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	Top Hit Descriptor	af25e08.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032710 31	Homo sapiens HSPC101 mRNA, partial cds	Cartine distemper virus strain A75/17, complete genome	Human catmodulin (CALM1) gene, eagns 2.3.4.5 and 6, and complete cds	601340661F1 NIH MGC 53 Homo saplens cDNA clone IMAGE:3683030 5	SO13 AMERICAN MGC Sta Homo septems CDNA clone IMAGE:3683030 5	OUISACOUT THE TRUE COLOR AND COLOR A	arbane duck parvenus KEF prousin (ref) ara unes capea prousin ver (ref) Barres, conspress de	X. laevis XFD2 mRNA for fork head protein	PROTEIN TRANSPORT PROTEIN HOFC HOMOLOG	II.3-HT0619-110700-210-C04 HT0819 Homo saplens cDNA	ee30f02.r1 Gessler Wilms furnor Homo sepiens cDNA done IMAGE:897339 5' similar to gb:MZZ362. MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);	agorino ri Gessler Wilms turnor Homo sapiens cDNA clone IMAGE:897339 5' similer to gb:M22382	MITOCHONDRIAL MATRIX PROTEIN P! PRECURSOR (HUMAN);	Homo sapiens putative hepatic transcription factor (WBSCR14) gene, complete cds	al75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 13766283'	ai75e08.cf Scares_testis_NHT Homo saptems aDNA clone 1376826 3'	a75a08.s1 Soares_testis_NHT Homo saptens cDNA clone 1376626 31	MR0HT0069-071099-001-c05 HT0069 Homo sapiens cDNA	FB20A6 Fetal brain, Stratagene Homo sapiens cDNA clone FB20A6 3'end	CELL-SURFACE RECEPTOR DAF-1 PRECURSOR	RC1-BT0254.090300-017-d09 BT0254 Hamo sepiens cDNA	Homo sapiens chromosome 21 segment HS21C068	Dictycstellum discoldeum myosin heavy chain kinase A (MHCK A) mRNA, complete cds	Pyrococcus abyssi complete genome; segment 5/6	Pyrocecus abyssi complete genome; segment 6/6	FB4A8 Fetal brain, Strategene Homo sapiens cDNA clone FB4A8 3 end similar to LINE-1	ah67105.srl Soares_testis_NHT Homo sapiens cDNA clone 13207053	EST387948 MAGE resequences, MAGN Homo septems cDNA	Mus musculus latent TGF bata binding protein (Tgfb), mRNA	Oncortynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1"01 altele, complete cds	og79e04.x1 Sceres_NPL_T_GBC_S1 Homo sapiens dJNA done IMAGE:18414063	HOMEOBOX PROTEIN HOX-D4 (CHOX-A)	H. SEPIENS UNA KO CAMIT prospriodestatese (exults 4-22.)
-	Top Hit Detablesse Source	EST_HUMAN 8	T F			T HI IMAN	LI BAAN	HOMAN			SWISSPROT	EST_HUMAN II	EST HUMAN	Т	EST_HUMAN	П	EST HUMAN	EST_HUMAN	EST HUMAN	T	Т		EST_HUMAN	Į.	) L		NT	EST HUMAN	HUMAN	EST_HUMAN		TN	П	ISSPROT	L <sub>N</sub>
	Top Hit Acession No.	6.9E-02 AA670269.1			Ī	Ţ.		-				6.9E-02 BF352899.1	6 RF-02 AA496759 1		6.8E-02 AA496759.1	6.8E-02 AF156673.1	6.8E-02 AA781996.1	6.8E-02 AA781996.1	6.8E-02 AA781998.1	8 RF-02 RF141076.1	6.8E-02 T03013.1	P20792	6.8E-02 BE061890.1	6.8E-02 AL163268.2	8.8E-02 U16856.1	6.8E-02 AJ248287.1	6.8E-02 AJ248287.1	6.8E-02 T03214.1	6.8E-02 AA758014.1	6.8E-02 AW975839.1	9910585 NT	8.7E-02 AF115538.1	6.7E-02 AI220285.1	P17278	6.7E-02 X62695.1
	Most Similar (Top) Hit BLAST E Vatue	8.9E-02/	8 OF 02 /	6.95-02	A OC 00 1142020 4	20108	0.95-02	6.9E-02	6.9E-02 U22987.1	6.9E-02 X74315.1	6.9E-02 P44621	6.9E-02	A AF.00	1	6.8E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02	S SF-02	6.8E-02	8 8 E-02 P 20792	6.8E-02	6.8E-02	8.8E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02	6.7E-02	6.7E-02	6.7E-02 P17278	6.7E-02
	Expression Signal	76.0	0 57	0 67	100	2.18	93.	1.08	0.55	2.17	1.75	3.69	4	2	1.18	4.7	1.05	1.05	185	7.0	0.78	990	1.05	7.18	0.64	5.44	6.44	3.73	2.52	1.68	2.35	1.83	1.80	4.34	1.01
-	ORF SEQ ID NO:	31041							36879			31648	97020		27919				L					33822			L						27830		34560
	SEQ ID NO:	18161	10100	2000		21336	2000	21865	22439	25141	25250	26631	44004	4354	14924	14946	1817A	18474	18174	47676		1			20889	21599	21699	25949	L.		<u> </u>				21153
	Probe SEQ ID NO:	5454	2000	20.00	2001	/8838	2000	688	9475	12343	12519	13112	Ş	200	180	3 6	3447	3447	1	202	2003		7887	7497	8	1538	<b>88</b>	12140	12274	12832	12894	1531	1910	3730	भक्ष

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Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)	Ab61c/11.x1 Scares_NFL_T_GBC_S1 Hamo sapiens cDNA clane IMAGE:2580788 31	UI-H-BIT-ecr-g-01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715453 3	1.H-Bi1-ear-g-01-0-Ui.s1 NCI_CGAP_Sub3 Homo septens cDNA clone IMAGE:2715433 3"	Drosophila melanogastar cactin mRNA, complete cds	Mus musculus Capri12 gene for calpain 12, exons 1-21, three atternative transcipts	y18b10.s1 Sources placenta NbZHP Homo sepiens cDNA done IMAGE:1395/93	Homo sepiens mesothelin (MSLN), transcript variant 1, mRNA	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA	Homo sepiens TESTIN 2 and TESTIN 3 genes, complete cds, attentatively spliced	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN HZ PRECURSOR (III HEAVY CHAIN HZ)	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN HZ PRECURSOR (III MEAY) CHAIN HZ)	P. vulgaris mRNA for chalcone synthase	MATERNAL EFFECT PROTEIN STAUFEN	MATERNAL EFFECT PROTEIN STAUFEN	Pentcillium unicas mitochondrial HRNA (large nRNA) gene and its franking region	Homo sepiens chemokine receptor CXCR4 gene, promoter region and complete cas	Dictycstellum discodeum darin (darA) gene, complete cds	Human nespiratory syncytial virus, complete genome	Human respiratory syncytial virus, complete genome	(1978) ST NCI_CGAP_LL24 Homo sepiens CDNA clone IMAGE:2149488 3	Homo saplens EWS, garZZ, mpZz and bamzz genes	Homo sepiens vinculin (VCL), mRNA	MR1-SN0064-010600-008-a12 SN0084 Homo sapiens cDIVA	C05789 Human pancreatic islet Homo sapiens cDNA clone hbc5156	Mus musculus DIPB gene (Dipb), mRNA	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5	Homo sapiens E2F-like protein (LOC51270), mRNA	Xenopus laevis alpha(E)-catenin mRNA, complete cds	Aquifex sectious section 96 of 109 of the complete genome	2246h12.s1 Soares overy tumor NbHOT Homo sepiens cDNA clone IMAGE:756743 3' similar to gb:M28038 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);	602118887F1 NIH_MGC_56 Hamo saplens cDNA clane IMAGE:4276028 5
	Top Hit Detrabase Source		EST_HUMAN x	EST_HUMAN L	EST_HUMAN L			T HUMAN				. 1	SWISSPROT			SWISSPROT	TN	EN EN				T_HUMAN	¥			EST_HUMAN			EST_HUMAN		NT	LN		EST_HUMAN
28110	Top Hit Acession No.		6.7E-02 AW082888.1	6.7E-02 AW137359.1	6.7E-02 AW137359.1	6.6E-02 AF245118.1	6.6E-02 AJ289241.1		7108357 NT	7108357 NT	8.6E-02 AF260225.1	261703	261703	X06411.1	25159	>25150	8.6E-02 D14567.1	8.6E-02 AF052572.1	6.6E-02 AF006055.1	9629198 NT	TN 9829198 NT	6.6E-02 AI458752.1	6.6E-02 Y07848.1	11430559 NT	6.6E-02 BF374248.1	6.6E-02 C05789.1	9837991 NT	6.6E-02 AF167430.1	6.5E-02 BF027639.1	TN 8909077	6.5E-02 U47624.1	6.5E-02 AE000784.1	8.5E-02 AA443891.1	6.5E-02 BF665340.1
	Most Similar (Top) Hit BLASTE Vaitue	6.7E-02 X62695.1	6.7E-02	6.7E-02	6.7E-02	6.GE-02	6.6E-02	6.6E-02 R64306.1	6.6E-02	6.6€-02	6.GE-02	6.6E-02 Q61703	6.6E-02 Q61703	6.6E-02 X06411.1	6.6E-02(P25159	6.6E-02 P25159	8.6E-02	8.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.8E-02	6.6E-02	6.6E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	8.5E-02
	Expression Signal	1.01	0.45	0.73	0.73	6.0	266	11.07	21	21	1.45	6.23	8.23	3.97	0.55	99.0	0.57	1.6	0.67	79.0	79'0	0.52	1.65	0.6	4.9	1.73	253	1.31	2.67	1.95	3.5	2.08	1.7.1	0.83
	ORF SEQ ID NO:	34561	35170	36347	36348	. 27376	28228	29447	29462	29463	90036	30913	30914	33073	33105	33106		34660	36209			38717	36860		37786				26586		<u> </u>			
	SEQ ID	21153	21748	22888	22886	14405	15207	16523	16637	16637	17141	18029	18029	19792	19823	19823	21090	21248	21784	22239	22239	23235	23369	23403	24260	24838	25373	25672	13652	14041	14426		1	Ш
	Probe SEQ ID NO:	8183	8781	9588	9568	1371	2182	3471	<u>8</u>	3491	4107	6016	5015	8738	2989	<b>2989</b>	8152	8279	8817	8273	8273	10311	10447	10481	11310	12063	12719	13024	282	686	1392	1749	8899	9999

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Top Hit Descriptor	Azotobacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partial cds	601656817R1 NIH_MGC_67 Hamo sepiens cDNA done IMAGE:3865637 3'	601656817R1 NIH_MGC_67 Homo sepiens cDNA clone IMAGE:3865637 3'	601823511F1 NIH_MGC_77 Hamo sapiens cDNA clane IMAGE:4043138 5	z32g05.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:085144 3"	Rabbit microsomal epodde hydrolase	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds	A.carterae precursor of pandinin-chlorophylla-protein (PCP) gene	Thermotoga maritima section 89 of 136 of the complete genome	Thermotoga maritima section 89 of 136 of the complete genome	Mus musculus histone deacetylese 5 (Hdac5), mRNA	z51604.r1 Soares_pregnant_uterus_NbHPU Homo saptens cONA clone IMAGE:505470 5' similar to	contains Alu repetitive element;	qe07b01,x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3	LTR8 repetitive element;	Mus muscutus IFN-response element binding factor 1 (IREBF-1), mRNA	Heterodera giyaines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds	Heterodera glychnes beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete ods	we73g12.xt Soares_Dieckgraafe_coton_NHCD Homo saptens cDNA clone IMAGE:2346790 3"	601680425FR2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 31	Neisseria meninglitdis serogroup A strain Z2491 complete genome; segment 67	Mus musculus chaperonin subunit Ga (zeta) (Cct6a), mRNA	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5	AF150185 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10	RC1-OT0083-150600-014-g06 OT0083 Hama saplens cDNA	Homo sepiens mRNA for KIAA0554 protein, partial cds	Hamo sepiens DNA topoisomenase II beta (TOP2B) gene, exans 16, 17, and 18	Homo sapiens DNA topotsomerase II beta (TOP2B) gene, exuns 16, 17, and 18	Human hereditary haemochromatosts region, histone 2A-lile protein gene, hereditary haemochromatosts (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPTS) gene, complete ods	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis Ann an base Base some and sodium phosphate hamanorter (NPT3) nears complete atts	(TLYTT) gars, nurse gars, an south prospinate usingware (1911) gars, whipper one
Top Hit Database Source	Ę	EST_HUMAN	EST_HUMAN		EST_HUMAN	¥		TN	¥	H	¥		EST_HUMAN	Г	EST_HUMAN	L	NT	NT	EST_HUMAN	EST_HUMAN	Į,		EST_HUMAN	EST_HUMAN	EST_HUMAN	Ν	NT	K	Ę	ì	Ž
Top Hit Acession No.	U22881.1	2	2	1	1		1.		1	1	TN 8289893		8.4E-02 AA147572.1		U191956.1	7305186 NT	6.4E-02 AF052733.1	.1	1		6.4E-02 AL162757.2	6753323 NT	6.4E-02 AA093305.1	6.4E-02 AF150185.1	6.4E-02 BE834083.1	6.4E-02 AB011128.1	6.4E-02 AF087150.1	6.4E-02 AF087150.1	J91328.1		J91328.1
Most Similar (Top) Hit BLAST E Vetue	8.5E-02 U	6.5E-02 BE963200	6.5E-02	6.5E-02 BF106300.	8.5E-02 AA195648	6.6E-02 M21498.1	6.5E-02 AF102983	6.4E-02 X94549.1	6.4E-02 AE001777.	6.4E-02	8.4E-02		8.4E-02		6.4E-02 A1191956.	8.4E-02	6.4E-02	6.4E-02	6.4E-02 AI672898.	6.4E-02	6.4E-02	6.4E-02	6.4E-02	6.4E-02	6.4E-02	6.4E-02	6.4E-02/	8.4E-02/	6.4E-02 U91328.1	!	6.4E-02 U91328.1
Expression Signal	1.17	0.65	0.65	0.53	4.51	4.18	7.31	1.74	0.83	0.83	1.16		258		1.19	1.15	4.16	4.16	0.72	4.64	0.52	2.79	4	0.92	0.61	1.75	0.59	0.59	2.18		2.18
ORF SEQ ID NO:	31241	36709	36710	37252	37492			28559			28007				31559	32285	32539	32540	32888	33542	34015					36472			38482		38483
SEQ ID	18396	23227	73227	ı	1		25255	13646	14775	L.,	L		18270		18624	19067			L		20651	21647	١		22871		23546	L.		L	24895
Probe SEQ ID NO:	7165	10302	10302	10832	11002	12164	12526	22	1748	1746	4933		5282		5525	2985	<b>823</b>	<b>6234</b>	6542	0669	288	82/38	9012	2483	4468	10075	10624	10624	12018		12018

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
12424	25881		5.38		6.4E-02 AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
12476	25224	31783	5.68		6.4E-02 AJZ77174.1	N	Drosophila melanogastar mRNA for mod(mdg4)51.4 protein
							Mus musculus major histocompatibility locus class III regions Hso70t gene, partial cds; smRNP, G7A, NG23,
1769	14798	27784	2.78		6.3E-02 AF109805.1	ᅜ	MutS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
3618	16662	-	277	6.3E-02 P37092	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6229	19332	32563	1.08		6.3E-02 BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_64 Hamo sepiens oDNA clane IMAGE:4097499 5"
7463	20419		1.39		6.3E-02 X97869.1	NT	H.saplens gene encoding La autoantigen
8846	22590	6609E	1.01		6.3E-02 AJ243916.1	N	Drosophila melanogaster Domina gena, exons 1-3
10874	23297		2.98	6.3E-02	6.3E-02 AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NSSA region), partial cds, strain: CMR-152
10634			0.81		6.3E-02 AV698070.1	EST_HUMAN	AV688070 GKC Homo septens cDNA clone GKCAHE01 5
11070	18332		276		6.3E-02 BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Hamo septems cDNA clane IMAGE:4097499 5
4278			2.48		6.2E-02 AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
	L						Rattus novegicus differentation-associated Na-dependent Inorganic phosphate cotransporter (DNPI) mRNA,
4365	17392		1.12		8.2E-02 AF271235.1	ᅜ	complete cds
4612	17633		6.56		Q62191	SWISSPROT	62 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO62)
8983	20188	33513	0.67		6.2E-02 D49530.1	F	Spirulina platensis DNA for adenylate cyclase, complete cds
7889	20833	34212	0.79		6.2E-02 U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete ods
8158	21096		0.58		8.2E-02 AL161545.2	NT	Arabidopsis fhaliana DNA chromosome 4, contig fragment No. 45
828	L		0.63		8.2E-02 M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cde
8896	22052	36106	0.53		اندا	EST_HUMAN	af20a06.s1 Scares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
9835	111777	36226	1.25		TN 8887788	LN.	Mus musculus stromal cell derived factor receptor 2 (Sdfr2), mRNA
12259	25979		15.66		6.2E-02 AE000750.1	NT	Aquifex eeclicus section 82 of 109 of the complete genome
12596	25299		1.38		6.2E-02 BE793085.1	EST_HUMAN	601583773F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937842 5
4.287B	DERAG	24.784	79 E		R 2F.112 BE112039 1	EST HUMAN	737h08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sepiens aDNA done IMAGE:3523815.3' similar to TR-09Y4S6 09Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1] :
256	ı				6.1E.02 D16471.1	Į.	Human mRNA, Xq terminal portion
4017	┸				6.1E-02 U73325.1	ᅜ	Arabidopsis thaliana K+ inward rectifying channel protein (AtKC1) gene, complete cds
8043	1_					¥	Homo sapiens KIAA1062 protein (KIAA1062), mRNA
8		32331	0.62		7662463 NT	INT	Homo sapiens KIAA1052 protein (KIAA1052), mRNA
	<u>L</u> _					ļ	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,
6235	- 1	١			N 0/0/0ch	Z	mentos o (omentos) montos.
9098	- 1	١			6.1E-02 X86Z68.1	1 N	FLESHERS BILLY NOT OF THE LOWER SOURCE AND HAND HAND THE CONTRACT OF THE LOWER SOURCE AND THE CONTRACT OF THE
8008	21974	35393	1.93		6.1E-02 BE971853.1	ESI HOMAN	OUTGOINGONT MIT MICH, OT FIGHT SEPTERS COLON CARROLL SOCION S

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Top Hit Descriptor  Signoricum mRNA for sethers cDNA clane IMAGE:2824604 8'  IL3-HTD618-110500-138-208 H19018 Hamo seplens cDNA clane IMAGE:282301 3'  IL3-HTD618-110500-138-208 H19018 Hamo seplens cDNA clane IMAGE:282301 3'  IL3-HTD618-110500-138-208 H19018 Hamo seplens cDNA clane IMAGE:282301 3'  Hamospies chromoson 21 segment IAS210007  Themrodoge meritime section 28 of 130 of the complete genome  EST380024 MAGE resequences, MAGJ Hamo seplens cDNA clane IMAGE:282310 5'  Themrodoge meritime section 89 of 130 of the complete genome  EST380024 MAGE resequences, MAGJ Hamo seplens cDNA clane IMAGE:282310 5'  Themrodoge meritime section 80 of 130 of the complete genome  EST380024 MAGE resequences, MAGJ Hamo seplens cDNA clane IMAGE:282310 5'  The resequences and MAGE resequences as the complete genome  EST380029 Colon adenocarchorna IV Homo seplens cDNA of and similar to tissue-specific protein  RC3-8170286 Colon adenocarchorna IV Homo seplens cDNA clane IMAGE:282810 5'  EST38209 Colon adenocarchorna IV Homo seplens cDNA done IMAGE:288673 3' similar to combans  L1 x1 L1 L1 topeditive element:  L1 x1 L1 to repetitive clanne captions cDNA done IMAGE:27082 5'  601874710F1 MIH_MGC_58 Homo seplens cDNA done IMAGE:270825 5'  601874710F1 MIH_MGC_58 Homo seplens cDNA done IMAGE:270828 5'  Recinomens anneticient mithorodomidin, complete genome  by Recinoment of CAP GOS Homo seplens cDNA done IMAGE:273782 3'  By Recinomens anneticient mithorodomidin, complete genome  by Recinomens anneticient mithorodomidin, complete genome  by Recinomens anneticient mithorodomidin, complete genome  by Recinomens anneticient mithorodomic, complete genome  by Recinomens anneticient mithorodomile, complete genome  by Recinomens anneticient mithorodomic anneticient to semiliar to semiliar to semiliar to semiliar to heat shock protein 1, 60 kDe-  EST180654 Jurket T-cells V Homo seple	Top Hit Detabese Source ST HUMAN STABBUT EST HUMAN EST HUMA	t Similar Ast E	Manage	Expression Signel 1.93 3.44 2.42 2.42 2.42 1.35 1.35 1.47 1.17 1.17 1.18 1.52 2.08 2.08 2.08 2.03 2.03 2.03 2.03 2.03 3.08 3.08 3.08 3.08 3.08 3.08 3.08 3	ORF SEQ ID NO: 35394 37596 22722 227222 227222 227222 227222 227222 227222 227222 22722 22	Ean SEQ ID NO: 21974 24044 24044 25697 25697 14302 15775 15775 15775 15775 20985 20987 225674	Production of the control of the con
w69hc3.x1 Soares_NFL_T_GBC_S1 Homo sepiens dDNA clone IMAGE:2350885 3' similar to TR:080298 080298 KIAA0551 PROTEIN ;	EST_HUMAN	6.0E-02 Al809273.1		3.16		25455	12845
WESTIGAT SOSTES_INTIL_1_CODU_ST FIGHTS SEPTENTS CLITAL CALTES IMMUSE_ASSUGGS & SETTING WITH COLUMN 10000000 B (IAA0567 PROTEIN)	EST HUMAN	AI809273.1		3.16			12845
WRSH03.x1 Source, NFL, T. GBC, S1 Horno septents cDNA clone IMAGE-2360885 3' similar to TR: 080298						L	
Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA	<u>5</u>	.11431702					12475
like	EST_HUMAN	AA309797.1					10285
EST180654 Juricat T-cells V Homo sapiens cDNA 5 end similar to similar to heat shock protein 1, 60 kDa-							
llice	EST_HUMAN	AA309797.1					10265
EST180654 Jurket T-cells V Homo septens cDNA 5' end stmilar to similar to heat shock protein 1, 60 kDa-							
Acipeneer baeri partial ICLV gene for Immunoglobulin light chain variable region, excres 1-2	¥	AJ245366.1	6.0E-02				9781
Acthenser baari partial ICEV gene for immunoglobulin light chain variable region, exons 1-2	LN.	AJ245365.1					9761
B/08/0XT NCI COAT GOO DOIN SEPRE CURA COM INVICE 2237 302.3	ESI HUMAN	ARZ3167.1					9627
LTD-00 -4 NO. COAR COR LICENSIA AND COARS OF		100000				1	38
ts78e06.x1 NCI_CGAP_GC8 Homo eapiens dDNA clone IMAGE:2237362 3'	EST HUMAN			1.17			1690
Reclinamonas americana mitochandrion, complete genome	LN			0.62			8786
प्रिक्षित08.x1 Scares_testis_NHT Homo sapiens cDNA clone IMACE::1754199 3'	EST_HUMAN	Al204275.1	6.0E-02	1.71			₹ 4
601874710F1 NIH_MGC_54 Homo septens cDNA clone IMAGE:4101074 6	EST HUMAN	BF210488.1	6.0E-02			•	7508
601815274-2 NIH_MGC_36 Homo septens cDNA clone IMAGE-4046226 5	EST_HUMAN	BF382349.1	,				300
Homo septiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA	¥	5174698					7180
Homo sapiens stimulated trans-acting factor (60 kDa) (STAF60) mRNA	K	5174898	6.0E-02				7180
L1.t1 L1 L1 repetitive element;	EST_HUMAN	AI807537.1	G.0E-02	0.98			88
wf48h05x1 Soares_NFL_T_GBC_S1 Homo explens cDNA clone IMAGE:2358873 3' strillar to contains							
RC3-BT0255-011189-013-b04-BT0253 Homo expiems cDNA	EST_HUMAN	AW370211.1		0.76			5472
EST84268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein	EST_HUMAN	AA372376.1		1.52			3243
EST84288 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein	EST_HUMAN	AA372376.1					3243
zp78c04.r1 Strategene HeLa cell 63 837216 Homo septiens dDNA done IMAGE:626310 6	EST_HUMAN	AA188730.1	6.0E-02				2948
zp78c04.r1 Strategene HeLa cell s3 937216 Homo septens cDNA clone IMACE:626310 5		AA188730.1	6.0E-02	1.47			2048
ATPasse subunit 6, and NADH dehydrogenasse subunit 2		AB031289.1		1.98			2783
Mesocestoides cart mitochandrial DNA, NADH dehydrogenase subunit 4, fRNA-Gin, fRNA-Phe, fRNA-Met,							
EST380924 MAGE resequences, MAGJ Hamo sapiens cDNA	EST_HUMAN	AW968848.1					2684
Thermotoga maritima section 89 of 136 of the complete genome	¥	AE001777.1					1267
Homo septens chromosome 21 eegment HS21C007	뉟	AL163207.2					12912
t56907_x1 NCI_CGAP_ON35 Homo sepiens cDNA clone IMAGE:2292801 31	EST_HUMAN	Al886611.1		1.35			12779
S japonicum mRNA for serine-enzyme	H	X70969.1		2.42			12218
IL3-HT0618-110500-136-C06 HT0618 Homo septens cDNA	EST_HUMAN	BE179543.1					11082
	ANADU TOD	DEB/ 1993.1					2002
601651086R1 NIH MGC 81 Homo sablens cDNA clone IMAGE:3834604 3'	EST HUMAN	BE974853 4	8 1F.00				Supp
	Source	호	BLAST E Value	Signal			ğ Ö Ö
Too Hit Descriptor	Top Hit Detabase	Top Hit Acession	Most Similar (Top) Hit	Expression			Probe
		-					

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Ingle Exon Plodes Expressed III doire mailow	Top Hit Descriptor	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced	Saccheromyces cerevisiae protein tyroshe phosphatase (PTP3) gene, complete cds	Drosophila metanogastar LD23107 sting (sting) mRNA, complete ods	Mus musculus frequeis related homeobox 5 (Drosophila) (In5), mRNA	601877609F1 NIH_MGC_55 Hamo saplens cDNA clane IMAGE:4105694 5	Mus musculus follistatin-like (Fsti), mRNA	Thichecillus ferroaddans merC, merA genes and URF-1	Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5	Thermotoga maritima section 87 of 138 of the complete genome	w/24c02 x1 NCL_CGAP_Kdd11 Homo sapiens cDNA done IMAGE:25446783'	W/24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3"	qh56f01x1 Soares_feta  Ilver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:18486973' stmiter to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);	qh56801.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:1848697.3' similar to	gb3M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);	Gellus galus tyrosine kinase JAK1 (JAK1) mPNA, complete cds	2p86a11.s1 Strategene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627088 3'	Human polymorphic microsatellite DNA	Human polymorphic microsatellite DNA	Homo sapiens chromosome 21 segment HS21C083	no/Jer11,s1 NCI_CGAP_AA1 Homo septems cDNA clane IMAGE:11128843'	out31005,s1 NCI_CGAP_Br2 Homo sepiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2	CE08811;	Home expiens deparmine transporter (SLC8A3) gene, complete cds	EST378865 MAGE resequences, MAGI Homo sapiens cDNA	Homo saplens partial stearin-1 gene	Mus musculus low density lipoprotein receptor (Ldir), mRNA	Homo septens ABCA1 (ABCA1) gene, complete cds	601447637F1 NIH_MGC_65 Hamo sapiens cDNA clane IMAGE:3851985 5	601447837F1 NIH_MGC_65 Hamo sepiens cDNA clane IMAGE:3851985 5	Xenopus taevis mRNA for fourth component of complement, complete cds	Xenopus Isavis mRNA for fourth component of complement, complete cds	Rattus norvegicus mRNA for potassium channel, alpha subunit (kr9.2 gene)	Mus musculus ect2 oncogene (Ect2), mRNA
Xon Flobes	Top Hat Darkabase Source	TN	L	NT		EST_HUMAN	L	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	IN	EST_HUMAN	IN	IN	Ĭ	EST_HUMAN		EST HUMAN	L	EST_HUMAN	IN	NT	NT	EST_HUMAN	EST_HUMAN	TN	TN	NT	¥
Single	Top Hit Acession No.	5.9E-02 AF190269.1	5.9E-02 AF008304.1	6.9E-02 AF146680.1	8055249 NT	3F242748.1	6.9E-02 6679870 NT	<b>390110.1</b>	5.8E-02 AJ223821.1	5.8E-02 AE001775.1		2			\I247505.1	5.8E-02 AF096284.1	5.8E-02 AA190994.1	A99150.1	A99150.1	NL163283.2	5.8E-02 AA604269.1		5.7E-02 Al081644.1	5.7E-02 AF119117.1	5.7E-02 AW968791.1	5.7E-02 AJ251973.1	6754525 NT	5.7E-02 AF275948.1	6.7E-02 BE871911.1	5.7E-02 BE871911.1	78003.1	78003.1	5.7E-02 AJ296090.1	6681260 NT
	Most Similer (Top) Hit BLAST E Value	5.9E-02	5.9E-02	6.9E-02	5.9E-02	5.9E-02	5.9E-02	5.8E-02 D90110.1	5.8E-02	5.8E-02	5.8E-02	5.8E-02	5.8E-02 AI247505.		5.8E-02 AI247505.	5.8E-02	5.8E-02	5.8E-02 M99150.1	5.8E-02 M99150.1	5.8E-02 AL163283	5.8E-02		5.7E-02/	5.7E-02	5.7E-02	5.7E-02/	5.7E-02	5.7E-02	6.7E-02	5.7E-02	5.7E-02 D78003.1	5.7E-02 D78003.1	5.7E-02	5.7E-02
	Expression Signal	3.42	16.0	0.62	1.82	0.82	3.23	6.03	66'0	1.32	5.33	5.33	4.73		4.73	2.83	0.53	252	2.52	0.59	10.6		1.27	1.51	2.47	0.91	1.18	0.69	0.69	0.59	99'0	0.68	1.74	0.65
	ORF SEQ ID NO:	28975	30814	33409	35355					20633	30292	30293	30495		30406		32288	34273	34274	35399			28039	28055	29761	31082			34025	34026	34111	34112		38621
	Exam SEO ID NO:	16054	17822	26874	21930	21129	24098	13986	15932	16719	17410	17410	17600		17600	17625	19097	20883	20883	21980	25968		16127	16143	16854	18208	18309	19084	20681	20681	20739	20739	21463	23134
,	Probe SEO ID NO:	9882	4905	707	8008 4008	9086	11138	88	2872	3676	4382	4382	4578		4578	4604	8014	<b>18</b>	致	8 4 19	12856		3070	3086	3814	5188	5306	62635	Ĕ	Ĕ	7188	7788	8495	10209

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Table 4
Single Exon Probes Expressed in Bone Marrow

It Top Hit Acession Database Source Source	5.7E-02 249983.1 NT Linedcana opb1 gene	6.7E-02 A1752885.1 EST_HUMAN cn18b09.y1 Normal Human Trabecular Bone Cells Homo septens cDNA clone NHTBC_cn18b09 random	5.7E-02 A1752685.1 EST_HUMAN an18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random	2 NT		I NT	5.7E-02 AF281280.1 NT Pan troglodyles apolipoprotein-E gene, complete cds	5.6E-02 AF094455.1 NT Hydrocotyle rotundifolia ribosomal protein L16 (rpl18) gene, intron; chloroplast gene for chloroplast product	5.6E-02 AB013100.1 NT Lycoperstoon esculentum LE-ACS8 mRNA for 1-eminocyclopropane-1-carboxylate synthase, complete cds	1 EST_HUMAN	1.1 EST_HUMAN	6E-02 AARRESTS 1 HUMAN repetitive element contains element L1 repetitive element;	1 EST HUMAN	I EST_HUMAN	1.1 EST_HUMAN	1 EST_HUMAN	Inf48d07.s1 NCI_CGAP_AM Home sepiens cDNA clone IMAGE:923245 shriter to TR:G768869 G769859 F-021 A4482884.1 EST HUMAN LAMINA ASSOCIATED POLYPEPTIDE 1C.;	П	¥	6755501 NT	L41581.1 NT	SWISSPROT	5.5E-02 001174 SWISSPROT TROPOMYOSIN ALPHA CHAIN, NON MUSCLE	6755902 NT	AF170911.1 NT		E-02 10947034 NT Homo septens elf-4E-transporter (4E-T), mRNA
Most Similar (Top) Hit Tc BLAST E	5.7E-02 Z4	6.7E-02 AI7	5.7E-02 AIT	5.7E-02 AL	5.7E-02 D5	5.7E-02 AF	5.7E-02 AF	5.0E-02 AF	5.6E-02 AB	5.6E-02 AA	5.6E-02/AV	5.GE-02 AA	5.6E-02 BE	5.6E-02 AI	5.0E-02 BE	5.6E-02 BE	5.0E-02.AA	5.6E-02 AF	6.6E-02 XB	5.5E-02	5.5E-02 L4	5.6E-02 Q	5.5E-02 Q0	5.5E-02	6.5E-02 AF	5.5E-02 AF	5.5E-02
Expression Signal	0.40	3.22	322	1.89	8.27	3.72	5.65	1.85	1.92	1.21	6.93	40	294	0.64	247	247	80.	1.87	828	3.44	1.13	3.09	3.81	1.85	0.69	0.69	0.63
ORF SEQ ID NO:	37365							27533	8/506			33407	23877				36576		28678					33925	34842		38405
SEQ ID	23850	24482	24462	L.	25782	25855	25858	14562	17692	17745	19871	20007	20328	27078	22120	22120	23098	24772	15680	16283	17273	L		20564	21426	21426	
Probe SEQ ID NO:	10930	11621	11521	11678	12573	12794	12930	1529	4671	4725	6817	7075	2368	8141	25.22	<b>M</b> 54	10171	11891	2882	3228	4244	6742	6141	7603	8457	8457	10013

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Table 4
Single Exon Probes Expressed in Bone Marrow

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rigie exon probes expressed in done maitow	Top Hit Descriptor	D. rento mRNA for zp-23 POU gene, splice warlant (neunula, 9-16 hpf and postsomitogenests, 20-28 hpf)	B.rerio pou(c) mRNA for transcription factor	H. sapiens mRNA for HMG-CoA-synthase	Homo sapiens maprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1	Homo septems pertial LMO1 gene for LIM domain only 1 protein, exon 1	Arabidopsis thalians putative dicarboxylate dilron protein (Crd1) mRNA, complete ods	Mus musculus cytokine inducible SH2-containing protein 3 (Cish3), mRNA	Human stardid hormane receptor Ner-I mRNA, complete cds	Saccharomyces cerewisiae Cdc54p (CDC54) gene, complete cds	wj80e04x1 NCI_CGAP_Lym12 Homo sepiems cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repetitive element ;	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA- BINDING GENE 18 PROTEIN)	Homo sapiens chromosome 21 segment HS21C004	Tumip mosaic virus genamic RNA for Cepsid protein, complete cds	Turnip mosatic virus genomic RNA for Capsid protein, complete cds	HSPD25097 HM3 Homo saplens cDNA clone s3000039A02	HSPD26097 HM3 Homo saplens cDNA clone s3000039A02	OXALOACETATE DECARBOXYLASE ALPHA CHAIN	DKFZp547D073_r1 547 (synonym: hfbr1) Homo septems cDNA ctone DKFZp547D073 5	Homo septems PBII gene for sativary profine-rich protein P-B, complete cds	HIV-1 patient 98 from Italy protease (pol) gene, complete cds	QV0-UM0051-250800-350-b08 UM0051 Hamo sepiens cDNA	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete ods	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds	Spodoptera littoralis mRNA for 3-dehydroecdysone 3beta-reductase	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CX 14)	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)	Candida albicans protein phosphatase Sed1 homolog (SSD1) gene, complete cds	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)	Homo sepiens ES18 mRNA, partial cds	Homo sapiens ES18 mRNA, partial cds
xon Probes Ext	Top Hit Database Source	rQ IN	NT B.r	NT H.		NT Ho	NT TN	NT		NT Hu	NT Sa	EST_HUMAN ME	SWISSPROT BIR	Γ	NT Tu		EST_HUMAN HS	EST_HUMAN HS	SWISSPROT OX	EST_HUMAN DK		NT H	EST_HUMAN  Q\	H	TN LN	ds IN	SWISSPROT KE	SWISSPROT KE		SWISSPROT AN		NT H
Single	Top Hit Acession No.	5.3E-02 Y07807.1	6.3E-02 X68432.1	5.3E-02 X66435.1	5031908 NT	5.2E-02 AJ277681.1	1	1	371757			5.2E-02 AIB30865.1		04.2						71.1	.1	5.1E-02 AF280369.1	5.1			1.1			38.1		_	5.1E-02 AF083930.1
	Most Similar (Top) Hit BLAST E Value	5.3E-02	6.3E-02	5.3E-02	5.2E-02	5.2€-02	5.2E-02	5.2€-02	5.2E-02	6.2E-02	5.2E-02	5.2E-02	5.0F_00 P36922	6.2E-02	5.2E-02	5.2E-02	5.2E-02	5.2E-02	5.2E-02 Q03030	5.1E-02	5.1E-02	5.1E-02	5.1E-02	5.1E-02	5.1E-02	5.1E-02	5.1E-02 P02533	5.1E-02 P02533	5.1E-02	5.1E-02 P40603	5.1E-02	5.1E-02
	Expression Signal	0.6	0.69	2.08	89.73	1.98	1.98	0.73	26'0	3.36	0.68	12	107	2.15	1.77	1.77	6.42	5.42	1.55	76.0	0.94	0.68	1.78	7.0	0.77	1.26	19.0	0.61	7.1	1.66	2.19	2.19
	ORF SEQ ID NO:		37111	38558		28097	86062	20915		30214	32310		23843		36487	38488	38357	38358				33175	31258	34978	34979	ĺ	35634	35635	36571	36959	37665	37666
	SEQ ID	23540	23617	24963	15305	16188	16188	17000	17002	17336	19108	18302	27.454	21886	23014	23014	24769	24789	25358	15380	18054	19884	18371	21584		21658	22203	22203		23464		24135
	Probe SEQ ID NO:	10618	10695	12092	2283	3131	3131	3960	3962	4307	6025	8238	7.480	8637	10087	10087	11888	11888	12693	2372	50.	<b>68830</b>	7039	888	8286	8890	1628	9237	10188	10542	11179	11179

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe	_						
SEO ID	Eogn SEO D	ORF SEO	Expression	Most Similar (Top) Hit	Top Hit Acession	Top Hit Defeablese	Too Hit Descriptor
NO.	Ö	Ö NÖ	Signal	BLAST E Vetue	<del>2</del>	Source	
12699	25359		1.75	5.1E-02	5.1E-02 AF062467.1	INT	Quoumis melo polygalacturonasa precursor (MPG3) mRNA, complete cds
12061	25531		1.8	5.1E-02	5.1E-02 AA534104.1	<b>EST_HUMAN</b>	nj73102.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:998139
483	13556	1848Z	2.18	5.0E-02	5.0E-02 AF098004.1	NT	Mus muscutus fatty acid amide hydrolase gene, excn 10
833	13988	86598	4.55	5.0E-02 233898.1	233898.1	NT	O. virginianus (HEL37) microsadeline DNA
1209	14247	27205	4.03	5.0E-02 Z89104.1	739104.1	NT	Bacillus subdifis complete genome (section 1 of 21); from 1 to 213080
2002	14028	Sense	70 7	4 OF 102 B03840	202840	LUddssims	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PRP-2/PRP-4) (PRP-2/PRP-4) (PRP-1/PRP-3) (PRP-2/PRP-4) (PRP-1/PRP-3) (PRP-2/PRP-4)
2828	<u>L</u>	2695	1.62	5.0E-02	-	NT	Oryclagus curiculus UDP-glucuronos/transferase (UGT2813) mRNA, complete cds
3348	L		1.34	5.0E-02	7305610 NT	Į,	Mus musculus Unc-51 like kinase 2 (C. elegans) (Uli/2), mRNA
3800			1.01	5.0E-02	5.0E-02 U32782.1	Į,	Haemophilius Influenzae Rd section 97 of 163 of the complete genome
3666			13.52	5.0E-02		NT	Antheraea pernyl period clock protein homolog mRNA, complete cds
භික			0.77	6.0E-02	1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6441	19506		1.25	5.0E-02	1	NT	Mus musculus Dmp-1 gene, exams 1-6
7181		31214	9.0	5.0E-02 P35616	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
7785	20738	34110	12.03	5.0E-02 P35616	535616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
8008			0.52	\$0E-02	5.0E-02 AW062464.1	<b>EST_HUMAN</b>	MR0-CT0064-100899-002-g10 CT0064 Homo saplens cDNA
10580	23482	36977	1.28	5.0E-02	5.0E-02 AF305238.1	INT	Mus musculus Fas-interacting serine/threcrine (chase 3 (Fist3) mRNA, complete cds
11820		38286	2.47	6.0E-02 U67600.1		TN	Methanococcus jannaschil section 142 of 150 of the complete genome
1228			6.4	5.0E-02 Q04047		SWISSPROT	NO-ON-TRANSIENT A PROTEIN
228			,,	4.9E-02		INT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
369	i	26384		4.9E-02	1	NT	Homo sapiens ABCA1 (ABCA1) gane, complete cds
369		26385	2.86	4.9E-02	48.1	NT	Hamo sapiens ABCA1 (ABCA1) gene, complete cds
3302	16355	28274	1.64	4.9E-02 P54258		SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN)
78372	16620		2.0	4 OF 10-	4 OF 02 A 4 4 8 8 9 4 0 4	EST HIMAN	zq48a12.e1 Stratagene hNT neuron (#837z33) Homo sapiens cDNA clone IMAGE:632826 3' similar to contains Alu moneffilm element contains element MSR1 moneffilm element
3805		28568	98.0	4.9E-02/	4.9E-02 AA400914.1	EST HUMAN	478ar03.s1 Scares testis NHT Homo septiens cDNA clone IMAGE:728428 3
3805		29667	96.0	4.9E-02/	4.9E-02 AA400914.1	EST HUMAN	zi78e03.s1 Scares, testis, NHT Homo sepiens cDNA clone IMAGE:728428 37
4877		30783	2.11	4.9E-02	4.9E-02 AW167821.1	Г	xg66g10.x1 NCI_CGAP_Ut4 Homo sepiens cDNA dane IMAGE:2832386 3'
4877	17894	30784	211	4.9E-02	H.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_Ut4 Homo septens cDNA clone IMAGE:2632388 3'
5444		31458	17.1	4.9E-02 L00122.1		NT	Rat elastase II gene, exon 6
5444	1		1.71	4.9E-02 1.00122.1		NT	Rat elestese II gene, exon 6
7348		33666	2.83	4.9E-02	1	Ę	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8963			0.91	4.9E-02	1	¥	Chlamydia munidarum, section 40 of 85 of the complete genome
9107	22073	36600	0.8	4.9E-02/	4.9E-02 AL161559.2	¥	Arabidopsis fhaliana DNA chromosome 4, config fragment No. 59

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exem SEQ ID NO:	ORF SEQ ID NO:	Expression	Most Similar (Top) Hit BLAST E Vetue	Tap Hit Acessian Na.	Top Hit Database Source	Top Hit Descriptor
10309	23233	36715	4.58	4.5E-02	4.5E-02 AA325216.1	EST_HUMAN	EST28167 Cerebellum II Hamo sapiens cDNA 6 and similar to similar to neuro-D4 protein
10460	23382	38875	67.0		4.5E-02 X95508.1	TN	A.europaeum mRNA for legumin-like protein
10577	23400	36891	0.81	4.5E-02	4.5E-02 AB000470.1	NT	Galtus galtus mRNA for alphan Integrin, complete cds
12440		31828	2.95	4.5E-02	11418013 NT	M	Homo saplens net finger protein-like 3 (RFPL3), mRNA
12823	25863	31440	7.3		4.5E-02 AA191097.1	EST_HUMAN	zq43f11_r1 Stratagene NNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632493 5
Ø	13322		4.84	4.4E-02	4.4E-02 BE972733.1	EST_HUMAN	601652154F1 NIH_MGC_82 Hamo sepiens cDNA clane IMAGE:3835388 5
2107	15124		86.38		P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2498					4.4E-02 AW875475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3854	16697	29612			4.4E-02 AF159160.1	NT	Myxococcus xanthus serine/threonine kinase Plan10 (plan10) gene, complete cds
4657	17678	30508	1.25		4.4E-02 AF108807.1	Ę	Homo sepiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
							Homo sepiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene,
4857	17678	30564	1.25		4.4E-02 AF109907.1	¥	partial ods
1774	17791		0.94	4.4E-02	4.4E-02 AJ222689.1	NT	Ovis aries CCAAT-enthancer binding protein gene
2325	20298	623628			4.4E-02 AF095824.1	M	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7325	20298	33640	0.59		4.4E-02 AF095824.1	TN	Cenis familiaris matrix metalioproteinase 9 (MMP-6) mRNA, partial cds
9105	22071	35497	2.17		4.4E-02 AA736969.1	EST_HUMAN	rw13h03.s1 NCL_CGAP_SS1 Hamo sepiens aDNA clane IMAGE:1239221 3'
[	2000	00000			A Coopean A		Hepatitis E whus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete
11408	3 2	3/900	3.73		4.4E-02 Arvevees.1	EST LIMAN	pactoms of General Wilms furnor Homo serieus cONA clone IMAGE-807631 5
3 5	11112		2.22		4.4E.02 ABA40028.4		Homo serviers mRNA for KIAA1463 protein pertial cds
12138	10000		1		4 AE-NO RE244245 4	EST HIMAN	BOIRTRAGET NIH MGC 55 Homo sepiens cDNA clone IMAGE:4107418 5
ě	13841	28786			4.3E-02 AF003249.1	- LN	Morane essettits myosin heavy chain FM3A (FM3A) mRNA, complete cds
2575	15678	28595			4.3E-02 AV704878.1	EST_HUMAN	AV704878 ADB Homo septens cDNA done ADBAOH08 5'
3443	16400	20400	8,93		4.3E-02 AL163210.2	¥	Homo sapiens chromosome 21 segment HS21C010
3671	16714		1.25		4.3E-02 AF080568.1	LN L	Homo sapiens promyelocytic leukernia zinc finger protein (PLZF) gens, complete cds
88 448	Į	32977	4.62	4.3E-02 P30427	P30427	SWISSPROT	PLECTIN
<b>88</b>		32878	4.62		P30427	SWISSPROT	PLECTIN
9689	19948		6 <u>7.</u> 0		4.3E-02 AA652268.1	EST_HUMAN	ns69c12.s1 NCI_CGAP_Prz Hamo sapiens cDNA clane IMAGE:1188886
8858	21825		6.0		4.3E-02 AF283359.1	MT	Hamo sepiens desmoodlin 3 (DSC3) gene, complete cds, alternatively spiloed
ଆଥ			0.95		4.3E-02 X55322.1	R	H. sapiens NCAM mRNA for neural cell achesion molecule
भछ					4.3E-02 X55322.1	7	H.saptens NCAM mRNA for neural cell acheston molecule
<b>88</b>	13881	26832			4.2E-02 AU123327.1	EST HUMAN	AU123327 NT2RM2 Homo saplens cDNA clone NT2RM2000020 6
867	13923		258	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo saplens cDNA clone NT2RM2000020 6

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				i	O PRINC		HIGH TYONG TYPE COOR III DOLLO MERION
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Shuilar (Top) Hit BLAST E Velue	Top Hit Acessian No.	Top Litt Database Source	Top Hit Descriptor
768	13952	28910	0.83		4.2E-02 AW003645.1	EST_HUMAN	w64g01.x1 NCI_CGAP_Pit1 Homo sepiens cDNA done IMAGE:25456843' similier to TR:Q63291 Q63291 L1 RETROPOSON, ORF2 MRNA ;contains L1.t3 L1 L1 repetitive element;
1733	14763		1.54	4.2E-02	4.2E-02 AL445068.1	¥	Thermoplasma acidophilum complete genome; segment 4/5
. 1783	14822		1.02	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
3677	16720		2.18		P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4774	17794		ez.0		4.2E-02 BF342895.1	EST_HUMAN	602017105F1 NCI_CGAP_Bm64 Hamo septems cDNA dane IMAGE:4152672 5
-			9			ł	Homo septens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial ods; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450
	18794	31867	0.83		4.ZE-02 AF-280107.1	Z	polybeproce o (CTPSAs) gene, peruel cos
2000	18784	31988	0.85		4.2E-02 AF280107.1	Ę	Homo sapiens cytochrome P450 potypeptide 43 (CYP3A43) gene, partial ods; cytochrome P450 potypeptide 4 (CYP3A4) genes, complete ods; and cytochrome P450 potypeptide 7 (CYP3A7) genes, complete ods; and cytochrome P450 potypeptide 5 (CYP3A5) gene, partial ods
7175	18406	31205	6.73	4.2E-02	4.2E-02 BE268285.1	EST_HUMAN	801124598F1 NIH_MGC_8 Hamo sepiens cDNA clone IMAGE-2988319 5
7768	20722	34094	4.62	4.2E-02	4.2E-02 AF276762.1	¥	Legionella pneumophila catalase-perceddase (katA) gene, complete cds
7783	20745	34118	0.61	4.2E-02	4.2E-02 AV730347.1	EST_HUMAN	AV730347 HTF Homo septens cDNA done HTFAVH04 5'
9162	1	35556	3.74	4.2E-02 P05095	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10525	23447	36945	1.19	4.2E-02 Q16650	Q16650	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)
							on33b11.s1 NCI_CGAP_LL6 Homo saplens cDNA clone IMAGE:1558491 3' similer to gb:M65290
11379		37855	1.58	4.2E-02	4.2E-02 AA976118.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
1687	24574	38138	2.65	4.2E-02	4.2E-02 BE815822.1	EST_HUMAN	PAKS-BND174-250500-009-d10 BND174 Homo septems cDNA
11637	24574	38139	2.65	4.2E-02	4.2E-02 BE815822.1	EST_HUMAN	PMS-BN0174-250500-009-d10 BN0174 Homo sepiens cDNA
12694	25908		5.62	4.2E-02	4.2E-02 AI983494.1	EST_HUMAN	w/48g10x1 NCI_CGAP_Pan1 Homo saplens cDNA clone IMAGE:2510850 3'
12890	25550		1.69	4.2E-02	4.2E-02 D14711.1	M	Staphylococcus aureus HSP10 and HSP80 genes
511	13582	26503	0.75	4.1E-02	4.1E-02 AF200629.1	M	Homo sapiens HPS1 gens, Intron 5
2082	15681	28699	1.16	4.1E-02	4.1E-02 AE002330.2	M	Chlamydla muridarum, section 60 of 85 of the complete genome
4489	17524		7.84		AW8934	84.1 EST_HUMAN	QV1-NN0012-180400-164-f06 NN0012 Homo sepiens cDNA
5302	18305	31168	0.62			N.	Homo septens SRY (sex-determining region Y)-box 10 (SOX10), mRNA
6728	18820	31999	1.08	4.1E-02	4.1E-02 BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_18 Homo saplens cDNA done IMAGE;3343856 57
57.28	18820	32000	1.08	4.1E-02	4.1E-02 BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Hamo sapiens cDNA dane IMAGE:3343856 5
2068	88007		6.0	4.1E-02	4.1E-02 X75881.1	M	A thallana mRNA for plasma membrane intrinsic protein 1a
7306		33615	1.19		4.1E-02 AE002132.1	M	Ureaplasma urealyticum section 33 of 58 of the complete genome
7756	20709	34078	2	4.1E-02	7862347 NT	NT	Homo sepiens KIAA0867 protein (KIAA0867), mRNA
7860	20804	34180	0.7	4.1E-02	4.1E-02 L02110.1	Ę	Mus musculus proviral retroviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, infron 1, with the proviral insert encompassing the env pseudogene (9' end) and 3' LTR
	L	l					

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SEQ ID SEQ ID NO:	34376 34286 34286 34288 34377 31614 27718 28001	Signal Si	Vetue  Vetue  Vetue  4.1E-02 AF0281: 4.1E-02 P97857  4.1E-02 P34887  4.1E-02 AA37733  4.1E-02 AB0408  4.0E-02 AF0388  4.0E-02 AF0388  4.0E-02 AF0009  4.0E-02 AB0003  3.9E-02 BF5161  3.9E-02 BF5161  3.9E-02 BF5161  3.9E-02 BF5161	Acession (c)	NT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT EST_HUMAN NT	Figu rubripes neural cell adhesion molecule L1 harndog (L1-CAM) gene, complete ods; putative protein 1 (PUT1) gene, perial cell adhesion molecule L1 harndog (L1-CAM) gene, complete ods; putative protein 1 (PUT1) gene, complete ods; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete ods; and calcium channel adhre-1 subunit?  ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTTES 1) (ADAM-TS 1)  MOTTES 1) (ADAMTE-1) (ADAM-TS 1)  Brassica naque glin gene for plastid glutamine synthrotase, complete ods, affamatively spiliced  Brassica naque glin gene for plastid glutamine synthrotase, complete ods, affamatively spiliced  Homo saplens SWARGAM isoform (SMARGAM) gene, complete ods, affamatively spiliced  Homo saplens mPRVM for MIAJ-17 protein, perial cds  ACM-TS 2017 (CICAAD-PAZB Homo sepiens CDNA chore IMAGE-2313745 3'  Homo saplens mPRVM for MIAJ-17 protein, perial cds  ACM-TS 2017 (CICAAD-PAZB Homo sepiens CDNA chore IMAGE-3568380 3' similar to TR-075299 075298  Brongylocentrotus purpuratus homolog of fuumen bore morphogenetic protein 1 (submp) mRNA, complete ods  Brongylocentrotus purpuratus homolog of fuumen bore morphogenetic protein 1 (submp) mRNA, complete ods  GLUCOHYDROLASE SIAS PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCONTOROLASE)  GLUCOHYDROLASE SIAS PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN Methanobacherium fremmosutatorphicum strain Merburg, Thiotfurnarate reductase subunit A Human mRVM for KPI-MORE gene, perial cds  Methanomyces lacking sport or Ca++ ATRES  ONe after sind RM MACGAP-Sub7 Homo sepiens cDNA chron IMAGE-3084134 3'  FAS ANTIGEN LIGAND  Brond Adam-Code adam-Charles adam-Charles and maken 15(0) (SINE)  Human mRVM of cell desmin-behaling fragment DesD7  Human mRVM of cell desmin-behaling fragm
	u. o. o.	2.12	l	4508862 NT	TAT	MRNA RCS CT0558-474100-094-094-094-094-094-094-094-094-09-09-09-09-09-09-09-09-09-09-09-09-09-
ı	24072	0.65	l	3 9F-02 AW392417 1	EST HUMAN	ROB-ST0258-171199-021-C09 ST0258 Homo sentiens cDNA

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	Top Hit Descriptor	Aeropyrum pernix genomio DNA, section 6/7	Xyella fastidiosa, section 121 of 229 of the complete genome	a55cop.s1 Soares parathyroid fumor NbHPA Homo sapiens cDNA clone 13609123'	801782117E1 NIH MGC 20 Homo saniens CDNA clone IMAGE-4024973 6	Union contone solide center family 22 (remain ceiter transporter), member 1 (SLC22A1), mRNA	TOTIO SEPARIS SOURCE CELLER LEILING ALL (U.Beillo Celler) and represent the celler of	H. wulgare Ss1 gene for sucrose synthase	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1 (j.104,co.3) of Homo samiens	supraise sessente reales contestino husaneriable minisatellites circumscome (0/10078.3) of Homo	nuito aquai a galantii ogisti ootimii ig iyra taasaa galana aasaa galana	C.giutamicum gap, pgk and tpi ganes for ghoaraidehyde-3-phosphate, phosphoghoarate kinase and	Troseprosprista	C.gtutarnicum gap, pgk and tol genes for glyceraldehyde-3-phosphate, phosphoglycerate knase and tricsephosphate isomerase	Homo saptens RU2AS (RU2) mRNA, complete cds	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA	CN2-EN0013-110500-192-b10 EN0013 Homo sepiens cDNA	Methanococcus jannaschii section 117 of 150 of the complete genome	Chromatium whosum suffur globule protein Ov2 precursor (sgp2) gene, complete cds	m/20e05.s1 NCI_CGAP_GCB0 Homo sepiens oDNA clone IMAGE:1241024 3' similar to gb:J00314_ma2	TUBULIN BETA-1 CHAIN (HUMAN);	MR0-H10158-030200-003-608 H10158 Hamo septems curva	Dictyostelium discoideum unidnown spore germination-epecitic protein-tike protein, ort1, ort2 and ort3 genes, complete cds	Dictyostelium discoideum unionown spore germination-specific protein-like protein, orff, orf2 and orf3 ganes,	complete cds	602020453F1 NCI_CGAP_Bm67 Hamo sapiens dDNA diane IMAGE:4100116 0	Drosophila melanogaster tiggrin mRNA, complete cds	Homo sapiens microsomal epodde hydrolase (EPHX1) gene, complete cds	602085136F1 NIH_MGC_83 Hamo sapiens cDNA clone IMAGE:4249377 5	602085136F1 NIH_MGC_83 Hamo saplens cDNA clone IMAGE:4249377 5	Thermotoga martitima section 85 of 136 of the complete genome	CYSTATHIONINE BETALYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
	Top Hit Detrabase Source	Ę	Į	T HIMAN	Τ			N.	5		Ę		Į,	¥	L	EST_HUMAN	EST_HUMAN	NT	Ę		EST_HUMAN	EST_HUMAN	Į.		M	EST_HUMAN	M	M	EST_HUMAN	EST_HUMAN	LN.	SWISSPROT
-	Top Hit Acession No.	3.7E-02 AP000063.1		T	Ī		1418392			3.0E-UZ ALUBOGUO.1	3.6E-02 AL096810.1		(59403.1	X59403.1	3.6E-02 AF181722.1	3.6E-02 AW945516.1	3.6E-02 AW945516.1	3.6E-02 U67575.1	3 AE NO A ENORGEO 4		3.6E-02 AA714521.1	3.6E-02 BE143078.1	3.6E-02 U20608.1		3.6E-02 U20608.1	3.6E-02 BF347588.1	3.5E-02 U09506.1	3.6E-02 AF263417.1	3.5E-02 BF678085.1	BF678085.1	3.6E-02 AE001773.1	P53780
	Most Similar (Top) Hit BLAST E Vatue	3.75-02/	2 TE AN	3.7E 02.7	0.77	3.7E-02	3.7E-02	3.6E-02 X73221.1	20 0	3.0E-02/	3.6E-02/		3.6E-02 X59403.1	3.6E-02 X59403.1	3.6E-02	3.6E-02	3.6E-02	3.6E-02	2 RE 02		3.6€-02	3.6E-02	3.6E-02		3.6E-02	3.6E-02	3.5E-02	3.6E-02	3.5E-02	3.5E-02	3.6E-02	3.5E-02 P53780
	Expression Signal	0.79	280	3 8	8,5	5.94	234	1.04		0.75	227		0.8	80	99.0	4.97	4.97	0.5	17	-	2.75	1.08	1.85		1.85	0.68	0.9	1.38	1.3	1.3	1.95	3.67
	ORF SEQ ID NO:		00070	140H			31520	29625		28631	31130		31514	31530			L				33853	34218			36143		İ					30253
	SEQ 10 NO:	25008	20000	1888	08787	25061	25762	16710		16717	1828		18801	18601	18674	10018	L		8	ST S		20838		1	22687	1_	L	L	L	1	L	17371
ľ	Probe SEQ ID NO:	7284		8	20/20	12225	12883	3867		3674	5253		250	559	6578	888	6865	7150	3	[8]	7527	7895	0748	3	9746	1768	968	1010	1566	1566	4241	4344

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Single Exon Probes Expressed in Bone Marrow

		-	-		_	<del>,</del>	_	_	_	_	_	_	_	_	<del></del>			_		_	_	_	_	,	-		_		<del>_</del>				_	~
	Top Hit Descriptor	HYPOTHETICAL 80.7 KD PROTEIN IN SOD1-CPA2 INTERGENIC REGION	Maize actin 1 gene (MAc1), complete cds	y944e05.r1 Soeres retina N2b5HR Homo sepiens cDNA clone IMAGE:190256 5' stmiler to contains Alu	repetitive element;	801644701R2 NIH_MGC_56 Hamo septens cDNA clane IMAGE:3929737 3'	Liacts MG1363 grpE and chalf genes	601344661F1 NIH_MGC_8 Hamo sapiens cDNA clane IMAGE:3677654 5	PM1-CT0326-291289-002-h03 CT0326 Homo septens cDNA	PM1-CT0326-291299-002-h03 CT0326 Homo septems cDNA	601178765F1 NH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'	Homo sapiens mRNA for FLJ00013 protein, partial ods	Homo sapiens mRNA for FLJ00013 protein, partial cds	Homo sepiens mRNA for FLJ00013 protein, pertial cds	Homo sepiens mRNA for FLJ00013 protein, pertial cds	xx28d07.x1 Scenes_NFL_T_GBC_S1 Home sapiens cDNA clone IMAGE-2814253 3' similar to	SW.CZ11_HUMAN POSSUI PUTATIVE SURTACE GLYCOPTROTEIN CZTURFT PRECURSOR;	Homo sapiens hypothetical protein FLJ13220 (HLJ13220), mrNNA	yc20e06.r1 Stratagene lung (#837210) Homo sapiens cDNA clone INAGE:81250 5' similar to contains MER29 repetitive element	Homo capiens chromosome 21 segment HS21C008	RC8-UM0015-210200-021-A10 UM0015 Homo sepiens cDNA	M.muscultus S-antigen gene promoter region	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTICEN HOMOLOG)	Ceenahabditis degans mRNA for DYS-1 protein, pertial	801820445F1 NIH_MGC_58 Hamo sapiens cDNA clone IMAGE:4052434 5	Human lysyl oxidase-like protein gene, exon 3	w69d04.x1 NCI_CGAP_Bm26 Hamo septens cDNA done IMAGE:2433031 3'	mu70/08.s1 NCI_CGAP_AM/ Homo saptens CDNA clone IMAGE:1216071 similar to contains Alu repetitive	element,contains element MLF/CD MELYCD repetitive element;	200411.s1 Strategene muscle 837209 Hamo sapiens cDNA clone IMAGE:628749 3' similar to	TR:G1017425 G1017425	IPPSGKPLPKYTLSRUGYPLKATMRFNTEITAENLTINLKESYTALAGAYYETTAANSSGTTKAFINVALDRPG IPPT GPVVISDITEESYTLKWEPPKYDGGSOVTNYILTKRETSTAVWTEVSATVARTIAAKVAAGA:	COSCHOR AT Scanes narethanid himor NIMPA Homo seniens cDNA clone IMAGE 1683519 3'	TOTALINOTE OFFICE THE TIME THE TOTALINO CONTROL OFFICE OFF
	Top Hit Detraberse Source	SWISSPROT	M		EST HUMAN	EST_HUMAN	NT	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	IN	IN	F	¥		EST_HUMAN	Ę	EST_HUMAN	¥	EST_HUMAN	١	SWISSPROT	N <sub>T</sub>	EST_HUMAN	NT	EST_HUMAN		EST_HUMAN			EST HIMAN	EST LINAN	ESI_NOMPA
26	Top Hit Acession No.	247144	101238.1		129951.1	3.5E-02 BE958970.1	C76642.1	3.5E-02 BE561042.1	3.5E-02 AW861641.1	3.5E-02 AW861641.1	3.6E-02 BE276948.1	3.4E-02 AK024424.1	3.4E-02 AK024424.1	3.4E-02 AK024424.1	3.4E-02 AK024424.1		3.4E-02 AW274020.1	11345459 NT	157160.1	3.4E-02 AL163208.2	3.4E-02 AW794952.1	(59799.1	226457	3.4E-02 AJ012489.1	3.4E-02 BF131628.1	J24393.1	3.4E-02 AI869629.1		3.4E-02 AA664886.1			3 4F-02   AA 194308 1	3.4E-02 ANISTOU. I	AIO92/19.1
	Most Similar (Top) Hit BLAST E Vatue	3.5E-02 P47144	3.5E-02 J01238.1		3.5E-02 H29961.1	3.5E-02	3.5E-02 X78642.1	3.5E-02	3.5E-02	3.5E-02	3.6E-02	3.4E-02	3.4E-02	3.4E-02	3.4E-02	į	3.4E-02/	3.4E-02	3.4E-02 T57160.1	3.4E-02	3.4E-02	3.4E-02 X59799.1	3.4E-02 Q26457	3.4E-02	3.4E-02	3.4E-02 U24393.1	3.4E-02	1	3.4E-021			4E-02	20,00	3.45-04
	Expression Signal	1.04	1.74		0.78	2.87	1.99	0.47	1.61	1.61	6.77	0.91	16.0	3.42	3.42		2.4	6.51	2.61	1.19	3.71	3.05	2.48	1.83	හ.0	3.97	3.14		1.56			6	750	0.64
	ORF SEQ ID NO:		32657				36777	36832		38289		20202					27049		28432					6660E		31251			36482				<u> </u>	
	Ean SEQ ID NO:	18273	19416		21279		23301	23347	24706		25806	13649	13649	13649	13849			14249	15408	16491	16982	17840	18110	18124	19400	18364	21672	<u></u>	22088			22224		23062
	Prabe SEQ ID NO:	6285	6347		8810	0268	1037B	10425	11823	11823	12877	289	280	581	584		1083	1211	2401	344	3942	4628	5100	5114	6330	7032	8604		9 8			800	2000	10136

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All Total I book Light County	ORF SEQ Expression (Top) Hit Top Hit Acesston Databases ID NO: Signal Value	9.24 3.3E-02 AA398735.1 EST_HUMAN	27166 14.49 3.3E-02 AB035867.1  NT	27650 1.73 3.3E-02 AF110763.1 NT	1.29 3.3E-02 AE000700.1  NT	3.3E-02 R09112.1 EST_HUMAN   y25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5	28485 1.31 3.3E-02 6755862 NT	28347 8.85 3.3E-02 H02389.1 EST_HUMAN	27650 2.36 3.3E-02 AF110769.1  NT	30407 1.81 3.3E-02 6755862 NT	30759 0.66 3.3E-02 AW275698.1  EST_HUMAN	32896 20.14 3.3E-02 BF245985.1 EST_HUMAN	32897 20.14 3.3E-02 BF245885.1   EST_HUMAN	36084 0.71 3.3E-02 BF115621.1	36085 0.71 3.3E-02 BF115621.1 EST_HUMAN	Ser 74 0 77 3 SELV2 AAABROOD 1 FST HILIMAN		36175 0.72 3.3E-02 AA488202.1 EST_HUMAN	0.46 3.3E-02 H38109.1 EST_HUMAN	37945 2.47 3.3E-02 BF691107.1  EST_HUMAN	3.71 3.3E-02 T96545.1 EST_HUMAN	1.69 3.3E-02 AF289665.1 NT	3.04 3.3E-02 M81890.1 NT	26168 1.27 3.2E-02 AJ002005.1 NT	27122 10.01 3.2E-02 AF096275.1 NT	27123 10.01 3.2E-02 AF096275.1 NT	3.6 3.2E-02 P28955 SWISSPROT	29122 9.61 3.2E-02 BE867353.1 EST_HUMAN	16.99 3.2E-02 X94768.1 NT	30712 3.75	1.34 3.2E-02 Y08824.1 NT	31866 1.56 3.2E-02 X68709.1 NT	Ш
			27166	27650	_		28485	28347	27650	30407	30759	32896	32897	36084	36085	30474	-	38175		37945				26168	27.122	27123		28122	_	30712		31866	31867
	Exen SEQ ID NO:	13458	14212	14677	3 14782	8 15113	15462	16422	3 14677	4 17519	17865	19630	19630	L				02222	23884	24398	5 25183	L	7 25286	13237	14171	14171	15144	16208	8 17275	l		3 18709	L.I
	Probe SEQ ID NO:	372	1171	1645	1753	2096	2458	3372	4206	4494	4848	6570	6570	7/96	229	0,40	100	8778	10964	11455	12425	12547	12577	132	1128	1128	2127	3151	4248	4801	230	5613	5613

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. Top Hit Descriptor	za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapians cDNA clone IMAGE:294906 5' shrillar to confains element TAR1 repetitive element;	za39a10.r1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:294906 6's similar to contains element TAR1 repetitive element;	Opprinus carpto mRNA for inducible nitric cadde synthase (INOS gene)	601512206F1 NIH_MGC_71 Hamo septens aDNA clane IMAGE:3913848 5	601512206F1 NIH_MGC_71 Hamo sepiens cDNA clone IMAGE:3913948 5	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-celis 1 (NFKB1) gene, complete cds	Homo sepiens nuclear factor of kappa light polypeptide gene enhancer in B-celis 1 (NFKB1) gene, complete cds	Human dystrophin gene	601854981F1 NIH_MGC_57 Hamo sapiens cDNA clone IMAGE:4074548 5	602154364F1 NIH_MGC_83 Hamo septens oDNA clone IMAGE:4295654 5	ILS-HT0704-290600-108-co4 HT0704 Homo septens cDNA	Omithorhynchus enatinus coagulation factor X mRNA, complete cds	Thermotoga maritima section 109 of 138 of the complete genome	Human coagulation factor VII (F7) gene excn 1 and factor X (F10) gene, excn 1	ne87704.s1 NCI_CGAP_Kid1 Hamo sepiens cDNA clane IMAGE:911.283	yh63d04.s1 Sogres placenta Nb2HP Homo sapiens cDNA clone IMAGE:1344073'	QV4-NN0038-270400-187-N05 NN0038 Hamo sapiens cDNA	Rattus norvegicus UDP-Gal:glucosyloaramide beta-1,4-galactosyltransferase mRNA, complete cds	Homo sepiens mitochondrial gutsdhione reductasse and cytosolic glutathione reductase (GRO1) gene, complete ods, eitematively spilced	01338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 57	801338428F1 NIH_MGC_53 Hamo sepiens cDNA clone IMAGE:3680695 5	Sheep gene for ultra high-sulphur keratin protein	yu07e10,r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5	Sus scrofa decoynthonuclease II mRNA, complete cds	601452661F1 NIH_MGC_66 Hamo saplens cDNA clane IMAGE:3856598 5	Neisseria meningitidis DNA for region 2 (fhaB- and fhaC-homologs, unknown genes) and flanking genes, strain FAM18	601140729F1 NIH_MGC_9 Homo sepiens cDNA clone IMAGE:3049830 5
Top Hit Database Source	EST_HUMAN e	EST_HUMAN e		П	EST_HUMAN (	¥ 5	¥		EST_HUMAN	EST_HUMAN		NT	TN	NT.	EST_HUMAN	EST HUMAN	EST_HUMAN (	NT	LN	T HUMAN	HUMAN		EST_HUMAN	TN	EST_HUMAN	Ę	THUMAN
Top Hit Acessian No.	VS9615.1	199815.1	3.0E-02 AJ242908.1	3.0E-02 BE889948.1	3.0E-02 BE889948.1	3.0E-02 AF213884.1	3.0E-02 AF213884.1	3.0E-02 M86524.1	3.0E-02 BF246361.1	3.0E-02 BF679706.1	3.0E-02 BF353889.1	3.0E-02 AF275654.1	3.0E-02 AE001797.1	3.0E-02 M81357.1	3.0E-02 AA483216.1	732019.1	3.0E-02 AW895565.1	3.0E-02 AF048687.1	2 QE-02   AF228703.1	2.9E-02 BE565644.1	2.9E-02 BE565644.1	X55294.1	2.9E-02 H72806.1	2,9E-02 AF080221.1	2.9E-02 BF032233.1	2.9E-02 AJ391284.1	2.9E-02 BE271437.1
Most Similar (Top) Hit BLAST E Veitue	3.0E-02 N99615.1	3.0E-02 N99815.1	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02 R32019.1	3.0E-02	3.0E-02	2.05-02	29E-02	2.9E-02	l		l	2.9E-02	2.9E-02	28E-02
Expression Signal	0.58	0.58	3.17	. 28	2.8	2.20	2.28	1.29	0.76	0.48	0.74	1.82	1.88	2.38	7.84	2.02	2.08	1.96	•	114	1.14	0.8	0.72	1,13	7.33	0.62	10.95
ORF SEQ ID NO:	32683	32894			33328	33310				-	35378		37248	38063		31316			78487	l	L						Ш
Exan SEQ ID NO:	19451	<u> </u>	1	20025	20025	1	l	1_	1	21432	L			24506	24874	25960	25470	25954		1	Ι.	┚		L	L		1 1
Probe SEQ ID NO:	888	888	6857	200	7097	7274	7274	7442	7836	8463	8868	9146	10826	11568	11997	12529	12888	12808	2442	3005	3008	3573	3950	6181	822	7142	7460

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Angle Form of the manner of the form	ORF SEQ Expression (Top) Hit Top Hit Accession Database ID NO: Signal Value Value	33982 0.67 2.9E-02 D28214.1   EST_HUMAN	34506 0.53 2.9E-02 AE003932.1  NT	The state of the s	34/16 U.83 Z.BE-UZ.AF 1.28Z/8.1 INI	34717 0.83 2.9E-02 AF1.28279.1 NT	36409 2.26 2.8E-02/AW875979.1 EST HUMAN	38410 2.26 2.9E-02 AW875979.1 EST_HUMAN	0.67 2.9E-02 AW976697.1 EST_HUMAN	37127 1.07 2.9E-02 AP000064.1 NT	29540 1.6 2.9E-02 X55294.1 NT	1.46 2.0E-02/AU135817.1 EST HUMAN	1.93 2.8E-02 AW970153.1 EST_HUMAN	28355 1.27 2.8E-02 AF066063.1 NT	29356 1.27 2.8E-02 AF066063.1 NT	0.67 2.8E-02 8393751 NT	31090 3.2	0.83 2.8E-02[M58493.1 NT	31622 10.89 2.8E-02 BE741083.1 EST_HUMAN	33533 1.13 2.8E-02 T78960.1 EST_HUMAN	35063 2.24 2.8E-02 AJ005820.1 NT	35766 0.82 2.8E-02 AA280762.1  EST_HUMAN	35974 1.03 2.8E-02 AF187872.1 NT	38071 0.71 2.8E-02 AE001092.1  NT	00 37413 0.42 2.8E-0.2 BF527244.1 EST_HUMAN 602039477F2 NCI_CCAP_Bm67 Homo saplens cDNA clone IMAGE:4177267 5	1.6 2.8E-02 R06968.1 EST_HUMAN	1.57 2.8E-02 X08322.1 NT	27491 1.07 2.7E-02 U66059.1 NT	29411 1.88 2.7E-02 AL.161494.2 NT	30143 2.01
		33982					L									<u> </u>			31622											
	S Essan S Es Es	57 20817	L		273000	31 21300	<u>.</u>		33 23 158	10 23632		31 25870	73637	L	L	17368	<u> </u>				L		33 22525	37 22820	30 23900		Ĺ.,			30 17259
	Probe SEQ ID NO:	7857	8169		23	16331	10016	10016	10233	10710	11388	12531	567	3380	3380	434	5208	5294	5565	<b>698</b>	8671	9371	5996	1996	10980	12809	12815	1485	3445	4230

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			_		T.sesstyvim pTTH20 mRNA for wheat type V thionin	Onyza sativa mRNA for ascorbate coddese, partial cds	A bisparus pgkA gene		Homo septens mRNA for FLJ00048 protein, partial cds	Mus musculus G21 protein (G21), mRNA	tc28g08.x1 Sceres_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to contains Atu repetitive element;			Mus muscutus histidine rich calcium binding protein (Hrc), mRNA	Mus musculus histidine rich calcium binding protein (Hrc), mRNA	Mus musculus MHC class III region RD gene, partial cds, Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC704,	╗		Chicken dorsalin-1 mRNA, complete cds	Detrococcus radiodurans R1 section 151 of 229 of the complete chromosome 1	xe52b04x1 NCI_CGAP_Ser4 Hamo sepiens cDNA done IMAGE:2570383 3" similar to SW:Y089_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0069;	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63			Vaccinia virus ORF1L, strain Wyeth	Vaccinia virus ORF1L, strain Wyeth	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA		П	Homo sepiens KIAA1070 protein (KIAA1070), mRNA
	Top Hit Detabase Source	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	NT	TN	NT	EST_HUMAN	LN	N	EST_HUMAN	Ę	<b>EST_HUMAN</b>	IN	IN	!	Z	EST_HUMAN	IN	NT	EST HUMAN	¥	١	<b>EST_HUMAN</b>	EST_HUMAN	NT	Z	NT	SWISSPROT	EST_HUMAN	노
	Top Hit Acession No.	2.7E-02 N47258.1	2.7E-02 BF245672.1	2.7E-02 R12246.1 ·	2.7E-02 X81670.1	2.7E-02 AB004799.1	2.7E-02 X97680.1	2.7E-02 AA893571.1	2.7E-02 AK024458.1	9266542 NT	2.7E-02 AI377036.1	2.8E-02 AL163282.2	2.6E-02 AA490021.1	6754241	6754241 NT		2.6E-02 AF109906.1	2.6E-02 AW181945.1	2.6E-02 L12032.1	2.6E-02 AE002014.1	2.6E-02 AW241154.1	2.6E-02 AL161563.2	2.8E-02 AL181563.2	2.6E-02 Al206030.1	2.6E-02 BE621748.1	2.6E-02 Z99064.1	2.6E-02 Z99064.1	6981271 NT	P21894	AA8609	11432020 NT
} !	Most Similar (Top) Hit BLAST E Vælue	27E-02	2.7E-02	2.7E-02	2.7E-02	2.7E-02	2.7E-02	2.7E-02	2.7E-02	2.7E-02	2.7E-02	2.8E-02	2.6E-02	2.0E-02	2.6E-02		2.6E-02	2.6E-02	2.6E-02	20E-02	2.6E-02	2.6E-02	2.8E-02	2.8E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02 P21894	2.6E-02	2.6E-02
	Expression Signal	2.01	0.52	1.89	0.68	0.51	1.03	1.83	0.53	0.69	123	1.25	2.54	3.05	3.05		1.52	0.91	3.26	1.8	3.05	0.6	0.55	6.36	1.88	0.82	0.82	6.03	0.55	0.71	121
-	ORF SEQ ID NO:	30144	31178			32379		33304		34407		26556		Ĺ	28407				30848		31014				32890	L	L				
	SEO ID NO:	17259	18425	l	ı	1	19808	20004	21077	21098	21065	13642	15382	ı	Į.	1	13984	17028	17968	ļ ·	18137	1	i.	l	L	L	L	1_	L	L	Ш
	Probe SEQ ID NO:	4230	5319	· 55616	8065	6087	6764	697,	8140	8180	8897	8	2374	2376	2376		2926	3088	4042	5104	6128	88	2885	8346	2838	ğ	ğ	2885	7516	8850	9715

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Single Excit Plobes Explessed in Dolle Mediow	Top Hit Descriptor	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II eipha chain (IAapha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds;	Chrysoprantike (NCS), bulyaphantike	Homo saplans gene for LEC12, complete cds	Homo septens similar to ALEX3 protein (H. septens) (LOC63634), mRNA	Homo explens mitogen-ectivated protein kinase kinase kinase 13 (MAP3K13), mRNA							T. thermophilia calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds	Г				(Chicken myristoylated alarnine-rich Cikinase substrate (MARCKS) mRNA, complete cds			Rat gene for uncoupling protein (UCP)	Rat gene for uncoupling protein (UCP)			IN RC3-ST0186-230300-019-h06 ST0186 Homo septens cDNA	Human retrotransposon 3' long terminal repeat	Г			٦	Barrella burgdorferi (section 11 of 70) of the complete gename		IN XIT repetitive element;
MOLL HOY	Top Hit Database Source	ļ	Z	Į.	5	¥	NT	EST_HUMAN	EST HUMAN	<b>EST_HUMAN</b>	SWISSPROT	SWISSPROT	TN	SWISSPROT	SWISSPROT	NT	EST_HUMAN	LN	NT	EST_HUMAN	TN	IN	SWISSPROT	TORPSIWS	EST_HUMAN	NT		EST HUMAN		EST_HUMAN	Ę		EST HUMAN
I BIRLING	Top Hit Accession No.		2.5E-02 AF050157.1		=	11433220 NT	2.5E-02 U80169.1	2.6E-02 BE973327.1	2.4E-02 AIS78582.1	2.4E-02 H85884.1	P01901	P01901	J05110.1	P01901	P01901	24E-02 AL161595.2	2.4E-02 W86680.1		2.4E-02 M31650.1	220573.1	2.4E-02 X12925.1	2.4E-02 X12925.1	P98092	P98092	2.4E-02 AW813007.1	2.4E-02 M16780.1		2.4E-02 H78376.1		2.4E-02 N69442.1	2.4E-02 AE001125.1		2.4E-02 AA625680.1
	Most Similar (Top) Hit BLAST E Value	1	2.35-02	255-02	2.6E-02	2.6E-02	2.5E-02	26€-02	2.45-02	2.4E-02	2.4E-02 P01901	2.45.02	2.4E-02 J05110.1	. 2.4E-02 P01901	2.4E-02 P01901	24E-02	2.45-02	2.4E-02	2.4E-02	2.4E-02	2.4E-02	2.45.02	2.4E-02 P98092	2.4E-02 P98092	2.4E-02	24E-02		2.4E-02	1	2.4E-02	24E-02	1	24E-02
	Expression Signal		20.5	147	3.36	1.47	2.24	3.42	0.69	2.24	1.73	1.73	1.43	1.43	1.43	6.0	26.0	0.65	0.65	1.38	1.05	1.05	0.52	0.62	0.57	0.58		0.53		11.43	0.49		0.81
	ORF SEQ ID NO:								26203	27810	28098	28099	30308	30461	30482		32650	32811	32812	33750	29755	89788	34495	34496							35731		35757
	SEQ ID		24180			25751			13276	14634	16884	15884	17424	17672	17572	18235	19409	19560	19560	86502	20414	20414	24097	24097	21191	21244		21751		- 1	22303		22328
	Probe SEQ ID NO:		1122/	12059	12416	12598	12686	12709	175	1602	2060	2060	4398	4540	4549	5227	6340	8496	6496	7431	7448	7448	8159	8169	8222	8275		8784		928	8338		888

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Single Exon Probes Expressed in Bone Marrow

							Bio Excel Flores Expressed III Codes Internow
Probe SEC ID S NO:	Ean SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detrábesse Source	Top Hit Descriptor
10050	77822	36443	0.48	2.4E-02	2.4E-02 AF124160.1	NT	Arabidopsts thatians motybdopterin synthese sulphunylese (crv6) gene, complete cds
10050	77822	36444	0.46	2.4E-02	2.4E-02 AF124160.1	NT	Arabidopsis theliana motybdopterin synthese sulphurylase (oroci) gene, complete cds
10165	23090	36588	2.67	2.4E-02	2.4E-02 AV892954.1	EST_HUMAN	AV692954 GKC Hamo sapiens cDNA clane GKCDSC03 5"
10340	23264	36743	2.78	2.4E-02	2.4E-02 AA483894.1	EST HUMAN	nh07b12.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similer to contains Alu repetitive element, contains element PTR5 repetitive element;
10976	23886		1.35	24E-02	24E-02 BE387111.1	EST_HUMAN	801274962F1 NIH_MGC_20 Hamo saplens cDNA clane IMAGE:3615902 5
11900	24781	38368	1.81	2.4E-02	2.4E-02 AF109905.1	NT	Mus musculus mejor histocompetibility locus class III regions Hsc70t gene, pertiel cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG26, and NG28 genes, complete cds; and unknown genes
11900	24781	38369	1.81	2.4E-02	AF10980	IN	Mus musculus major histocompetibility locus class III regions Hac/70t gene, partial cds; smRNP, G7A, NG23, Mus homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
12209	25050		2.39	2.4E-02	TN 6067296	Į.	Bacteriophage bll.87, complete genome
12383	26152	31855	1.7	2.4E-02		¥	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
12418	25188	31823	3.48	2.4E-02	BE92886	EST HUMAN	MR0-FT0175-310800-202-e06 FT0175 Homo sapiens cDNA
12474	25222	31791	1.59	2.4E-02	2.4E-02 U78167.1	NT	Rattus norvegicus cAMP-regulated guantine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
12474	25252	31833	1.59	2.4E-02	2.4E-02 U78167.1	NT	Rattus norvegicus cAMP-regulated guantine nucleotide exchange factor I (cAMP-CEFI) mRNA, complete cds
12843	25327		7.88	2.4E-02	2.4E-02 AB008689.1	Ę	Ceenorhabdilis elegans mRNA for tron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cde
1888	14913		5.28	2.3E-02	2.3E-02 W05340.1	EST_HUMAN	za84g08.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299294 5
1904	14928		8.44	23E-02	U94165.1	TN	4 Homo saplens mammary fumor-essociated protein INT6 (INT6) gene, exon 4
2358	15366	28388	3.16	23E-02	274293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
3694	16737	29650	4.2	2.3E-02	7.20377.1	EST_HUMAN	HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA
4178	17207	30083	0.8	2.3E-02	1.24799.1	NT	Gallus gallus correctn 45.6 (Cx45.6) gene, complete cds
4178	17207	30094	0.8	2.3E-02		NT	Gallus gallus connedn 45.6 (CX45.6) gene, complete cds
4450	17478	30364	1.52	2.3E-02	1	EST_HUMAN	CM4-NN0080-280400-160-b04 NN0080 Hamo saptens cDNA
4477	17503	30388	0.78	2.3E-02	2.3E-02 BE835225.1	EST_HUMAN	CM2-MT0118-010900-318-g07 MT0118 Hamo saplens cDNA
4477	17503	30389	0.78	2.3E-02	2.3E-02 BE935225.1	EST_HUMAN	CM2-MT0118-010900-318-g07 MT0118 Hamo septens cDNA
4478	18317	30380	1.23	2.3E-02	2.3E-02 AW583683.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U12 Hamo septiens aDNA dane IMAGE-2770671 3'
4478	18317	30391	1.23	2.3E-02	2.3E-02 AW 593693.1		xx25d08.x1 NCI_CGAP_Ut2 Homo sepiens cDNA done IMAGE:2770671 3'
4625	17646		2.80	23E-02	2.3E-02 BF026487.1		601672278F1 NIH_MGC_20 Homo septems cDNA clone IMAGE:3855388 5
4625	17846	30535	289	2.3E-02	2.3E-02 BF026487.1	EST_HUMAN	601672278F1 NIH_MGC_20 Hano sepiens cDNA dane IMAQE:3855388 5

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	Top Hit Descriptor	Rettus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds	Rattus norvegicus guantre rucleotide binding protein gamma subunit 11 mRNA, complete cds	Cautobacter crescentus topotsomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA	carboxylase beta chain (pccB) homolog gene, partial cds	601822921R1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042829 3'	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17	MR0-HT0080-011099-002-c09 HT0080 Hamo sepiens dDNA	Homo sapiens chromosome 21 segment HS21C103	Human plactin (PLEC1) gene, excns 3-32, and complete cds	Homo septens PDX1 gene for lipoyl-containing component X, exons 1-11	Hamo sapiens PDX1 gene for lipoyl-combining component X, exans 1-11	wa76h10.x1 Scares_NFL_T_GBC_S1 Homo septems cDNA clone IMAGE:2302147 3*	wa78h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'	HYPOTHETICAL 55.8 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR	CHROMOSOME ASSEMBLY PROTEIN XCAP-C	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome	GLUCOANYLASE S1/82 PRECURSOR (GLUCAN 1,4-ALPHA-CLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)	601178958F1 NIH_MGC_21 Hano sepiens cDNA clone IMAGE:3548567 6	602043629F1 NCL_CGAP_Bm67 Homo saplens cDNA clane IMAGE:4181454 5	602043629F1 NCI_CGAP_Bm67 Homo septens cDNA clone IMAGE:4181454 5	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds	Dictyostelium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds	Homo sapiens dead ringer (Drosophila)-like 1 (DRIL1), mRNA	Columba livia nucleoside diphosphate ktrase (NDPK) gene, nuclear gene encoding mitochondrial protein, commiste cds.	Lorns emisse chromodymain belines DNA binfing protein 2 (CHD2) mRNA	any expense an university decreased by the present of the formal process of the formal p	Optionistics by the air year campinates	m.24804.81 NCI_CGAP_Gas1 Homo sapiens cun/a done IMAGE:1084782.3	Infectious bursal disease virus segment B strain 11.4 VP1 gane, complete ods	PMU-B10340-170100-004-b03 B10340 Hamo septens GJ/VA	S. CATEMISIA GALGING STATE OF TOTAL AND THE OFFE TO
	Top Hit Database Source	NT R	NT R			T_HUMAN	N A	EST HUMAN M	エ		I F		EST_HUMAN W	EST_HUMAN   w	SWISSPROT H	SWISSPROT C	NT	NT	SWISSPROT G	EST_HUMAN &	EST_HUMAN 6	EST_HUMAN 6	S						Т	EST HUMAN IN	_	T HUMAN	
	Top Hit Acessian No.	2.3E-02 AF257110.1	2.3E-02 AF257110.1					2.3E-02 BE141475.1	.2				2.3E-02 AIG85380.1				2.3E-02 AE000199.1	2.3E-02 AE000199.1		31.1	2.3E-02 BF528462.1	2.3E-02 BF528462.1	2.3E-02 U39394.1		2.3E-02 11428388 NT		27170	900/440			1		2.2E-02 Z74283.1
	Most Similar (Top) Hit BLAST E Vætue	2.3E-02	2.3E-02		2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3€-02	2.3E-02	23E-02	2.3E-02	2.3E-02 P41996	2.3E-02 P50532	2.3E-02	23E-02	2.3E-02 P08640	2.3E-02	23E-02	2.35-02	2.3E-02	2.3E-02	2.3E-02	2.25.00	20 20 0	ZZE-0Z	222-02	2.2€-02	2.2€-02	2.2€-02	2.2E-02
	Expression Signal	1.19	1.19		3.35	0.55	4.22	0.84	0.52	99.9	0.87	0.87	0.74	0.74	0.89	0.77	1.47	1.47	1.71	7.99	1.5	1.5	3.2	2.48	1.82			8.	1.08	2.15	3.48	1.26	0.74
	ORF SEQ ID NO:	31086	31087		31463	32675	33112	31201	34016	34686	35207	35208	35431			38632	38794	36792	37624		31756	31756	31724			i i		1	28065			29814	╝
	Exan SEO ID NO:	18212	18212		18551	19432	19829	18403	20653	21178	L	l	I_	L	22457	L	L	23312	24095	25738	25392	25392	25453	25983	25833		L						16981
	Probe SEQ ID NO:	5203	5233		5449	සහ	6774	7172	7895	8028	8815	8815	8	48	200	102/18	10380	10330	11135	12336	12742	12742	12843	12897	13100	1	3	1782	2031	3448	3660	3867	3941

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Top Hit Descriptor Source	S.cerevisiae chronosome XVI reading frame ORF YPL241c	EST_HUMAN   AV689721 GKB Homo sapiens cDNA clone GKBAND03 3'	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27	P.vulgata etpha tub 2 mRNA	Home septens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	Homo sepiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	Mus musculus Sjogren syndrome artigen A1 (Ssaf), mRNA	EST_HUMAN   601684308F1 NIH_MGC_7 Hamo septiens cDNA clane IMAGE:3838571 5'	ne47h07.s1 NCI_CGAP_Cc3 Homo septens cDNA clone IMAGE;900541 3' similar to contains Alu repetitive	Т	Т	Becillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore cost protein CottM (cottM) genes, complete ds	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5 flanking region and partial cds	Mus muscuhus macrophage migration hinbitory factor (MIF) gene, 5' flanking region and partial cds	SWISSPROT   KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A		SWISSPROT   KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A			EST_HUMAN   PM2-870546-120100-001-f11 BT0548 Homo saplens cDNA	EST_HUMAN   nc21g03.r1 NCL_CGAP_Pr1 Hamo septiens cDNA clame IMAGE:1008820 /	EST_HUMAN   yx43h07.r1 Sogres melanocyte 2NbHM Home septens cDNA clone IMAGE:284541 5'	EST_HUMAN PM2-BT0546-120100-001-f11 BT0546 Hamo septens cDNA	EST_HUMAN   PM2-BT0546-120100-001-f11 BT0546 Homo saplens cDNA	EST_HUMAN   zd3b09.r1 Sogres_total_fetus_Nb2HF8_9w Homo septens cDNA chone IMAGE:786121 5		NT S.cerewisiae chromosome IV reading frame ORF YDL245c	T HUMAN	NT Borrella burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes
Most Similar (Top) Hit Acession Signal BLAST E No.	1.17 2.2E-02 Z73597.1  NT							2.26 2.2E-02 AB026898.1 NT	0.91 2.2E-02 6678140 NT	BE797601.1		2 1F-02 AV781502 1	2.1E-02 AF029726.1	8.8 2.1E-02 U72073.1 NT	2.1E-02 AF204395.1	L					2.1E-02 BE072546.1		2.1E-02 AA225095.1	2.1E-02 N29268.1	2.1E-02 BE072546.1		2.1E-02 AA461271.1	2.1E-02 BF203457.1		2.1E-02 BF343655.1	2.15 2.1E-02 U44914.1
Moost Similar Expression (Top) Hit Signal BLAST E Vetue	2.2E-02 Z73597.1	2.2E-02 AV699721.1	2.28 2.2E-02 AL181515.2	2.28 2.2E-02 AL161515.2	0.77 2.2E-02 X79468.1	2.26 2.2E-02 AB026898.1		2.2E-02 AB026898.1	0.91 2.25-02 667	2.2E-02 BE797601.1	2 2F AD AABTREES 1	2 1F-02 AV781502 1	2.1E-02 AF029726.1	2.1E-02 U72073.1	0.89 2.1E-02 AF204395.1	2.1E-02 AF204395.1	2.1E-02 P02438	2.1E-02 P02438	2.1E-02 P02438	2.1E-02 AF190899.1	0.9 2.1E-02 BE072546.1	2.1E-02 BE072548.1	2.1E-02 AA225095.1	2.1E-02 N29268.1	2.1E-02 BE072546.1	2.1E-02 BE072546.1	2.1E-02 AA461271.1	2.1E-02 BF203457.1	2.1E-02 Z74283.1	1.4 2.1E-02 BF343655.1	
A Expression (Top) Hit Signal BLAST E	1.17 2.2E-02 Z73597.1	3.37 2.2E-02 AV699721.1	35109 2.28 2.2E-02 AL181515.2	21682 35110 2.28 2.2E-02 AL161515.2	22127 35555 0.77 2.2E-02 X79468.1	22872 38488 2.26 2.2E.02.AB028898.1		2.26 2.2E-02 AB026898.1	0.91 2.25-02 667	1.8 2.2E-02 BE797601.1	2 2F AD AABTREES 1	13492 537 2 1F-02 AV781502 1	13522 8.77 2.1E-02 AF028128.1	8.3 2.1E-02[U72073.1	14420 27389 0.89 2.1E-02 AF204385.1	0.99 2.1E-02 AF204395.1	1.26 2.1E-02 P02438	1.26 2.1E-02 P02438	14828 27813 1.26 2.1E-02[P02438	15001 28004 1.01 2.1E-02 AF190899.1	15069 28089 0.9 2.1E-02 BE072546.1	15069 28090 0.9 2.1E-02 BE072546.1	1.04 2.1E-02 AA225095.1	13839 26784 4.45 2.1E-02 N29268.1	28089 1.02 2.1E-02 BE072546.1	28090 1.02 2.1E-02 BE072546.1	0.98 2.1E-02 AA461271.1	17066 28967 0.97 2.1E-02 BF203457.1	0.64 2.1E-02 274283.1	17368 30249 1.4 2.1E-02 BF343655.1	30384 2.15

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	Top Hit Descriptor	iy46d04.x1 Socres_NSF_FB_9W_OT_PA_P_S1 Homo sepiens cDNA clone IMAGE:2144651 3' similar to contains Alu repetitive element;	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters	Meleagris galiopavo paramonase-2 (PON2) mRNA, complete cds	Drosophila kanekol gene for glycard-3-phosphate dehydrogenase, complete cds	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1	Netsserla meningitidis serogroup A strain Z2491 completa genome; segment 37	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds	601852385F1 NIH_MGC_56 Hamo septens cDNA clone IMAGE:4076253 5	yyddh08.s1 Soares_muttiple_sclerosis_2NbHMSP Hamo sepiens cDNA clane IMAGE:276839 3'	Synechocystis sp. PCC8803 camplets gename, 20/27, 2538000-2844794	Hirudo medichalis Intermediate filament gilarin mRNA, complete cds	H. saplens MUC18 gene excn 16	hn52c06.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element. MER29 repetitive element :	601884329F1 NIH MGC 17 Homo septens CDNA dane IMAGE:4139983 5	H.francisci mRNA for myelin basic protein (MBP)	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome	te52a09.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090298 3"	MR1-OT0011-280300-009-404 OT0011 Homo sapiens oDNA	MR1-070011-280300-009-g04 OT0011 Homo sapiens cDNA	al/24h04,s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406835 31	QV4-DT0021-301299-071-b11 DT0021 Homo sepiens cDNA	HYPOTHETICAL PROTEIN DJ845024.2	Oryza sativa putative histone deacetylase HD2 mRNA, complete cds	Neisseria meningitidis serogroup B strain MC58 section 160 of 208 of the complete genome	Neisseria meningifidis serogroup B strain MC58 section 160 of 206 of the complete genome	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW SREGION	601763288F1 NIH_MGC_20 Hamo espiens cDNA clane IMAGE:4028280 5	601763268F1 NIH_MGC_20 Hamo sapiens cDNA clane IMAGE:4028280 5	Mus musculus carbonic anhydrase IV gene, complete cds
	Top Hit Database Source	EST_HUMAN o	NT	N FA	NT	NT TN	H LN	NT TN	NT	EST_HUMAN 6		EST_HUMAN 6	EST_HUMAN	אנ	II LN	+ LN	I NAMIN TSE	T		HT	EST_HUMAN I	EST_HUMAN N		EST_HUMAN	EST_HUMAN (	SWISSPROT	NT	INT	NT	SWISSPROT		T_HUMAN	Į.
	Top Hit Acession No.	1.9E-02 AH52999.1	1.9E-02 AL161550.2		L47572.1	AB019507.1	1.9E-02 U19241.1	1.8E-02 U19241.1	1.9E-02 AL162754.2	1.9E-02 BF316129.1	1.9E-02 L10114.1	1.9E-02 BP895832.1	1.9E-02 N39160.1	1.9E-02 D64001.1	1.9E-02 AF101085.1	1.9E-02 X68271.1	1 8F.02 AW771104 1	1 RF-02 BF308122 1	1.8E-02 X17884.1	1.8E-02 AE004544.1	1.8E-02 Al805829.1	1.8E-02 AW879122.1	1.8E-02 AW878122.1	1.8E-02 AA861448.1	1.8E-02 AWS36363.1	060810	1.8E-02 AF255711.1	1.8E-02 AE002518.1	1.8E-02 AE002518.1	P14310	1.8E-02 BF125690.1	1.8E-02 BF125690.1	U37091.1
	Most Similar (Top) Hit BLAST E Value	1.9E-02	1.9E-02	1.9E-02	1.9E-02	1.9E-02	l			1.9E-02	1.9E-02	1.9E-02	1.9E-02	1.9E-02	1.9E-02	1.9E-02	1 85-772	4 RF-02	1.8E-02	1.8E-02		1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02   O60810	1.8E-02	1.8E-02	1.8E-02	1.8E-02 P14310	1.8E-02		
	Expression Signal	3.65	2.68	0.94	1.25	1.24	1.34	1.34	1.2	0.78	0.43	1.09	0.46	0.5	3.14	1.4	1 95	4 30	1.87	1.78	1.06	1.01	1.01	1.04	1.49	0.98	0.68	0.59	0.59	4.59	0.65	0.58	0.77
	ORF SEQ ID NO:	30488		31369	31581		33817			36096		36811					1.30 ESC	l				29863			30374	30895		32845	32846	33534	34021	34021	
	SEQ ID NO:	17594	L	L				ı				23327		L					_	L	L	16942	16942	L			L	19587				20657	$\mathbf{L}_{-}\mathbf{l}$
Г	Probe SEQ ID NO:	4572	5048	5389	554	5885	7308	18	<b>8917</b>	8888	1007	10405	1950	10614	12372	13026	376	3 8	12	2887	3224	18	3902	4113	4461	4992	5287	6524	6524	6982	7689	7722	8467

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Single Exon Probes Expressed in Bone Marrow

Top Hill Descriptor	QV2-NN1073-220400-159-h09 NN1073 Hamo septens cDNA	Mus musculus microtubule-essociated protein 2 (Mtap2), mRNA	601877028F1 NIH_MGC_55 Hamo sapiens cDNA dane IMACE:4105303 5	601877028F1 NIH_MGC_55 Hamo sapiens aDNA dane IMACE:4105303 5	aj62f08.s1 Scenes_testis_NHT Homo sepiens cDNA clone IMAGE:1384821 3' stmiter to gb:L11672 ZINC FINGER PROTEIN 91 (HUMAN);	601463545F1 NIH_MGC_67 Hamo sepiens cDNA clane IMAGE:386963 5	Letagnalis mRNA for myomodulin neuropeptide precursor	Homo sepiens mRNA for KIAA0339 protein, partial cds	Homo septens mRNA for KIAA0839 protein, partial cds	Pyrococcus haritoshii OT3 genamic DNA, 1168001-1485000 nt. position (877)	Zee mays acidic ribosomal protein P2a-3 (rpp2a-3) mRNA, pertial cds	y/80d01.s1 Scares infant brain 1NIB Homo sepiens cDNA clone IMAGE:28986 3' similar to gb:IM62783 ALPHA-N-ACETYLGALACTOSAMINIDASE PRECURSOR (HUMAN);	y/80d01.s1 Scares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28985 3' similar to gb:M62783 ALPHA-N-ACETYLGALACTOSAMINIDASE PRECURSOR (HUMAN);	801310828F1 NIH_MGC_44 Homo sepiens cDNA done IMAGE:3632190 5	ht34eD3.x1 Scenes_NPL_T_GBC_S1 Hamo septens cDNA clone IMAGE:2833740 3' similar to contains L1.t1 L1 repetitive element;	hf34a03.x1 Scares_NRT_GBC_S1 Hamo septens cDNA clone IMAGE:2833740 3' similar to contains	L1.t1 L1 repetitive element;	Homo sapiens chromosome 21 segment HS21C004	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds	(microsatellite INRA41) [Ovis anies≕sheep, Genomic, 361 nt, segment 1 of 2]	Homo sepiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA	qb22s08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'	hm45a94.x1 NCL_CCAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element;	ac19f04.s1 Stratagene overy (#837217) Homo sepiens cDNA clone IMAGE:856927 3' similar to contains Alu	repetitive element; contains element MER24 repetitive element;	ye86108.r1 Scares fetal liver spleen 1NFLS Hamo septens cDNA clane IMAGE:124847 5	qm08g07.x1 NCI_CGAP_Lu5 Homo sepiens dDNA done IMAGE:1881276 3' similer to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);
Top Hit Detabase Source	EST_HUMAN	NT	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	EST HUMAN	Þ	N	IN	NT	IN	EST_HUMAN	EST HUMAN	<b>EST HUMAN</b>	EST HUMAN		<b>EST_HUMAN</b>	IN	NT	IN	IN	EST HUMAN	EST HUMAN		EST HUMAN	<b>EST_HUMAN</b>	EST_HUMAN
Top Hit Acession No.	1.8E-02 AW905327.1	6678943 NT	1.8E-02 BF241924.1	1.8E-02 BF241924.1	1.8E-02 AA897543.1	1.8E-02 BE778274.1	1.8E-02 X96933.1	1.8E-02 AB002337.2	1.8E-02 AB002337.2	1.8E-02 AP000006.1	1.8E-02 U62749.1	1.8E-02 R40255.1	1.8E-02 R40255.1	1.7E-02 BE394869.1	1.7E-02 AW573183.1		1.7E-02 AW573183.1	1.7E-02 AL163204.2	1.7E-02 AB004818.1	1.7E-02 S74188.1	7667495 NT	1.7E-02 A1147815.1	1.7E-02 AW827368.1		1.7E-02 AA669618.1	1.7E-02 R02508.1	1.7E-02 Al305279.1
Most Simitar (Top) Hit BLAST E Value	1.8E-02	1.85-02	1.8E-02	1.8E-02	1.85-02	1.8E-02	1.8E-02	1.8€-02	1.8E-02	1.8E-02	1.8E-02	1.85-02	1.8E-02	1.7E-02	1.7E-02		1.7E-02	1.7E-02	1.7E-02	1.7E-02	1.7E-02	1.7E-02	1.7E-02		1.7E-02	1.7E-02	1.7E-02
Expression Signal	0.79	0.75	9.0	0.5	2.03	1.65	1.2	1.7	1.7	2.73	3.16	1.35	1.35	0.8	2.15		2.15	4.23	11.19	1.03	1.18	96'0	5.52		96'0	2.04	0.7
ORF SEQ ID NO:		35247				36830			37439				31881				27824			28333		28990					30396
Exan SEQ ID NO:	21778	21824	22785	L	12827		23508	23920	23920	24816	24827	22826	1	I			14834	14912	15138	15313	15645	16069	16589		17229	17257	17507
Probe SEQ ID NO:	8811	8857	9849	9849	1000 000	10423	10586	11786	11785	11835	11948	13105	13105	200	1806		1806	1887	되되	2301	2848	3011	3523		4198	4228	4482

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Single Exon Probes Expressed in Bone Marrow

ngie exon probes expressed in done mailow	Top Hit Descriptor Source	ht34e03x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2833740 3' similar to contains EST_HUMAN L1.th L1 repetitive element;		EST_HUMAN   0v61e02.c1 Scares_testis_NHT Homo capiens cDNA clone IMAGE:1640858 31	Rettus norvegicus N-arginine dibasic convertase 1 (Nrd1), mRNA		wg35f09.x1 Sogres_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' struiter to contains Atu repetitive element;		EST_HUMAN   0/65h03x1 Soeres_fetal_iner_spieen_1NFLS_S1 Homo saptens cJNA clone IMAGE:1672861 3'		Homo sapiens nebulin (NEB), mRNA	Human apolipoprotein (a) gene, excn 1				EST_HUMAN   DKFZp434l0314_r1 434 (synonym: hbss3) Homo eaplens cDNA done DKFZp434l0314 6		EST HUMAN CMA-NN1030-040400-130-608 NN1030 Homo sepiens cDNA	oe08d04,s1 NCI_CGAP_Ov2 Hamo sepiens dDNA cione IMAGE:1385287 similar to contains element MSR1 EST_HUMAN repetitive element;	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162			T_HUMAN		EST HUMAN IL3-CT0219-160200-063-C07 CT0219 Homo saplens cDNA				EST_HUMAN   qu42b09.x1 NCI_CGAP_Lym5 Hamo sapiens cDNA crone IMAGE:195/417 3
Single EX	Top Hit Acesston No.	<u>-</u> .			6981289 NT	1229041.1 NT				=190930.1 NT	8400716 NT	L07899.1 NT	7899.1 NT	1010770.1 NT	21854.1 NT	1	5902007 NT	1.7E-02 AW903482.1 ES	-	_	I8889.1	J006345.1 NT	1	1.6E-02 AB014534.1 NT	7.	Ţ	7.7		
	Most Similar (Top) Hit BLAST E Vatue	1.7E-02 AW573183	1.7E-02 V00641.1	1.7E-02 AI015078.1	1.7E-02	1.7E-02 AJ229041.1	1.7E-02 AI769247.1	1.7E-02 Z28383.1	1.7E-02 Al038280.1	1.7E-02 AF190930.	1.7E-02	1.7E-02 LC	1.7E-02 L07899.1	1.7E-02 AJ010770	1.7E-02 U21854.1	1.7E-02 AL040554.	1.7E-02	1.7E-02 A	1.7E-02 A	1.8E-02 AL021829.	1.6E-02 Y18889.1	1.6E-02 AJ006345.	1.6E-02 AA484872.	1.6E-02	1.6E-02 AW850652	1.6E-02 AF110520	1.6E-02 AW875407	1.6E-02 N80156.1	1.6E-02 AI281385.
	Expression Signal	1.52	1.54	7.05	0.74	Ю.О	1.68	0.64	1.37	1.31	1.85	0.85	0.85	1.98	0.94	1.31	1.59	3.15		222	0.91	0.95	1.46	1.37	4.46	2.14	96'0	0.76	0.49
	ORF SEQ ID NO:	30471	30658		30989		32551		33065	33284			33903		34514	36453		31424			27673				29506		30245		31183
	SEQ ID	17580	17764	17868	18116	18237	18324	19678	19787	19388	20378	20543	20543	20954	2114	22884	24956	26910	25605	13583	14697	16673	15648	15700	16583		17357		18431
	Probe SEQ ID NO:	4567	4744	4851	5106	223	845	8618	6731	7251	7411	7681	7581	8016	9794	10057	12084	12910	1305	512	1000	2572	2861	202	3537	4204	4329	5172	6325

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Cirigia Evol F100as Expressed iii Dura iviai Ow	Similar Top Hit Acession Detablesse Source Source	6671715 NT	1,8E-02 AB015281.1 INT Cendida elbicans CeGGR3 gene, complete cds	1.8E-02 AB027571.1 NT Seccharomyces cerevisias CAD2 gene for cadmitum resistance protein, complete cds	LΝ	1.6E-02/AL161508.2 NT Arebidopsis thaliene DNA chromosome 4, contig fregment No. 20	1.6E-02 AJZ77882.1 NT Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein	¥	1.6E-02 AF078764.1 NT Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds	1.6E-02 AA572818.1 EST_HUMAN   P28284 TELOKIN. [1];	1.6E-02 AA572818.1 EST HUMAN P29294 TELOKIN [1];		1.6E-02/AL161508.2 NT Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20	1.6E-02 AL161508.2 NT Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20	I.6E-02/AI373558.1 EST_HUMAN   \$28610.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442.3'	SWISSPROT	SWISSPROT	3823734 NT	EST. HUMAN	1.6E-02 AL161994.2 NT Arabidopsis thellana DNA chromosome 4, contig fregment No. 90	NT	1,5E-02 AJ008216.1 NT Homo sepiens CACNA1F gene, exons 1 to 48	1.5E-02 BF092942.1 [EST_HUMAN  MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA	1.5E-02 Q09711 SWISSPROT HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME I	11467282 NT	11418713 NT Homo sapiens KIAA1009 protein (KIAA1009), mRNA		.5E-02 11417739 NT Homo sepiens wald-tRNA synthetase 2 (VARS2), mRNA	1.6E-02 BF345554.1   EST_HUMAN   602019136F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154504.57	1.1 NT	IN	1.5E-02 R32867.1 [EST_HUMAN   yh54b10.r1 Soares placenta Nb2HP Homo septiens cDNA clone IMAGE:133531 5
	Most Similar (Top) Hit BLAST E No	1.6E-02 6	1.6E-02 AB015281	1.6E-02 AB027571	1.6E-02 AB027571	1.6E-02 AL161508	1.6E-02 AJ277682	1.6E-02 X05151.1	1.6E-02 AF079764	1.6E-02 AA572818	1.6E-02 AA572818	1.6E-02 Z94828.1	1.6E-02 AL161508	1.6E-02 AL161508	1.6E-02 AI373558.1	1.6E-02 Q64176	1.6E-02 Q64176	1.5E-02 8	1.5E-02 N39521.1	1.5E-02 AL161594	1.5E-02 AJ006218	1.5E-02 AJ008216.	1.5E-02 BF092942	Q09711	1.5E-02 11	1.5E-02 11	1.5E-02 AL163303	1.5E-02 11	1.5E-02 BF345554	1.5E-02 AF096774	1.5E-02 D44606.1	1.5E-02 R32687.1
	Expression Signal	1.33	2.07	0.93	0.93	1.08	0.72	1.5	1.98	1.2	1.2	1.83	1.7	1.7	1.66	1.39	1.39	20.75	4.44	1.82	2.54	2.54	1.06	1.33	1.59	1.38	1.5	4.62	0.93	0.58	1.58	0.95
	ORF SEQ ID NO:	31977	33138		33355	34308	34844			37208	37207	37730	38042	38043	38307	31172	31173				29043	29044	28982	32745		33954		34593	35675			36574
	Esan SEQ ID NO:	18800	19853	20051	20051	20917	2427	21487	ZZ8ZZ	23706	23708	26705	24488	24488	24722	18834	18334	13813		15200		16131	16779	19493	20504	20591		21182	22148		Ш	23095
	Prabe SEQ ID NO:	6705	6739	7117	7117	7978	8458	8519	10400	10785	10785	11256	11547	11547	11839	12347	12347	752	2152	2185	3074	3074	3737	6428	7541	7831	8228	8213	9182	8823	8828	10170

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Single Exon Probes Expressed in Bone Marrow

Probe SEO ID NO:	Elean SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Veitue	Top Hit Acession No.	Top Hitt Deviabase Source	Top Hit Descriptor
10170	23095	36575	0.95		1.6E-02 R32867.1	EST_HUMAN	yh54b10.r1 Sogres placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5
11503	24445	37997	2.75		1.5E-02 [.40809.1	¥	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
11537	L		2,52		1.6E-02 AL111238.1	NT	Botry6s charea strain T4 cDNA library under conditions of nitrogen deprivation
12564			2.04		1.5E-02 AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
13078	25840		13		1.6E-02 AI783127.1	EST HUMAN	w06Nt3.x1 NCI_CGAP_CLL1 Homo saplens cDNA clone IMAGE:2389463 3' similar to conteins Atu repolitive element,contains element MER26 MSR1 repolitive element;
417	1		1,99		1.4E-02 AE002230.2	¥	Chlamydophila pneumoniae AR39, section 58 of 84 of the complete genome
1128		27115			TN05980 NT	LN	Homo sapiens NESH protein (LOC51225), mRNA
1261	14296		1.74		1.4E-02 U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1301	14337		3.4		1.4E-02 U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1520	14562		1.03		1.4E-02 AV723785.1	EST_HUMAN	AV723785 HTB Hamo septens cDNA clane HTBAHH11 5'
			•			ļ	Bifidobacterium longum Na+/H+ antiporter (nhaB), cytosine dearninase, and alpha-galactosidase (agil.)
3226			2.04		1.4E-02 AF160509.2	Z	galles, cultime usa, and recognitive states in the state of second and second s
3409			0.98		1.4E-02 AW074212.1	EST HUMAN	X000009X1 NCI_CGAP_GUT Hamo septens curva cione IMAGEL.20/0/83 3
3496					1.4E-02 AL161566.2	N	Andropes training Live Grantoning 4, Wing Ingline in the
3496					1.4E-02 AL161586.2	L.	Arabdopsis thallana DNA chromosome 4, contig tregment No. 82
3880	16712	20627	69'9	1.4E-02	6006918 NT	Ę	Mus musculus histocompetibility 2, complement component factor B (H2-Bf), mRNA
4516	17541	30427	6.1		1.4E-02 AW962688.1	EST HUMAN	EST374761 MAGE resequences, MAGG Homo sapiens cONA
4516	17341	30428	0.1		1.4E-02 AW962688.1	EST_HUMAN	EST374761 MAGE resequences, MAGG Homo sepiens cDNA
491	17928	30818	80.8		1.4E-02 BE733142.1	<b>EST_HUMAN</b>	601567403F1 NIH_MGC_21 Hamo septems cDNA clane IMAGE:3842280 5
491	17928		80.8		1.4E-02 BE733142.1	EST_HUMAN	801567403F1 NIH_MGC_21 Hamo sapiens cDNA clone IMAGE:3842280 5
5130	18139	31017	1.01		1.4E-02 AW948453.1	EST_HUMAN	CMO-FN0041-120500-370-h09 FN0041 Homo sepiens cDNA
2888	25992		96'0		1.4E-02 X91338.1	NT	H.sapiens La/SS-B pseudogene 3
							n11c04.s1 NCI_CGAP_Br2 Homo sepiens dDNA clone IMAGE:1023880 3' similar to contains Alu repetitive
9555	19915	32880	4.9		1.4E-02 AA559030.1	EST HUMAN	element;
	L.						n11c04.s1 NCI_CGAP_Br2 Homo septems cDNA clone IMAGE:1028890 3' similar to contains Alu repetitive
9299	19616	32881	4.9		1.4E-02 AA559030.1	EST_HUMAN	element,
8478	21447		1.61		1.4E-02 AL022073.1	INT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
9249		35645			1.4E-02 M81702.1	NT	Candida boldinii methandi oxidasse (AOD1) gene, complete cds
9510		35917	6.0		1.4E-02 AJ272266.1	TN	Hamo sapiens SPP2 gene for secreted phosphaprotein 24 precursor, exans 1-8
9755		38153	2.15		1.4E-02 BE544581.1	EST_HUMAN	601078239F1 NIH_MGC_12 Hamo saplens cDNA clane IMAGE:3464241 5
10923			0.58		1.4E-02 AL163218.2	IN	Homo sapiens chromosome 21 segment HS21C018
						:	

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Top Hit Descriptor	Human IFNAR gans for Interferon alpha/beta receptor	Arabidopsis thaliana F21 J9.2 mRNA, complete cds	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA	Homo sapiens chromosome 21 segment HS21C001	602129475F1 NIH_MGC_56 Hamo sapiens cDNA clane IMAGE:4286203 5	802129475F1 NIH_MGC_56 Hamo sapiens cDNA clane IMAGE:4286203 5	Mus musculus bela-sarcoglycan gene, complete cds	GENERAL TOWNS TO THE PROPERTY OF THE PROPERTY	Intuition general 1-deal receptor uses divisit Force 173 in 11, 1 CADV 201, 1 CADV 100 II., 1 CADV 250 II., 1 CABV 165 III., 1 CABV 165 III	TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2>	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc	finger protein 92, mmaq28orf	Mus musculus chromosome X configB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finar motate 02 mmm/204f	Impar process of interpretation for the PARTING Acres models and monthods inhibition	Train separate passe unated part taum 2 pm (suzpm) gans, pausa cos, train in approve unitarial protein (nata) and survival motor neuron protein (smn) genes, complete cds	C.reinhardtii ribulose 1,5-bisphosphate carboxylasseloxygenase activase mRNA, complete ods	Arabidopsis thatiana DNA chromosome 4, contig fragment No. 48	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48	ow08g05.x1 Soares_parathyrold_turnor_NbHPA Horno sepiens cDNA clone IMAGE:1646072.3' similar to contains. Au repetitive element,	Homo sapiens human endogencus retrovirus W gagC3.37 G gag (gag) gene, complete cds	Mouse kidney androgen-regulated protein (KAP) gene, complete cds	Chlemydla trachomatis section 31 of 87 of the complete genome	zh24a07.s1 Soares_pinsal_gland_N3HPG Homo sapiens cDNA clone IMAGE:412880 3*	xx34e03.x1 Sceres_NFL_T_GBC_S1 Hamo sepiens cDNA clane IMAGE:2815036 3'	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'	Bacillus subiliis complete genome (section 14 of 21); from 2569451 to 2812870	Human herpesvirus 6B, complete genome	Homo sapiens V1b vasopressin receptor (VPR3) gane, complete cds	H.seplens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
Top Hit Database Source	NT	ĮŅ.	NT	NT	EST_HUMAN	<b>EST_HUMAN</b>	F			Ę		닐	Ę		Į,	NT	NT	¥	EST HUMAN	FA FA	M	Į,	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN.	F	NT	F
Top Hit Acession No.	1.4E-02 X60459.1	1.4E-02 AF324985.1	11426968 NT	1.3E-02 AL163201.2	1.3E-02 BF697081.1	1.3E-02 BF697081.1	1.3E-02 AF169288.1			1.3E-02 U66061.1		1.3E-02 AL049868.2	4 25 00 41 040000 3	LLV48000.2	1.3E-02 U80017.1	1.3E-02 M62862.1	1.3E-02 AL161546.2	1.3E-02 AL161546.2	1.3E-02 Al031593.1	1.3E-02 AF156961.1	1.3E-02 M63707.1	1.3E-02 AE001304.1	1.3E-02 AA707741.1	1.3E-02 AW268563.1		299117.1	TN 69033069 NT	1.3E-02 AF152238.1	1.2E-02 X87344.1
Most Similar (Top) Hit BLAST E Value	1.4E-02	1.4E-02	1.4E-02	1.3E-02	1.35-02	1.3E-02	1.3E-02		_	1.3E-02		1.3E-02	20 10	1.35-02	1.3E-02	1.3E-02	1.3E-02	1.3E-02	1.35-02	1.3E-02	1.3E-02	1.3E-02	1.3E-02	1.3E-02	1.3E-02	1.3E-02 299117.1	1.3E-02	1.3E-02	1.2E-02
Expression Signal	2.14	1.47	1.96	2.05	2.31	2.31	1.38			1.08		1.79	,	R/:	1.21	2.0	125	1.25	4.86	1.48	2.18	0.63	0.44	3.74	3.74	1.4	2.51	16.88	0.67
ORF SEQ ID NO:	38172			27894		29206				30860		31225			32597	32634		31229	34455					37809					
SEQ ID NO:	25080			<u>l</u>	16282	L	170333			17879		18423		2862	18360	19393		18386			23489	23563	<u> </u>		L			L	
Probe SEQ ID NO:	12254	12616	12882	1972	3227	3227	3963			4984		5317	1	2	8829	68222	7164	757	882	8838	10567	10641	10988	11336	11336	12622	12714	12886	214

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO: NO: 2180 2180 2180 2260 2605 2605 2605 2605 2605 6121 6121 6121 6123 6238 7203 7203 7203 7203 7203	Exan SEQ ID NO: NO: 13443 13528 15454 16508 15454 16508 16508 1654 1654 1654 1654 1654 1654 1654 1654	28476 28476 28476 28225 282476 28225 282476 28225 282476 28535 28535 28535 30858 33858 33858 33858 33858 34131	Signal Si	Most Similar (Top Hit BLAST E Vatue L. Z02 AA0592	Top Hit Aco No. No. No. No. No. No. No. No. No. No	Top Hit Delaboses Source Source Source Source SWISSPROT EST HUMAN EST HUMAN EST HUMAN EST HUMAN NT EST HUMAN	Top Hit Descriptor  Top Hit Source retine N2A-HR Homo septens cDNA cione IMAGE:381940 5' striliar to contains element  EST HUMAN  Li repeditive element:  Source  Sour
8330	- 1			1.2E-02 Q11205	Q11205	SWISSPROT	GALNACALPHA-23-SIALYLTRANSFERASE) (ST3GALA-2) (SIAT4-B)
8534 153	11		1.31	1.2E-02	1.2E-02 AF183612.1	F	Homo sepiens fitnge protein mRNA, partial cds Homo sepiens fitnes protein mRNA, partial cds
9242	2022Z		1.1	1.2E-02	1.2E-02   176987.1	EST_HUMAN	yd72c08.s1 Soares felal liver spleen 1NRLS Homo sapiens cDNA clone IMAGE:113774 3*

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Indie Exori Probes Expressed in Bolie Mailow	Top Hit Descriptor	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)	WR1-ST0111-111199-011-h06 ST0111 Homo sepiens cDNA	Cempylobacter jejuni NCTC11168 complete genome; segment 2/6	Mus musculus fusion 2 (human) (Fus2), mRNA	QV1-BT0677-040400-131-g03 BT0677 Homo sepiens cDNA	801475619F1 NIH_MGC_68 Hamo sepiens cDNA clane IMAGE:3878405 5	S.carevisiae chronosome X reading frame ORF YJR152w	CMALNIVO119-300600-223-b05 NN0119 Homo septens cDNA	od80a09.s1 NCI_CGAP_Ov2 Homo septens dDNA dane IMAGE:1374232	od80809.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232	Homo sapiens melanoma-associated antigen (MAGE-C1) gena, complete cds	Oryctolagus cuniculus elF-2a kinase mRNA, complete cds	Homo septems ABCG1 geme for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1),	complete cds	Cryptosparidium parvum HC-10 gene, complete ads	Cryptospandium parvum HC-10 gene, complete cds	Glycine max glutathione S-transferase GST 21 mRNA, partial cds	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5	FORKHEAD BOX PROTEIN D3 (HINF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NIJCI EAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2)	ab70b09,s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'	xx21b02.x1 Sceres_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2813739 3'	EST382826 MAGE resequences, MAGA Homo sepiens cDNA	EST362826 MAGE resequences, MAGA Homo sepiens cDNA	HISTIDINE-RICH CLYCOPROTEIN PRECURSOR	qf34h02xt Scares_testis_NHT Homo sepiens cDNA clone IMAGE:1751955 3"	UI-H-Bi3-ekb-c-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds	UI-H-BI3-akb-c-10-0-UI.s1 NCI_CGAP_Sub5 Homo sepiens cDNA clone IMAGE:2733691 3'	Dictyostefium discoideum multidrug resistance transporter/Ser protease (tegC) mRNA, complete ods
TYOU LIONS	Top Hit Database Source	SWISSPROT	EST_HUMAN	NT	M	EST_HUMAN	EST_HUMAN	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	IN		M	NT	IN	NT	EST_HUMAN	SWISSPROT	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN	Ę	EST_HUMAN	Ę
Single	Top Hit Acession No.	288160	8.0E-03 AW808692.1	8.0E-03 AL139075.2	TN 958956 NT	8.0E-03 BE086509.1	8.0E-03 BE788441.1	249652.1	8.0E-03 BF363327.1	8.0E-03 AA828817.1	8.0E-03 AA828817.1	8.0E-03 AF084589.1	8.0E-03 M69035.1		8.0E-03 AB038161.1	7.0E-03 AF097183.1	7.0E-03 AF097183.1	7.0E-03 AF243378.1	7.0E-03 AV731712.1	DRYCHO	7.0E-03 AA688298.1	7.0E-03 AW303599.1	7.0E-03 AW950556.1	7.0E-03 AW950556.1	P04929	7.0E-03 AI150273.1	7.0E-03 AW44463.1	7.0E-03 AF196344.1	7.0E-03 AW44463.1	7.0E-03 U60086.1
	Most Similar (Top) Hit BLAST E Vatue	8.0E-03 P98160	8.0E-03	8.0E-03	8.0E-03	8.0E-03	B.0E-03	8.0E-03   249652.1	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03		8.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7 05-08	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03 P04929	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03
	Expression Signal	0.58	3.77	0.52	0.58	5.16	1.96	2.66	2.69	1.55	1.55	3.74	2.04		2.6	18.14	18.14	4.66	4.38	4.	3.03	3.04	1.03	1.03	2.08	0.67	56.0	1.45	0.83	0.96
	ORF SEQ ID NO:	35631	35657	35665			37602		38156	38252	38253	ĺ				28887	26688	26983	27113		27390							29769		
Ī	Exem SEQ ID NO:	22201	12227	22236	22286	23232	24078	24280	24586	24675	24675	24000	25047		25077	13757	13757	14029	14162	44400	14430	14535			15888	ı	16820	16865	16820	17393
	Probe SEQ ID NO:	8235	<b>1928</b>	8270	9331	10308	11118	11330	11649	11710	11710	12024	12205		12249	88	895	978	1138	. 1986	130	1502	1756	1756	2267	3571	3778	3825	4048	4366

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WOLLDAY OF THE PROPERTY OF THE	ORF SEQ Expression (Top) Hit Acession ID No: Signal BLAST E No. Source	xe34f09.x1 NCI_CGAP_Ut1 Homo sepiens dDNA done IMAGE:2809033 3' similar to TR:Q12387 Q12387 A C12387 Q12387	1.47 7.0E-03 AW630888.1 EST HUMAN hh89s05.y1 NCI_CGAP_GU1 Homo saplens cDNA clone IMAGE:2969936 57	1.81 7.0E-03 AL163278.2	31108 1.4 7.0E-03 AV724419.1 EST_HUMAN	31109 1.4 7.0E-03 AV724419.1 EST_HUMAN		0.83 7.0E-03 H71108.1 EST_HUMAN	6.11 7.0E-03 AW861059.1  EST_HUMAN	32762 1.38 7.0E-08 W68251.1 EST_HUMAN	33019 3.16 7.0E-03 AA327129.1  EST_HUMAN	33052	33387 1.92 7.0E-03 BE928133.1 EST_HUMAN	34088 5.31 7.0E-03 Z35838.1 NT		34557 0.45 7.0E-03 AJ229043.1 NT	34558 0.45 7.0E-03 AJ229043.1 NT	34830 2.46 7.0E-03 BE175687.1 EST_HUMAN	35354 0.49 7.0E-03 AF281074.1 NT	0.71 7.0E-03 AF111168.2 NT	NYTHIN AND TOCKNESS OF STREET	30344 0.63) 7.0E-US N32370.1	36476 2.84 7.0E-03 P48982 SWISSPROT	1.06 7.0E-03 AV687379.1 EST HUMAN	0.85 7.0E-03 A1789734.1 EST_HUMAN	2 37682 2.23 7.0E-03 AB008862.1 NT Bos teurus mRNA for NDP52, complete cds	1 37722 1.51 7.0E-03 AJ004862.1 INT Homo septens partial MUC6B gene, exon 1-29	1 37723 1.51 7.0E-03 AJ004862.1 NT Homo septems partial MUCSB gene, exon 1-29	1.53 7.0E-03 H94065.1 EST HUMAN	1.91 7.0E-03 BE2863253.1 EST_HUMAIN	1 1.99 7.0E-03 Y17455.1 INT Homo sepiers LSFR2 gene, penuftimate exon
		-			31108	31109				32762	33019	33052	33387	34088	34089	34557	34558	34830	35354		77686	30344	36476			37662	37722	37723	 +		
	Exan SEQ ID NO:	5 17588	17650	18038	8 18234	18234	ŀ		3 25656	7 19512	19744	19773		3 20716	3 20716	21150		3 21417	12812	22683		23002	1_	L			3 24201	3 24201	$\bot$	┙	25451
	Probe SEQ ID NO:	4565	4629	5024	5228	8228		5918	6233	6447	6887	6717	7284	7768	7763	8180	8180	8448	8961	9752	8	4502	10078	10668	10853	11176	11248	11248	1273	12741	12834

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Expression (Top) Hit Top Hit Acession Database Signal BLAST E No. Source	29153 1.22 5.0E-03 R71794.1 EST_HUMAN ly88g02.s1 Scares breast 2NbHBst Homo sapiens cDNA clone IMAGE:155666 3"	0.94 5.0E-03 AJ297357.1 INT Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene	2 NT	28670 4.03 5.0E-03 AF147449.2 NT Pseudomonas aaruginosa strain PAO1 peniciliin-binding protein 1B (ponB) gene, complete cds	1 5.0E-03 U38914.1 NT	2 5.0E-03 AA299675.1 EST_HUMAN	30246 0.69 5.0E-03 H78355.1 EST_HUMAN   yu79g10.r1 Soares fetal liver spleen (INFLS Hamo sapiens cDNA clane IMAGE 240068 5"	28722 1.02 6.0E-03 U38914.1 NT Citrus shrensls seed storage protein citrin mRNA, complete cds	30515 1.02 5.0E-03   U46851.1   NT   Human pubative chromatin structure regulator (SUPTGH) mRNA, complete cds	30546 1.13 6.0E-03 AJ131016.1  NT Hamo sapiens SCL gene locus	30885 1.34 5.0E-03 AI752367.1 EST_HUMAN can15c02.x1 Normal Human Trabecular Bone Cells Homo sepiens cDNA cione NHTBC_can15c02 random	30876 1.08 6.0E-03 P16286 SWISSPROT SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)	6754029 NT	32/172 5.69 5.0E-03 P35500 SWISSPROT SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)	Po	T	5.0F-03 BE300091.1   EST HUMAN	5.0E-03 AB025024.1 NT	0.82 6.0E-03 AB038287.1 NT	5.0E-03 6763651 NT		34047 0.62 6.0E-03 105124.1 EST HUMAN CONTRACTORS AND ISPOSITE AND SERVICE CONTRACTORS OF A 4.7 E. ACT. AND SERVICE AND SERVIC	5 0F-03 AB016816.1 NT	TOGGOSINA		0.49 6.0E-03 Q9R001 SWISSPROT	SWISSPROT	5.83 5.0E-03 M61132.1 INT IMause complement receptor (CR2) mRNA, 3" and
CON ORF SEQ	16236 29153	16344		16756 28670			17361 30246	16813 29722	17622 30515	17659 30546	17769 30665	17985 30875	18230 31105			19237 32468	19801						34378		TOTAL STATE	21033 34432		21925
Probe Exan SEQ ID SEQ ID NO: NO:	3181 16	L				<u>L</u>		_	4601 17	4638 17	4749 17		ı	5883 18		6162 19	1		L.,		<u> </u>		200	1	17	8097 21	8581 21	2050

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Top Hit Descriptor		Escherichia coli genomic DNA, (19.1 - 19.4 min)	Rabbit uteroglobin (UGL) gene, excn 1	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds	RC0-ST0379-210100-032-c02 ST0379 Homo sepiens cDNA	ny48h10.s1 NCI_CGAP_Pr9 Hamo sapiens cDNA clane IMAGE:385587	Homo sapiens PR00471 protein (PR00471), mRNA	ag48c10.s1 Gessler Wilms turnor Homo saplens cDNA clone IMAGE:1128290 3"	694F Heart Hamo sapiens cDNA clane 684	xn59g05.x1 Soares_NHCeC_cervicel_tumor Homo saplens cDNA clone IMAGE:2698040 3' similar to	xn59c05x1 Soares NHCeC cervical tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to	contains L1.12 L1 repetitive element;	y608e04.r1 Strategene placenta (#637225) Homo sapiens cDNA clone IMAGE:70686 5	1248c04.y1 NCI_CGAP_Bm62 Homo septens cDNA clone IMAGE:2291622 5	Gallus galius giyoaraldehyde-3-phosphate dehydrogenase mRNA, complete cds	Brugia malayi Y chromosome marker	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cots	2/75a/3.s1 Soares overy tumor NbHOT Homo septens cDNA clone IMAGE:809548 3' stmilar to SW DXA2 MOUSE P14885 PROBABLE DIPHENOL OXIDASE A2 COMPONENT	602077774F1 NIH_MGC_62 Hamo sepiens cDNA clane IMAGE:4252002 6	UHH-BIS-ekf-f-08-0-UI,s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'	UHIF-BNO-eko-h-04-0-UI-ri NIH_MGC_50 Hamo sapiens cDNA clane IMAGE:3078831 5	yg51e04.s1 Soares Infant brain 1NIB Homo sapiens cDNA done IMAGE:35988 3"	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PR-KINASE) (PTDINS-3-KINASE) (PRK)	on75g12.s1 Soares_NFL_T_GBC_S1 Hamo septens cDNA clane IMAGE:1562566 3"	yg51e04.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:35988 3"	RC3-BT0333-110100-012-101 BT0339 Homo sepiens cDNA	zi81a08.r1 Stratagana colon (#837204) Homo sapiens cDNA clone IMAGE:510898 5"	RC8-UM0014-170400-023-G01 UM0014 Hamo septens cDNA	2558a01.r1 NCI_CGAP_GCB1 Homo septens aDNA done IMAGE:701736 5	AV708305 ADC Hamo septens cDNA clane ADCAKB06 5	Rattus norvegicus type 1 astrocyte and offactory-limblo associated protein AT1-46 mRNA, complete ods	z/81g08.r1 Strategene colon (#637204) Homo saplens cDNA clone IMAGE:510898 5
Top Hit Dartebesso	Source	H	FA	¥	EST_HUMAN	T_HUMAN		EST_HUMAN	EST_HUMAN	Cet Ullian	Т	EST HUMAN	EST_HUMAN	EST HUMAN	Ę	Ę	Į.	EST HUMAN	Т	EST_HUMAN		EST_HUMAN	SWISSPROT			EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN
Top Hit Acession No.					5.0E-03 AW821888.1		7862557 NT	5.0E-03 AA653281.1	r19596.1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SOCTOR I LONGT.	5.0E-03 AW170334.1	149163.1	5.0E-03 BE048055.1	-	6.0E-03 AF067253.1		5 OF OR AA456597.1	5.0E-03 BF572332.1	5.0E-03 AW449109.1	4.0E-03 AW600198.1	346482.1	54675	4.0E-03 AA939339.1	346482.1	4.0E-03 AW749101.1	4.0E-03 AA099777.1	4.0E-03 AW794740.1	4.0E-03 AA284374.1	4.0E-03 AV708305.1		4.0E-03 AA099777.1
Most Similar (Top) Hit BLAST E	Vatue	5.0E-03 D90723.1	5.0E-03 M25090.1	5.0E-03 L21710.1	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03 T19596.1	200	0.0E-001	5.0E-03	6.0E-03 T49163.1	5.0E-03	5.0E-03	6.0E-03	5.0E-03 L10347.1	5.05-03	5.0E-03	5.0E-03	4.0E-03	4.0E-03 R46482.1	4.0E-03 P54675	4.0E-03	4.0E-03 R46482.1	4.0E-03	4.0E-03	4.0E-03/	4.0E-03	4.0E-03	4.0E-03 U33472.1	4.0E-03
Expression Signal	,	1.08	0.61	76.0	99.0	0.44	0.47	0.51	4.17	2.46	21.7	2.15	1.66	3.62	5.42	3.7	3.19	8	5.67	3.21	2.6	2.12	1.15	4.63	1.9	3.64	27.01	1.92	1.5	1.64	2.38	11.42
ORF SEQ.		35554	35688				37112	L			5//6	37765	37857							31702			28449	26586	28892		27147				27772	
Exan SEQ ID	ö	22125	22258	23124	23254		L			1	10047	24237	24328	24595	25938	25298	26355	26372	25752	25408	13335	13413	13518	13672	13933	13967	14185	14214	l	L	14787	15053
Probe SEQ ID	Ö Z	9459	2828	10189	10330	10518	10696	10844	11075	1	Ì	11287	11381	11659	12463	12595	12688	4274R	12743	12922	385	321	443	88	878	912	1153	1173	1306	1580	1758	2034

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igie exon Probes expressed in Bone Marrow	Top Hit Descriptor	601304161F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3638510 5	RC8-UM0014-170400-023-G01 UM0014 Hamo sepiens cDNA	Homo sepiens X28 region neer ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ce2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), advended/odystrophy protein >	Homo septens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ce2+/Celmodulin-dependent protein kinese I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrendeukodystrophy protein >	Homo sapiens polygiutamine-containing C14ORF4 gene	Homo explens polyglutamine-containing C140RF4 gene	Hamo sepiens chromosome 21 segment HS21C084	PM1-HT0340-151289-003-h08 HT0340 Homo septems cDNA	PM1-HT0340-151289-003-h08 HT0340 Homo sepiens cDNA	xf88f04.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2885279 31	xj98f04.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2865279 3'	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)	Homo sepiens TNNT1 gene, excns 1-11 (and joined CDS)	ab18a08x5 Strategene lung (#337210) Homo saplens cDNA clone IMAGE:841142 3' shrillar to contains Atu repetitive element,	Homo sepiens chromosome 21 segment HS21C084	xe83d03.x1 NCI_CGAP_Bm35 Homo septens cDNA done INAGE:2614469 3' stmiter to conteins L1.t1 L1	L1 repetitive element;	z68601.s1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4360093'	Foot and mouth disease virus serotype A-12 119ab capaid protein VP3	Drosophila melanogaster anon207 (anon207) mRNA, complete cds	Rattus norvegicus beta-catanin binding protein mRNA, complete cds	(HPRG)	MAJOR SURFACE-LABELED TROPHOZOITE ANTIGEN PRECURSOR	DKFZp781H014_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761H014 5	Rattus norvegicus opsin gene, complete ods	46c07.x1 NCI_CGAP_GC8 Hamo sapiens cDNA done IMAGE:29486523*	601076015F1 NIH_MGC_12 Hamo sepiens cDNA dane IMAGE:3461954 5	a)32/11.s1 Soares_testis_NHT Homo sapiens cDNA clone 139/2045 3	Lycopersicon esculentum knotted 3 protein (TKn3) mtRNA, comprete cas
xou Probes Ext	Top Hit Database Source	EST_HUMAN 60	EST_HUMAN RC	<u> </u>			H IN	NT H	EST_HUMAN PA	EST_HUMAN PA			SWISSPROT OF	XI N	EST HUMAN 12	Т	Г	EST_HUMAN L1	EST HUMAN	NT Fo	NT Dr		SWISSPROT (H	SWISSPROT M	EST_HUMAN DA		EST_HUMAN ho		T HUMAN	NT
Single	Top Hit Acessian No.	4.0E-03 BE410558.1		4.0E-03 U62111.2 ·		2			4.0E-03 BE154134.1	4.0E-03 BE154134.1	-	128.1		4.0E-03 AJ011712.1	4.0E-03 AI732764.1			4.0E-03 AW103719.1	4.0E-03 AA69995.1	4.0E-03 J02187.1	4.0E-03 AF005859.1	4.0E-03 AF169825.1	P04198	P21849	4.0E-03 AL133871.1	4.0E-03 U22180.1	4.0E-03 AW590572.1	4.0E-03 BE548453.1	4.0E-03 AA813222.1	4.0E-03 U76408.1
	Most Similer (Top) Hit BLAST E Vatue	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03 Q13608	4.0E-03	4.0E-03	4.0E-03		4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03 P04198	4.0E-03 P21849	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03
	Expression Signal	1.68	1.53	1.75	8.5	3.92	3.92	1.68	1.04	1.04	8.0	0.8	0.64	2.14	++	5.8		0.98	0.63	9.93	1.56	23.1	2.72	1.63	0.87	3.56	F	1.78	0.87	1.5
	ORF SEQ ID NO:		28323		28599	28712	28713	28716			29510	20511	29597		30553	30717		31059	31102	31142	31324	31482	32474		<u> </u>		32673	32757		
	Exam SEQ ID NO:	1_	15299		L	Ĺ	15697		L	L		16687	16682	17058		L		18182	18228	18278	18463	L		1_	L	<b>!</b>				20168
	Probe SEQ ID NO:	2259	2288	252	2578	2701	2701	2707	3230	3239	3541	3541	3639	4020	4843	4805		5173	5220	5272	5348	5473	5891	9889	2883	8203	838	6442	6827	6942

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Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C078	Homo saplens chromosome 21 segment HS21C078	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)	bs7g12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:22718143'	Г		ADAM-TS 6 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 6) [ADAM-TS-6] (ADAM-TS-5] (ADAM-TS-5] (ADAM-TS-5] (ADAM-TS-5) (	Dictyostetium discotteum AX4 development protein DG1122 (DG1122) gene, partial cds	Homo sepiens KIAA0345 gene product (KIAA0345), mRNA	1649611.x1 Scares_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:2080013 3' stmillar to contains Aburrocettifive element:	Homo sepiens chromosome 21 segment HS210008	Homo sepiens chromosome 21 segment HS210078	yp42g12.r1 Sogres retina N2b6HR Homo sapiens cDNA clone IMAGE:190150 5	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65	xx47h04x1 NCI_CGAP_Ut1 Homo septens cDNA clone IMAGE:2707159 3'	Homo sapiens chromosome 21 segment HS21C008	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA	601118164F1 NIH_MGC_17 Homo septens cDNA clone IMAGE:3028086 5	UHIF-BND-alp-g-04-0-ULM NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 6	7q74c09x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' strailar to contains Alu repetitive	Marinal Countries against Michael Home against 1, Marina MACE 2053032 3' similar to combas element		Г	Homo sepiens Grb2-essociated binder 2 (KIAA0571), mRNA	Homo saplens protein kinase CK2 catalytic subunit alpha gene, exon 1	Homo sepiens protein kinese CK2 catalytic subunit alpha gene, exon 1	Inc73c05.s1 NCI_CGAP_Pr2 Hamo sepiens cDNA clone IMAGE:782984 similar to contains Alu repetitive	element	Homo sapiens MHC class 1 region	S.careale (cv. Halo) mRNA for tricsephosphate isomerase	Mus musculus intestinal trefoil factor gene, partial cds
Top Hit Detabase Source	TN	H	SWISSPROT	EST_HUMAN	EST_HUMAN	<u>F</u>	SWISSPROT	뉟	Ę	EST HUMAN	NT	¥	EST HUMAN	Z	EST_HUMAN	Į,	EST_HUMAN	EST_HUMAN	EST_HUMAN	1445	EST TIOMAIN	EST HUMAN	EST HUMAN	Į.	Į.	¥		EST_HUMAN	TN	N	N
Top Hit Acession No.	4.0E-03 AL163278.2	4.0E-03 AL163278.2	202817	AJ681483.1	4.0E-03 BE670170.1	4.0E-03 X92109.1	287180	4.0E-03 AF111944.1	T862067 NT	4.0E-03 AI553083.1	4.0E-03 AL 163209.2	4.0E-03 AL 163278.2	4.0E-03 H30664.1	4L161555.2	4.0E-03 AW513635.1	4.0E-03 AL163206.2	4.0E-03 BE815173.1	4.0E-03 BE298290.1	4.0E-03 AW504273.1	7 307700	4.UE-US BF-ZZ41Z3.1	4.0E-08 AW614596.1	4.0E-03 AW819141.1		3.0E-03 AF011920.1	3.0E-03 AF011920.1		3.0E-03 AA468110.1	3.0E-03 AF055068.1	732521.1	3.0E-03 U46858.1
Most Similar (Top) Hit BLAST E Value	4.0E-03	4.0E-03	4.0E-03 Q02817	4.0E-03	4.0E-03	4.0E-03	4.0E-03 C9TT92	4.0E-03	4.0E-03	4.05.08	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	70 10	4.UE-US	4.0E-03	4.0E-03	4.0E-03	3.0E-03	3.0E-03		3.0E-03	3.0E-03	3.0E-03 Z32521.1	3.0E-03
Expression	1.22	122	4.12	0.89	0.72	99.0	0.49	90.9	1.92	7.41	4.72	3.66	0.57	0.79	1.65	4.53	1.62	3.2	2.13		77	3.31	2.73	6.48	1.69	3.09		5.52	1.58	8.08	1.3
ORF SEQ ID NO:					33860		34655			35453		35646				37954								31675		ĺ_		27678			28334
Eson SEQ ID NO:	20008	20008			20626		21243		21513	22030	22207	Ł	1	ı		24407	25958	25213	25259	30,50	<b>R</b>	25866	25437	25619	13457	13935		14701	16281	15314	16315
Probe SEQ ID NO:	2273	7273	7404	7865	7667	7977	8774	8383	8545	8087	8241	9250	10287	10742	11178	11464	12431	12454	12533		12/30	12801	12814	13083	371	88		1669	2268	2302	2303

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Top Hit Descriptor	Mus musculus intestinal trefoil factor gene, partial cds	Arabidopsis thallana rpoMt gene	601237982F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3609833 5	11.2-UM0076-240300-056-D03 UM0076 Homo capiens cDNA	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, excn 1 and 2	C.elegans samdc gene	AV762392 MDS Hamo sapiens cDNA clane MDSBSG01 5	AV762392 MDS Hamo sepiens cDNA clane MDSBSG01 57	aho4108.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 6	S.cereale (cv. Helo) mRNA for tricesphosphate isomerase	Rattus norvegicus gdnf gene	xu8,P10,H3 conorm Homo sepiens cDNA 3'	eb18e08x5 Stretagene lung (#837210) Homo sepiens cDNA clone IMAGE:841142 3' similar to contains Alu	repetitive element	601482715F1 NIH_MGC_68 Hano saplens cDNA clane IMAGE:3885483 5	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mKNA	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)	Mus muscutus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-	Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cas	sat3f10_r1 Sogres NitrHMPu_S1 Hamo sapiens curva clane IMAUCE: 813103 0	Fugu rubripes mRNA for sodium channel alpha subumit, perital cas	Kluyveromyces mandanus pcpi3 gane for purine-cytosine permease	Oryzza satiwa gene for bZIP protein, complete cds	DNA REPAIR HELICASE RAD15 (RHP3)	RC0-BT0812-250900-032-e07 BT0812 Homo septens cDNA	RC0-BT0812-250600-032-607 BT0812 Homo sepiens cDNA	zb27604.s1 Sogres parathyroid_tumor_NbHPA Homo sepiens cDNA clone IMAGE:304783 3	S.carevisiae UGA35 gene, complete cds	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HINRNP A2(A))	Hamo sapiens chromosome 21 segment HS210068	NONSTRUCTURAL PROTEIN V	hh80f10 x1 NCI_CGAP_GU1 Homo capiens cDNA done INAGE:2889131 3' similar to contains L1.f1 L1	repetitive element;	Arabidopsis thaliana DNA chromosome 4, contig tragiment No. 63
Top Hit Database Source	E E		EST HUMAN	EST HUMAN		¥	EST_HUMAN /	EST_HUMAN /	EST_HUMAN	NT IN	) LN	EST_HUMAN D	П		T_HUMAN		NT			T HUMAN	NT				EST_HUMAN	EST_HUMAN	EST_HUMAN	- 1	SWISSPROT	Г	ISSPROT	Т	EST_HUMAN	_
Top Hit Acession No.			3 0E-03 BE379298.1			112500.1	3.0E-03 AV762392.1	3.0E-03 AV762392.1	3.0E-03 AI792278.1	232521.1	3.0E-03 AJ011432.1	3.0E-03 AI636141.1		3.0E-03 AIT32754.1	3.0E-03 BE787945.1	N 6822499 NT	3.0E-03 AJ249981.1		3.0E-03 U35323.1	3.0E-03 AA456701.1	3.0E-03 D37977.1	3.0E-03 AJ011419.1	3.0E-03 AB021736.1	P28859	3.0E-03 BF333058.1	3.0E-03 BF333058.1	3.0E-03 N92580.1	3.0E-03 M63408.1	P51989	3 0F-03 AI 163268.2	3 OF AS OBOMB1			3.0E-03 AL161589.2
Most Similar (Top) Hit BLAST E Vatue	3.0E-03 U46858.1	3.0E-03 Y09006.1	3.0F-03	3.0E-03	3.0E-03 U34606.1	3.0E-03 Y12500.1	3.0E-03	3.0E-03	3.0E-03	3.0E-03 Z32521.1	3.0€-03	3.0E-03		3.0E-03	3.0E-03	3.0E-03	3.0E-03		3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03 P26659	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03 P51989	3 OF-03	3 OF -03	3	3.0E-03	3.0E-03
Expression Signal	13	80	8 4	25.5	1.62	6.72	7.18	7.18	1.47	1.08	3.8	6.58		1.74	5.49	3.42	122		0.95	10.04	0.65	1.37	3.16	0.49	16.0	16.0	131	0.77	1.18	18	1.25	291	10.07	4.04
ORF SEQ ID NO:	28335		09000	20136	20395		20049	22050	29995		30342	30458		30776	30796	31196	31893		31980	33040	33580	<u> </u>							35197					35797
SEQ ID NO:	45245	18084	48468	46224	16478	16486	17041	1381	17103	17208	17451	ŀ		17888	1_		1	٠[_	18803	19761		ı	ı	L			1	1	ı		L			H
Probe SEO ID NO:	2203	300	300	8 8	2628	3430	4002	4002	4067	4177	4424	4546		4871	4890	5338	5635		2708	6705	7224	7412	7765	8145	8270	8270	PADS.	8888	8874			3	9343	9400

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igie Exciti i coco Expressoa ili coro ilimitati	Top Hit Descriptor	Hamo sepiens procellagen-lysine, 2-axoglutarate 5-diaxygenase (lysine hydraxylase, Ehlere-Danlos syndrome type VI) (PLOD) mRNA	COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR	zx42a10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 6	Mus musculus myelin expression factor-3-like protein gene, partial cds	Homo sepiens chromosome 21 segment HS21C102	UI-H-BI1-adig-10-0-UI.st NCI_CGAP_Sub3 Hamo sapiens oDNA alone IMAGE:2717010 3	zet2a10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'	H.sepiens DWA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 denes	Raftus novegicus mRNA for SREB1, complete cds	ENV POLYPROTEIN (CONTAINS: COAT PROTEIN GP62; COAT PROTEIN GP36)	zp13h01,r1 Strategene fetal retina 937202 Homo saptens cDNA clone IMAGE:009361 5	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds	UI-H-BW0-cair-g-03-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3"	HA0507 Human fetal liver cDNA library Homo sapiens cDNA	Drosophila melanogaster shortsighted class 2 (shs) mRNA, complete cds	Drosophila melanogaster shortsighted class 2 (shs) mRNA, complete ods	Homo sepiens caldum chamal alpha1E subunit (CACNA1E) gene, exons 7-49, and partial ods, alternativaly spiload	ye45e02.s1 Scares adult brain N2b4HB55Y Homo saplens cDNA clone IMAGE:180890 3'	Homo sepiens X-linked antitutrative ectodermal dysplasia protein gene (EDA), excn 2 and flanking repeat	regions	8 Hamo sapiens concentrative nucleoside transporter (CALLI) gane, exact 12	Homo sapiens gene for cholecystokinin type-A receptor, complete cds	601878385F1 NIH_MGC_55 Hamo septens cDNA clane IMA(3E:4104682 5	Hamo septems mRNA for KIAA0693 protein, pertial cds	WR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA	MR2-UM0025-300300-102-f02 UM0025 Homo sepiens oDNA	Xenopus laevis xefitin mRNA, complete ods	ATP-DEPENDENT NUCLEASE SUBUNIT B	ATP-DEPENDENT NUCLEASE SUBUNIT B	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
	Top Hit Database Source		SWISSPROT	EST_HUMAN 2	NT		╗	$\neg$	EST_HUMAN (	<u> </u>		/ISSPROT			EST_HUMAN	EST_HUMAN	NT	L	<u> </u>	EST HUMAN				╗	EST_HUMAN	NT TN	EST_HUMAN	EST_HUMAN			П	SWISSPROT
- Cirigina	Top Hit Acession No.	4557836 NT		20E-03 AA450138.1	2.0E-03 AF302691.1		2.0E-03 AW137782.1	20E-03 AA450138.1	20E-03 BF568955.1		1.		83.1		2.0E-03 AW297380.1	2.0E-03 Al084748.1	20E-03 L42512.1	2.0E-03 L42512.1	2 0E-03 AF223391.1	2.0E-03 R87773.1		2.0E-03 AF003528.1	2.0E-03 AF187974.1	2.0E-03 D85608.1	2.0E-03 BF241410.1	2.0E-03 AB014593.1	2.0E-03 AW798111.1	2.0E-03 AW796111.1	20E-03 U63711.1	P23477	P23477	095203
	Most Similer (Top) Hit BLAST E Vetue	2.0E-03	20E-03 P29400	2.0E-03	2.0E-03	20E-03	2.0E-03	2.0E-03	20E-03	2 0F-03 X87344 1	20E-03	2.0E-03 P03374	2.0E-03	2.0E-03	2.0E-03	2.0E-03	20E-03	2.0E-03	2.05-03	20E-03		2.0E-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03	20E-03	2.0E-03 P23477	2.0E-03 P23477	2.0E-03 0.95203
	Expression Signal	3.03	8.7	1.28	1.52	1.02	4.02	4.82	8.0	ě	0 85	21	128	9.31	1.01	1.11	1.89	1.89	8	2		0.75	1.02	2.26	1.33	2.18	0.64	0.64	1.73	3.79	3.79	15.16
	ORF SEQ ID NO:	27523		27800	28042	28299		29394	29400	80800	20002	3002	30122			30375	30493	30494	30549			30945	31051	31149	31607					32536		32793
ļ	Exem SEQ ID NO:	14551	14627	14815	15032	15275	15585	16475	16481	18773	1	1777	17234	17277	17484	17488	17500	17500	1775	47760		18088	18172	18287	١	١.	١_	1_	1	18305	L	19545
	Probe SEQ ID NO:	1519	1595	1786	201	283	2584	3427	3434	600	3 6	4140	4203	4248	4468	4462	4577	4677	4735	4740		5054	5163	5281	5564	2709	92/9	582	2797	6231	6231	6480

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Single Extri Fludes Expressed in Doire Mariow	Most Similar  Expression (Top) Hit Top Hit Accession Signal BLASTE No. Source	32794 15.16 2.0E-03 Q95203 SWISSPROT CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)	7.38 2.0E-03 BF308187.1 EST_HUMAN	32842 2.28 2.0E-03 Q9UKP4 SWISSPROT MOTIFS 7) (ADAMTS-7) (ADAMTS7)		1.36 2.0E-03 X94451.1	EST_HUMAN	33133 0.71 2.0E-03 AA677831.1 EST_HUMAN	1 TM	33371 2.86 2.0E-03 BE067986.1 EST_HUMAN   CAM4-BT0368-061299-054-001 BT0368 Homo septiens cDNA	0.64 2.0E-03 AI298883.1  EST_HUMAN	33837 0.77 2.0E-03 T96569.1 EST_HUMAN  yd77g10.r1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:114306 6"	34198 1.55 2.0E-03 P07354 SWISSPROT PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)	4783 1.96 2.0E-03 AW592004.1 EST_HUMAN QC0976 JERKY.;	34947 6.01 2.0E-03 N20287.1 EST_HUMAN L1.b2 L1 repetitive element;	EST HUMAN	34880 0.57 2.0E-03 Q92350 SWISSPROT HYPOTHETICAL 32.8 KD PROTEIN C6G9.05 IN CHROMOSOME I	SWISSPROT	0.77 2.0E-03 6005855 NT	0.77 2.0E-03 6005855 NT	35102 0.81 2.0E-03 AU136879.1 EST_HUMAN AU138879 PLACE1 Homo septems cDNA clone PLACE1004839 5	Homo sepiens ASCL3 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene, C11orf16 gene and C11orf17 gene	2.0E-03 AW796111.1 EST HUMAN	0.68 2.0E-03 AW786111.1 EST HUMAN	0.68 2.0E-03 AF224669.1 NT	EST_HUMAN	36292 0.97 2.0E-03 H50832.1 EST_HUMAN ly98609.s1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA done IMAGE:194296 3"
	ORF SEQ ID NO:																										
	B Econ ID SEQ ID NO:	ı	19547			54 19814	56 19810	l		87 20064		11 20476		24365	21528		1		L.	84 21652		24729			<u> </u>	L	84 22837
	Probe SEQ ID NO:	2	6482		6522	6554	6756	67	7151	72	Ŕ	7511	7877	8386	8580	888	88	86239	8684	8684	8709	8782	88	9560	9898	9884	9884

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					Sign Sign		
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Velue	Top Hit Acessian No.	Top Hit Dafrabesse Source	Тक Hit Descriptor
	1			2000	Kerke	TOGGSSIMS	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIA-C) (TN-C)
92.00	22/3/	30180	3.31		P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
40028	1				P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10081					2.0E-03 AF097732.1	NT	Homo sepiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
10081	<u> </u>		0.65		2.0E-03 AF097732.1	NT	Homo sepiens caspase recruitment domain-containing protein (BCL-10) gene, complete cds
10275	L				2.0E-03 AW884269.1	EST_HUMAN	QV3-OT0064-060400-144-e01 OT0084 Homo septens eDNA
10402	<u> </u>		6.44	•	2.0E-03 AA251378.1	EST_HUMAN	zs 10a06.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:084754 3'
10781		37200	0.45		2.0E-03 BF367386.1	EST_HUMAN	MR2.GN0030-140600-001-e05 GN0030 Homo sapiens cDNA
10969	23889	37401	0.43		2.0E-03 AW361178.1	EST_HUMAN	RC1-CT0251-141099-012-d01 CT0251 Homo sepiens dDNA
10969	1_		0.43		2.0E-03 AW361178.1	EST_HUMAN	RC1-CT0251-141099-012-d01 CT0251 Homo septens dDNA
11356	L		24		2.0E-03 M86524.1	TN	Human dystrophin gene
11817	L	34198			P07354	SWISSPROT	PROTEOCLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11870	1				2.0E-03 BF330909.1	EST_HUMAN	RC3-8T0333-310800-115-g04 BT0333 Homo capterts cDNA
11876		38342	10.47		2.0E-03 Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
8			200		2 NE-13 AB25745 1	EST HUMAN	tyG5h03.x1 NCI_CGAP_Kd41 Hamo sepiens cDNA clane IMAGE:2283989 3' similer to SW:VATG_MANSE   025532 VACUOLAR ATP SYNTHASE SUBUNIT G ;
12/07		38873			2.0E-03 AF167516.2	Z	Homo sepiens SEL1L (SEL1L) gene, partial cds
			į				ow3o08.s1 Source paraffirmed furnor NibHPA Homo suplens oDNA clone IMAGE:1669634 3' similar to
12220	25057	38827	1.75		2.0E-03 AI084325.1	<b>EST_HUMAN</b>	TR-P97535 P97535 PS-PLÁ1 PRECURSOR;
12241	18349		11.57		2.0E-03 AJ245167.1	NT	Cametus dromedartus cyhp19 gene for immunoglobulin heavy chain variable region
12459	25932		2.03		2.0E-03 AV697968.1	EST HUMAN	AV697966 CKC Hama sepiens cDNA clane GKCGXD05 6
12550		31777	1.83		2.0E-03 Y00508.1	NT	H. sapiens M1 gene for muscamitic ecelylicholine receptor
12683			1.33		2.0E-03 AL163203.2	NT	Homo sapiens chromosome 21 segment HS210003
	L						1266702.x1 Soeres_total_fatus_Nb24F8_9w Homo expiens cDNA clone IMAGE:2049051 3' similar to
12710	25795		1.55		2.0E-03 AI375037.1	EST_HUMAN	contains Alu repetitive element;
13838	SAAAR				2 OF-08 AF129738 1	<u> </u>	Homo sepiens MSH55 gene, partial cds; and CLICH, DDAH, G8b, G8c, G5b, G8d, G9e, G8f, BAT5, G5b, CSK2B, BAT4, C4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
1300	L		18		2 OF AN AVERTAGE 1	EST HUMAN	AV697968 GKC Hamo sapiens cDNA date GKCGXD05 5
13095	1_		1.4		2.0E-03 P04797	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (GAPDH)
430	L	26444			1.0E-03 H96471.1	EST HUMAN	y98c08.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone INAGE-232334 67
	1	l					

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Top Hit Descriptor	Epstein-Barr virus (AG878 isolate) U2-IR2 domein encoding nuclear protein EBNA2, complete ods	601589841F1 NIH_MGC_7 Hamo sapiens cDNA dane IMAGE:3943954 57	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)	y07h06.r1 Soares melancoyte 2NbHM Homo sapiens cDNA clone IMAGE:270587 6' similar to contains element MER8 repetitive element;	yyOTh08.rf Sogres metenocyte ZNbHM Homo septens cDNA clone IMAGE:270587 5' similar to contains element MER8 repetitive element;	ab65g12.s1 Strategene lung cardinoma 837218 Home septens cDNA clone IMAGE:845734 3'	602088042F1 NIH_MGC_38 Hamo sepiens cDNA clone IMAGE:4086907 5	Mouse nucleoin gene	601657519R1 NIH_MGC_68 Hamo sapiens cDNA dane IMAGE:3875683 3'	Homo sapiens T-cell lymphoma Invasion and metastasts 1 (TIAM1), mRNA	yd33a11.r1 Scares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:115772 5	QV3-NN1024-260400-171-g05 NN1024 Hamo sapiens aDNA	Homo septems DiGearge syndrame critical region, centrameric end	Human gene for fourth somatostatin receptor subtype	Homo sepiens 969 ldo contig between AML1 and CBR1 on chromosome 21q22, segment 2/3	Homo septems X28 region near ALD tocus containing dual specificity phosphatase 9 (DUSP9), ribosomal	protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR),	CDM protein (CDM), adrendeukodystrophy protein >	Human TRPM-2 proteth gene, exons 1,2 and 3	601491081F1 NIH_MGC_69 Hamo septens cDNA clone IMAGE:3893276 5	Hamo sapiens prolactin-releasing peptide receptor gene, 5' flanking region	Homo sapiens partial stearth-1 gene	zk97c09.s1 Soares_pregnant_uterus_NtHPU Homo sapiens cDNA clone IMAGE:490788 3' similar to	contains L1.t1 L1 repetitive element;	Homo sapiens excetoses-like protein 1 (EXTL1) gene, exans 2 through 11, and complete ods	Rattus norvegicus plasma membrane Ce2+ ATPase Isoform 3 (PMCA3) gene, 5' flanking region	zh82e06.s1 Soares fetal Ilver spleen 1NFLS_S1 Homo sapiens cDNA ctone IMAGE:427810 3'	zh82e06.s1 Soares_fetal_liver_splean_1NFLS_S1 Hamo sapiens cDNA clone IMAGE:427810 3'	V.carteri gene encoding volvocopsin	CM3-LT0079-170200-092-607 LT0079 Homo sepiens cDNA
Top Hit Detabase Source	Ŋ	EST_HUMAN	SWISSPROT	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	N.	EST_HUMAN	Z	EST_HUMAN	EST_HUMAN	ᅜ	NT	IN			TN.	TN	<b>EST_HUMAN</b>	TN	N		EST_HUMAN	TN	MT	EST_HUMAN	EST_HUMAN	ŢN	EST_HUMAN
Top Hit Acession No.	(03332.1	1.0E-03 BE798491.1	202388	441974.1	141974 1	1.0E-03 AA773352.1	1.0E-03 BF541639.1	07699.1	1.0E-03 BE963939.2	11528176 NT	F87761.1	1.0E-03 AW902585.1	<i>-7757</i> 0.1	016826.1	1.0E-03 AJ229042.1			1.0E-03 U52111.2	1.0E-03 M63378.1	1.0E-03 BE880044.1	1.0E-03 AF274581.1	1.0E-03 AJ251973.1		1.0E-03 AA122270.1	1.0E-03 AF153980.1	1.0E-03 U29397.1	1.0E-03 AA001613.1	1.0E-03 AA001613.1	1.0E-03 Y11204.1	1.0E-03 AW840353.1
Most Similar (Top) Hit BLAST E Vaiue	1.0E-03 K03332.1	1.0E-03	1.0E-03 Q02388	1.0E-03 N41974.1	1 0F-03 N41974 1	1.0E-03	1.0E-03	1.0E-03 X07699.1	1.0E-03	1.0E-03	1.0E-03 T87761.1	1.0E-03	1.0E-03 L77570.1	1.0E-03 D16826.1	1.0E-03/			1.0E-03	1.0E-03	1.05-03	1.05-03	1.0E-03		1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03
Expression Signal	1.77	0.83	1.76	0.7	0.7	0.56	0.52	2.67	1.06	8.39	1.06	1.69	1.18	2.43	236			1.71	3.18	0.87	0.55	5.32		1.01	2.42	0.7	0.63	0.53	1.37	0.6
ORF SEQ ID NO:	31588	31916	31921						32485		32781		33268	33678				34228	34305					34869			35331		Ì	36716
SEQ D	18828	18748	18754	18810	1884	18078	19701	19213	19252	19387	19633	19610	19970	20329	20685			20844	20914	20070	21190	21251		21451	21554	21740	21907	21907	72281	22286
Probe SEO ID NO:	5531	5652	2658	57.16	574R	2002	8	6136	6177	8316	8488	8548	8919	7369	7728			7904	7976	8083	22	8282		8483	8588	8773	<u>2</u>	88	9828	<b>6</b> 824

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Top Hit Descriptor	nk27e11.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014784 3' similar to conteins Alu repetitive element,	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)	Bos taurus micromoler calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	zo33b08.r1 Stratagene colon (#897204) Homo sapiens cDNA clone IMAGE:588683 5	Gorilla gorilla involucrin gene medium allele, complete cds	qd13f08.x1 Scares_placenta_8to9wedcs_2NbHP8to9W Homo saplens cDNA clone IMAGE:1723619 3' similar to gb:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN);contains Alu repetitive element;	ob86602.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338226 3' similar to contains element MER22 repetitive element;	aj56h03.s1 Scares_testis_NHT Homo sapiens cDNA done IMAGE:1394357 3'	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5'shrilar to REPETITIVE ELEMENT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR	xs08e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'	Human familial Alzheimer's disease (STM2) gene, complete cds	DKFZp586M2024_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M2024	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	nf16h02.s1 NC_CGAP_P11 Homo septens cDNA clone IMAGE:013875	Haemophilus influenzae Rd section 63 of 163 of the complete genome	es70b08.x1 Berstead colon HPLRB7 Homo septens cDNA ctone IMAGE-2334039 3' striiber to TR-013825 013825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE;	as 70008.x1 Barstead colon HPLRB7 Homo septens CDNA clone IMAGE:2334039 3' similar to TR:Q13825	Q13825 AU-BINDING PROTEINENOYL-COA HYDKATASE.;	RC3-CT0254-130100-023-f01 CT0254 Hamo sepiens cDNA	Homo sapiens chromosome 21 segment HS21C078	DKFZp434D059_r1 434 (synanym: htes3) Homo sapiens aDNA clane DKFZp434D059 5	SERICIN-2 (SILK GUM PROTEIN 2)	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, atternatively spicoed
Top Hit Detablesse Source	EST_HUMAN	SWISSPROT N	¥	EST_HUMAN 2	IN	EST_HUMAN (	EST HUMAN N			SWISSPROT	EST_HUMAN x	INT IN	EST_HUMAN [		EST_HUMAN I		EST_HUMAN C	Г	╗	T HUMAN	± E		ISSPROT	- L
Top Hit Acessian No.	5.0E-04 AA548931.1	29UKP4	5.0E-04 AF248054.1	5.0E-04 AA156080.1	5.0E-04 M23604.1	5.0E-04 Al188382.1	5.0E-04 AA814519.1	5.0E-04 AA846545.1	6.0E-04 N83786.1		5.0E-04 AWZ70838.1	5.0E-04 U50871.1	5.0E-04 AL048507.2	6.0E-04 AF248054.1	5.0E-04 AA588513.1		4.0E-04 AI720263.1		4.0E-04 AI720263.1		4.0E-04 AL163278.2	4.0E-04 AL048704.1		4.0E-04 AF281074.1
Most Similar (Top) Hit BLAST E Value	5.0E-04	5.0E-04 Q9UKP4	5.0E-04	5.0E-04	5.0E-04	5.0E-04	5.05-04	5.0E-04	5.0E-04	5.0E-04 P29128	5.0E-04	5.0E-04	5.0E-04	5.0E-04	5.0E-04	4.0E-04	4.0E-04		4.0E-04	4.0E-04	4.0E-04	4.0E-04	4.0E-04 096815	4.0E-04
Expression Signal	1.28	0.95	237	5.64	10.72	4.95	0.92	1.57	0.62	0.54	4.55	0.47	1.94	10.61	4.4	1.46	1.6		1.6	2.78	1.57	0.99	1.66	1.8
ORF SEQ ID NO:	28394	29082				34669	35036							31588		26665				27468	28133			29150
SEQ ID NO:	16472	167.70			1	21258	21614	22576	22754	22829	22895	23562	24270	18846	l	L.	13904	ł _	13904	14494	15112	15160	1 1	16233
Probe SEO ID NO:	3424	3728	6549	6784	7602	8289	8646	9632	9726	9876	8888	10840	11320	12022	12296	874	28		848	1461	2082	2143	2835	3178

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Single Exon Probes Expressed in Bone Marrow

- W21121 T-GELL		ļ	
Top Hit Descriptor  Inhitoerto st NCI_CCAP_Cof Homo sepiens cDNA clane IMAGE:96(1930 % similar to gb:MZ1121 T-CELL  SPECIPIC RANTES PROTEIN PRECURSOR (HUMAN);  Inhitoerto st NCI_CCAP_Cof Homo sepiens cDNA clane IMAGE:96(1930 % similar to gb:MZ1121 T-CELL  SPECIPIC RANTES PROTEIN PRECURSOR (HUMAN);  Inhitoerto st NCI_CCAP_Cof Homo sepiens cDNA clane IMAGE:96(1930 % similar to gb:MZ1121 T-CELL  SPECIPIC RANTES PROTEIN PRECURSOR (HUMAN);  Indicator st NCI_CCAP_Cof Homo sepiens cDNA clane IMAGE:96(1930 % similar to gb:MZ1121 T-CELL  SPECIPIC RANTES PROTEIN PRECURSOR (HUMAN);  Indicator st NCI_CCAP_Cof Homo sepiens cDNA clane IMAGE:96(1930 % similar to gb:MZ1121 T-CELL  SPECIPIC RANTES PROTEIN PRECURSOR (HUMAN);  EXTRACTOR SACTIONA-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL  CALCULUA-SENSING RECEPTOR)  Arabidossis theliane DNA chromesome 4, config fregment No. 66  AUTIZO770 MAMIMA1 Homo sepiens cDNA clane IMAGE:144341 3'  MAIN musculus neutropiin-Zelt T) mRA, alternatively spicod, complete cds, alternatively spicod  DRCZ-PRIFUZZI T 781 (syncaym: Insmy2) Homo sepiens cDNA clane IMAGE:119082 3'  INTERNALIN B PRECURSOR  GLUTAMATE DEHYDROGENES 2 PRECURSOR (GDH)  Homo sepiens SWARCA ISO14 Homo sepiens cDNA clane IMAGE:2119082 3'  INTERNALIN B PRECURSOR  GLUTAMATE DEHYDROGENES 2 PRECURSOR (GDH)  Homo sepiens Square A pecudoculaceanal region; segment 1/2  RCO-HT0014.510599 c28 HT0014 Homo sepiens cDNA  PMACHTR839.190200-007-472 HT0339 segment 1/2  Homo sepiens Superior St personal region; segment 2/2  Homo sepiens Superior St personal region; segment 1/2  Homo sepiens Superior St segment HS210078	RC4-NN027-060400-011-b08 NN0027 Homo saplens cDNA	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)	PERCORAST GROW IN TACLOR RECEIPED STREETS ON COLOR STREET
Top Hit Defeabese Source ST HUMAN ST HUMAN ST HUMAN ST HUMAN SWISSPROT NT EST HUMAN SWISSPROT SWISSPR	EST HUMAN	SWISSPROT	SWISSPROT EST_HUMAN
2	3.0E-04 AW893981.1	P23468	3.0E-04 P22807 3.0E-04 AA454055.1
養6男	3.0E-04		
Signal 3,23 3,23 3,23 1,111 1,111 1,111 1,165 1,		0.77	5.18
30257 30257 30258 30484 31010 34321 34321 34321 34321 26187 26286 26895 27878 26895 27878			36589
20020 17378 17378 17378 17378 17378 17378 17328 13280 13280 17328 14882 17482 17757			23205
NO:	7183	7847	10280

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					ı		
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
10538	23460	36957	0.58	3.0E-04	3.0E-04 AI992139.1	EST_HUMAN	wt75s11.x1 Seares_thymus_NHFTh Homo sepiens cDNA clone IMAGE-2513276 3'
10825	23746	37247	7.72		3.0E-04 AA781201.1	EST_HUMAN	e/24g05.s1 Scenes_bestis_NHT Homo sepiens cDNA clone 1391288 3' similar to gtxM36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
12246	26967	31316	3.88	3.0E-04	3.0E-04 AA228301.1	EST HUMAN	nc38e04.rf NCL_CGAP_Pr2 Homo sepiens cDNA clone IMAGE:1010430 similar to contains L1.t2 L1 repetitive element:
12823	1			3.0E-04	3.0E-04 AB018292.1	Ę	Hamo sapiens mRNA for KIAA0749 protein, partial cds
13014			4.33	3.0E-04	3.0E-04 AL134483.1	EST_HUMAN	DKFZp547L185_r1 547 (synonym: hfbr1) Homo sepiens cDNA clone DKFZp547L185 5
177	13278	28204	1.28	2.0E-04	2.0E-04 AF217786.1	ᅜ	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete ods
479			3.55	2.0E-04	AU146707.1	EST_HUMAN	AU146707 HEMBB1 Hamo saplens cDNA clone HEMBB1001253 3'
88			4.01	2.0E-04	2.0E-04 M86524.1	LN LN	Human dystrophin gene
808	13963		4.01	2.0E-04	2.0E-04 M86524.1	Į.	Human dystrophin gene
1183	14224			2.0E-04	2.0E-04 AI286021.1	EST HUMAN	dh88e11.x1 Sogres_NFL_T_GBC_S1 Homo septiens cDNA clone IMAGE:1855052.3' shrilar to contains MER3.b2 MER3 repetitive element:
1180			2.5	20E-04		NT.	Hamo saplens chromosome 21 segment HS21C003
1849	14875		1.19	20E-04		Į.	Mus muscutus 6' flanking region of Pib.3 gene
2194	15209		1.03	20E-04	20E-04 AA478980.1	EST_HUMAN	2139b05.s1 Soeres ovary fumor NICHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element,
							Human garmline T-call receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV16S1, TCRBV14S1, TCRBV3S1, TCRBV14S1,
2381			4.05	20E-04		Ę	TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2>
3000				20E-04	2.0E-04 AH24529.1	EST_HUMAN	am58c09.x1 Johnston frontal contax Homo sapiens cDNA clone IMAGE:1639760 3'
3440		20413		2.0E-04		EST_HUMAN	QV2-BT0638-070500-194-b07 BT0638 Hamo sepiens cDNA
3832	- 1			20E-04	=	EST HUMAN	EST390550 MAGE resequences, MAGP Homo septens cDNA
410/	17747	30812	1 24	205-04	2.0E-04 001028.1	EST HIMAN	Prinsectus wagans mutate requested (PVNVX) gare, comprete cas wadanta ri Scenes, phresi niand NRWPG Home seniens r-DNA done MARE-272558 F
4656	1			20E-04	2.0E-04 H98285.1	EST HUMAN	yu01e11.rl Soares, pineal, gland, N3HPG Homo sapiens cDNA clone IMAGE-232556 5
4834	17851		1.46	20E-04		Ę	Gallus gallus proteasome 28 kDa subunit homotog mRNA, complete cds
02.05	18080	19608	1.21	20E-04	20E-04 H85683.1	EST HUMAN	ys68b08.r1 Soares refina N2b4HR Homo sepiens cDNA clone IMAGE:219927 5' similær to contains L1 repositive element :
5098		30981	1.85	2.0E-04		NT	Danto rerio hagaromo gene, exons 1 to 6, partial cds
5623	L			2.0E-04		EST_HUMAN	AV864352 GLC Hamo sepiens cDNA clone GLCDUH10 3'
5636	18732	31894	1.78	20E-04	20E-04 AIG90862.1	EST_HUMAN	tqQ3b11.x1 NCI_CGAP_U3 Home sepiens dDNA done IMAGE:22077093'

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	Top Hit Descriptor	EST11191 Uterus Homo saptens cDNA 5 and similar to EST containing O family repeat	Homo saptens cell cycle progression 3 protein (UNJ3) mirtyA	Mus musculus G protein coupled receptor gene, complete cas; and unknown gene	AU121712 MAMIMA1 Homo sapiens cDNA clone MAMMA1000/98 5	QV0-CT0387-180300-167-e10 CT0387 Homo septens cDNA	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN- ASSOCIATED PROTEIN)	DKFZp434L2023_r1 494 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2023 5	DKFZp484[2023_r1 484 (synanym: https://doi.org/pians.gDNA.dane.DKFZp484L2023.o	Solanum Iyooparsicum phylochrome F (PHYF) gene, partial cds	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds	Hamo sepiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, camplete cds)	Homo sepiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	Homo sepiens FRA3B common fregile region, diadenosine triphosphate hydrolese (FHIT) gene, exon 5	Human immunoglobulin C(mu) and C(deita) heavy chain genes (constant regions)	arzzarz. st Soares, testis, NHT Homo septers cONA done 1343518 3"	GASTRULA ZINC FINGER PROTEIN ALCURZO.1	RC3-H10254-151089-011-005 H10254 From Septemb CLIVA	ALGOCITATI Sogresa Testis THTI Transportation Court With Call Property Court C	AV/SUS/S DIF TRUITS SEAFRED CLICK AND THE TOTAL SEAFRED CL	HOMO Septems per use 0-11 to recognicing genes, covains a color.	IDITALIXI NCI_CGAP_GGB4 FKING BEPREIS CLAVA GATE IMACL_LITAZAG S Settled in California Fall information	UI-H-BI1-edm-c-04-0-UI.s1 NCI_CGAP_Sub3 Homo sepiens cDNA clone IMAGE:2717190 3'	yz26c09.s1 Soares melanocyte zNbHiM Homo sapiens cDNA clone IMAGE:282864.3' similar to contains	L1,t1 L1 repetitive element;	PERICENTRIN	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCAIL TASE, ENDONUCLEASE)	UI-H-BIO-gab-e-09-0-UI:s1 NCI_CGAP_Sub1 Hamo sepiens curva dane IMAGETZ/U8625 3
	Top Hit Database Source	T_HUMAN		$\neg$	EST_HUMAN		SWISSPROT	SWISSPROT	EST HUMAN	EST_HUMAN	NT	NT	Ę	NT	TA	ᅜ	EST_HUMAN	SWISSPROT	EST HUMAN	EST_HUMAN	EST_HUMAN	¥	EST HUMAN	EST HUMAN		EST_HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN
ORINO	Top Hit Acession No.	2.0E-04 AA296652.1	4758179 NT	2.0E-04 AF140708.1		1	2.0E-04 P08548	54298	2.0E-04 AL043272.2	2.0E-04 AL043272.2	J32444.2	2.0E-04 U32444.2	2.0E-04 AB026898.1	2.0E-04 AB026898.1	2.0E-04 AF020503.1	X57381.1	2.0E-04 AA725700.1	P18715	2.0E-04 BE148303.1	2.0E-04 AA405777.1	2.0E-04 AV730373.1	AJ243213.1	2 OE DA A1440282 4	2.0E-04 AW136740.1		1.0E-04 H99846.1	P48725	P11369	1.0E-04 AW013847.1
	Most Similar (Top) Hit BLAST E Value	20E-04	2.0E-04	2.0E-04 /	2.0E-04	2.0E-04	2.0E-04	2.0E-04 P54298	2.0E-04	2.0E-04	2.0E-04 U32444.2	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04 X57331.1	2.0E-04	2.0E-04 P18715	2.0E-04	2.0E-04	2.0E-04	2.0E-04				1.0E-04	1.0E-04 P48725	1.0E-04 P11369	1.05.04
	Expression Signal	1.15	0.88	0.8	254	0.64	151	124	0.63	0.53	213	213	121	121	1.9	0.58	0.51	99'0	1.21	2.74	3.58	2.59		240	2.7	0.81	2.03	2.61	
	ORF SEQ ID NO:	32417		32878				34215			L	34688	ļ ·					36170	36735		37683			OS LOS		26771			
	SEO ID	18933	19138	19435	20407	20509	20826	20836	21109	21109	21257	21257	2/595	7 596		1	1.				24162	24451	l	24672		13827	L	L_	ΙI
Ī	Probe SEQ ID NO:	5843	6057	8388	545	248	7882	780	1 2	8170	888	8288	8677	8877	894	2000	896	9774	10834	10377	11197	11510		11636	8	88	8	1078	1116

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Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Acession No.	Top Hit Databese Source	Top Hit Descriptor
1118	14160	27111	4.21	1.0E-04	1.0E-04 AW013847.1	EST_HUMAN	UIH-HBIO-eab-609-0-UI.st NCI_CGAP_Sub1 Hamo septems aDNA done IMAGE:2708825 3'
1335	14369		3.08		1.0E-04 U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gena, complete ods
							Kaposi's sercome essociated herpesvirus ORF 68 gene, partial ods; and ORF 69, kaposin, v-RLIP, v-cyclin, latent nuclear antigen, ORF K14, v-QPCR, putative phosphoribosyfromylghornamidine synthese, and LAMP
1632	14685	27840	3.19		1.0E-04 AF148805.1	¥	(LAMP) genes, complete cds
							Kaposi's serooma-associated herpesvirus ORF 68 gene, partial ods; and ORF 69, kaposin, v-FLIP, v-cyclin, ident nuclear antigen, ORF K14, v-GPCR, putative phosphoribosytformylghornamidine synthase, and LAMP
1632	14665	27641	3.19			ΝŢ	(LAMP) genes, complete cds
1878	14903	27903	2.37		1.0E-04 AB048342.1	NT	Equus cabaltus DNA, chromosome 24q14, microsatalitia TKY36
2698	15894				1.0E-04 BE218833.1	EST_HUMAN	hw45c08x1 NCI_CGAP_Lu24 Homo septens cDNA clone INACE:3176368 3
2898	15694	28711	1.05		1.0E-04 BE218833.1	EST_HUMAN	hw45c08.x1 NCI_CGAP_Lu24 Hamo sepiens cDNA clane IMAGE:3176366 3'
3287	16350	28270	1.14		1.0E-04 Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
							tion in the contains Albano septens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive
3748	16790	29702			1	EST_HUMAN	element
4089	17123	30017	2.07	L	1.0E-04 M14042.1	NT	Mouse eights 1 type-IV collegen mRNA
4109	17143	30037	1.04		1.0E-04 AV647727.1	EST_HUMAN	AV647727 GLC Hamo sapiens cDNA dane GLCBBD043'
5132	18141	31019	1.87		7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5132	18141	31020	1.87	L	1.0E-04 7682015 NT	NT	Homo sepiens KIAA0237 gene product (KIAA0237), mRNA
5137	18148	31026	0.92		AB57156.1	EST_HUMAN	φ62h04x1 NCL_CGAP_GC4 Homo septens cDNA done IMAGE:2006975 3*
888	19045			_	1.0E-04 P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6033	19116				1.0E-04 T19815.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
8888	19118		0.52		1.0E-04 T19815.1	EST_HUMAN	76SF Heart Homo sapiens cONA clone 763
6279	19639				1.0E-04 AA177111.1	EST_HUMAN	no02e12.s1 NCI_CGAP_Pr3 Homo seplens cDNA done IMAGE:252
7042	20138	33466	0.68		1.0E-04 AA564561.1	EST HUMAN	n/25e04.s1 NCL_CGAP_AA1 Homo saptens cDNA clone IMAGE:883488 S' stritter to git:M97252 KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); conteitns Alu repetitive element,
7392	1				1.0E-04 AI251980.1	EST HUMAN	qv67d10.x1 NCI_CGAP_Ov62 Homo sapiens cDNA clone IMAGE:1985683 3'
28	•					EST_HUMAN	qv57d10x1 NCI_CGAP_Ov82 Hamo septens cDNA clone IMAGE:1985683.3'
8228	ı				1.0E-04 AA630453.1	<b>EST_HUMAN</b>	ab94g08.s1 Strategene lung (#837210) Hamo septens cDNA clone IMAGE:854654 3'
2696	22845	36102	2.18		1.0E-04 Al806220.1	EST_HUMAN	wf28e08x1 Sogree_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE-2256742 3"
9703	L		1.47		1.0E-04 O88969	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9780	22721		0.63		177163	EST_HUMAN	yd72c08.rf Soares fetal liver spleen 1NPLS Homo saplens cDNA clone IMAGE:113774 5
10004	22831	36394			10863876 NT	¥	Hamo sepiens phospholipid scramblase 1 (PLSCR1), mRNA
10539	23461				1.0E-04 P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10578	23498	36350	0.91		1.0E-04 P08548	SWISSPROT	UNE-1 REVERSE TRANSCRIPTASE HOMOLOG

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Table 4
Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor	Mouse alpha leukocyte interferon gene, complete cds	Homo eaplens mRNA for KIAA1142 protein, partial cds	xw48g12.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'	NEURONAL-GLAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)	NEURONAL-GLAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)	722810.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:3296058 3' stmiler to contains L1.3 L1	repetitive element ;	PM4-NN0091-190700-004-f11 NN0091 Homo sapiens cDNA	ah45c11.s1 Scenes_testis_NHT Homo sepiens cDNA clone 1292468 3'	QV4-SN0023-070400-168-bo4 SN0023 Homo septems cDNA	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR	UI-H-BI1-eer-4-05-0-UI.s1 NCI_CGAP_Sub3 Hamo sepiens cDNA dane IMAGE:2720289 3"	UI-H-BI1-eer-4-05-0-UI.s1 NCI_CGAP_Sub3 Hamo sapiens cDNA done IMAGE-2720289 3'	Homo sepiens gene for cholecystoldnin type-A receptor, complete cds	Homo septens methyl-CpG binding protein 1 (MBO1) gene, expn 15b	xs34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA done IMAGE:2568728 3' similar to contains L1.12.L1	rapetitive etement;	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR	Homo sapiens MSH55 gene, partial ods; and CLIC1, DDAH, G6b, G6c, G6b, G6d, G8e, G6f, BAT5, G5b, CSf(28, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete ods	Pisum sativum mRNA for befa-1,3 glucanase (gns2 gene)	Pisum satiwum mRNA for beta-1,3 glucanase (gns2 gene)	Human platelet-derived growth factor A chain (PDGFA) gene, exons only	wy78a04.x1 Soares_NSF_FB_9W_OT_PA_P_S1 Hamo saplens cDNA clone IMAGE:2554638 37	Mus musculus gene for hexoldnase II, exon 1 (and joined CDS)	Humen heptoglobin and haptoglobin-related protein (HP and HPR) genes, complete ods	2588h01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704583 3' similiar to contains Alu	repetitive element, contains element MSR1 repetitive element;	RC3-CT0208-220899-011-E04 CT0208 Hamo sapiens cDNA	RC3-CT0208-220899-011-E04 CT0208 Hamo sapiens cDNA	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HHU072014	HUM072014F Human foves cDNA Homo sapiens cDNA done EST HFD072014
Top Hit Database Source	IN	FZ.	EST_HUMAN	SWISSPROT	SWISSPROT		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	EST HUMAN	Ę	N		EST HUMAN	SWISSPROT	Ę	Ę	۲	NT	<b>EST_HUMAN</b>	NT	N.		EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	1.0E-04 M28587.1	1.0E-04 AB032968.1	1.0E-04 AW269061.1	203696	203696	-	1.0E-04 BE676399.1	1.0E-04 BE700353.1	9.0E-05 AA718933.1	9.0E-05 AW868218.1	260716	9.0E-05 AW204968.1	9.0E-05 AW204958.1	9.0E-05 D85606.1	9.0E-05 AF120982.1		9.0E-05 AW073078.1	260716	9.0E-05 AF129758.1	8.0E-05 AJ261648.1	8.0E-05 AJ251648.1	8.0E-05 M83575.1	8.0E-05 AW044605.1	8.0E-05 Y11606.1	8.0E-05 M69197.1		8.0E-05 AAZ79333.1	7.0E-05 AW847445.1	7.0E-05 AW847445.1	7.0E-05 L49075.1	7.0E-05 L49075.1
Most Similar (Top) Hit BLAST E Value	1.0E-04	1.0E-04	1.05-04	1.0E-04 Q03696	1.0E-04 Q03696		1.00.04	1.0E-04	9.0E-05	9.0E-05	9.0E-05 Q60716	9.0E-05	9.0E-05	9.0E-05	9.0E-05		9.0E-05	9.0E-05 Q60716	9.0E-05	8.0E-05	8.0E-05	8.0E-05	8.0E-05	8.0E-05	8.0E-05		8.0E-05	7.0E-05	7.0E-05	7.0E-05	7.0E-05
Expression Signal	1.74	1.5	1.46	1.81	1.81		24	1.38	2.39	1.09	1.58	0.67	0.67	2.89	3.13		2.03	3.21	3.02	1.73	7.38	16.0	0.87	0.48	3.06		2.74	6.11	6.11	1	F
ORF SEQ ID NO:		38433		l	38503					28052		L			36137		37864			26831			30415	35493				26358	26359		
Exam SEQ ID NO:	24603	24840	24876				25770	25597	13761	15041	19155	20776	20776	22680	22682		24415	L	25832	13880	ł	ı	17532	22067	24428		25815	13438	13436	13639	13639
Probe SEQ ID NO:	11687	11961	11889	12032	12032		12413	13061	88	2020	6074	78.28	7828	9831	8833		11472	11938	12465	822	865	2961	4507	9101	11485		13050	347	347	989	6993

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Single Exon Probes Expressed in Bone Marrow

Probe Exm NO:	28080 28708 28708 30813 30813 30813 30813 30813 30813 30813 30813 30887 30880 30880 30880 30881	Signal 1,47 1,47 1,53 1,53 1,53 1,53 1,53 1,53 1,53 1,53		Single of hit Acession No.  No.  No.  No.  AL 163278.2  AB000000.1  AL 163278.2  AL 163278.2  AL 163278.2  AL 163278.2  AL 163241.2  AL 163249.2  AL 163264.1  AL 16326.1  AL 163260.1   TOP HIT DEST SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE STANDAN NT EST HUMAN	TOP HIS Detabase Source  PROBABLE QLYCEROL-3-PHOSPHAITE ACYLTRANISFERASE, MITOCHONDRAL PRECURSOR  SWESSPROT (CPAT)  Heno septems chromosome 21 segment HSZICOM  EST HUMAN WIGHOR Test brain, Strategene cDNA clane BMAGE-980893  EST HUMAN NO septems seroughcan the septems CDNA clane BMAGE-980893  EST HUMAN NO SEPTEMBER STRANDSON HERSICOM  MI Heno septems chromosome 21 segment HSZICOM  EST HUMAN NO SEPTEMBER SEROUGHCAN CORD (CRORPS) mRNA clane BMAGE-980893  EST HUMAN NO SEPTEMBER SEROUGHCAN CORD (CRORPS) mRNA clane BMAGE-980893  EST HUMAN NO SEPTEMBER SEROUGHCAN CORD (CRORPS) mRNA clane BMAGE-980893  MI Humo septems chromosome 21 segment HSZICOM  MI Heapless flow-sorted chromosome 6 throat in segmen cDNA clane BMAGE-2808013 semilar to septems chromosome 6 throat in segmen cDNA clane BMAGE-2808013 semilar to septems chromosome 6 throat in segmen cDNA clane BMAGE-2808013 semilar to septems chromosome 6 throat in segmen cDNA clane BMAGE-2808013 semilar to septems chromosome 6 throat in segmen cDNA clane BMAGE-2808013 semilar to septems chromosome 6 throat in segmen cDNA clane BMAGE-2808013 semilar to throat segmen cDNA clane BMAGE-2808013 semilar to throat segmen cDNA clane BMAGE-2808013 semilar to throat segmen cDNA clane BMAGE-2808013 semilar to confront AVTZ2842 TITB Homo septems cDNA clane HTBBEDTS 6  SWISSPROT CONFACTIN PRECURSOR (CLYCOPROTEIN OFFICE)  EST HUMAN AVTZ2842 TITB Homo septems cDNA clane BMAGE-2808013 semilar to confront AVTZ2842 TITB Homo septems cDNA clane BMAGE-2808014 CDNACTIN PRECURSOR (CLYCOPROTEIN OFFICE)  EST HUMAN AVTZ2842 TITB Homo septems cDNA clane BMAGE-2808016 CDNACTIN PRECURSOR (CLYCOPROTEIN OFFICE)  EST HUMAN AVTZ2842 TITB Homo septems cDNA clane BMAGE-2808016 CDNACTIN PRECURSOR (CLYCOPROTEIN OFFICE)  EST HUMAN AVTZ2842 TITB Homo septems cDNA clane BMAGE-2808016 CDNACTIN PRECURSOR (CLYCOPROTEIN OFFICE)  EST HUMAN AVTZ2842 TITB Homo septems cDNA clane BMAGE-2808016 CDNACTIN PRECURSOR (CLYCOPROTEIN OFFICE)  EST HUMAN AVTZ2842 TITB Homo septems cDNACTIN PRECURSOR (CLYCOPROTEIN OFFICE)  EST	
Example 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	- I fine I alaka hakalalah kalal alahahahahalahahalah musimini		Same Series Seri	Host Nost Nost Nost Nost Nost Nost Nost N	Signes (Top) Hit Acoust Similar (Top) Hit Acoust Signes (Top) Hit Acoust Signe	Signes (Top) Hit Acoust Similar (Top) Hit Acoust Signes (Top) Hit Acoust Signe

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Single Exon Probes Expressed in Bone Marrow

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					CIR III		Igle Later I come Lapresca III come Internation
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Defaberse Source	Top Hit Descriptor
4483	17518	30405	2.41	3.0E-05	3.0E-05 AA368679.1	EST_HUMAN	EST79996 Placenta I Homo sepiens cDNA similar to similar to p53-associated protein
4483	17518	30406	2.41	3.0E-05	3.0E-05 AA368679.1	EST_HUMAN	EST79996 Placenta I Homo septens cDNA similar to similar to p53-associated protein
<del>8</del> 28	17841		2.0	3.0E-05	3.0E-05 AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2887	18733	31895	1.76	3.0E-05	11072102 NT	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Mylc2pl), mRNA
<b>1209</b>	16671		1.18	3.0E-05	3.0E-05 AJ225782.1	Ŋ	Homo sapiens SYBL1 gene, exons 6-8
6024	10071	33268	1.18	3.0E-05	3.0E-05 AJ225782.1	F	Homo sapiens SYBL1 gene, exons 6-8
08230	L.		2.48	3.0E-05	BE733157.1	EST_HUMAN	601667451F1 NIH_MGC_21 Home sepiens cDNA dane IMAGE:3842202 6
8695	L		1.68		3.0E-05 AA284049.1	EST_HUMAN	zs60b05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
8244		35641	1.54		3.0E-05 AW770982.1	EST_HUMAN	hB4e08 x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
9248	22214		1.37	3.0E-05	6912431 NT	INT	Homo sapiens interfeukin-1 receptor entagonist homolog 1 (IL1HY1), mRNA
9252	22218	35649	0.59	3.0E-05 P43361	P43361	SWISSPROT	MELANOWA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
<b>8</b>	. 22450		0.51	3.0E-05	3.0E-05 X03273.1	IN	Human Alti-family cluster 5' of alpha(1) ecid glycoprotein gene
8875	22628	38081	12	3.0E-05	3.0E-05 AA372562.1	EST_HUMAN	EST8475 Colon adenocarcinoma IV Homo sapiens cDNA 6' end
10021	22948		3.24	3.0E-05	3.0E-05 Al769331.1	EST_HUMAN	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Horrio sapiens cDNA clone IMAGE:2367209.3'
10901	23821	37330	08.0	3.0E-05	3.0E-05 Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
10901	23821	37331	0.89	3.0E-05 Q62918	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
12353	25147		1.49	3.0E-05	3.0E-05 L77570.1	INT	Homo sepiens DiGeorge syndrome critical region, centromeric end
							ch88e11.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone INAGE:1855052.3' similar to contains
2332	- 1			١	2.0E-05 AI286021.1	EST_HUMAN	MLKS.DZ MLKS repetutve evennent;
2587	15588	28605	2.2	20E-05	20E-05 M13792.1	NT.	Human adenceine deaminase (ADA) gene, complete cds
2726	16719		86.7	2.0E-05	2.0E-06 AA180582.1	EST HUMAN	zq48a12.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632734 6' similiar to contains Alu repetitive element, contains element L1 repetitive element;
3152	L	28128	1.15	2.0E-05	2.0E-05 BE088038.1	EST HUMAN	RC3-BT0319-120200-014-h08 BT0319 Homo sepiens cDNA
3359	16409		0.88	2.0E-05	2.0E-05 AF184614.1	N	Homo sapiens p47-phox (NCF1) gene, complete cds
3382		28359	1.35	2.0E-05	20E-05 X89211.1	INT	H, saplens DNA for endogenous retroviral like element
3505	16552		0.7	20E-05	2.0E-05 X95465.1	ħ	S.cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3820	L.		69.0	2.0E-05	2.0E-05 AI.039107.1	EST_HUMAN	DKFZp568i084_r1 568 (synonym: hffat2) Homo sapiens cDNA clone DKFZp568i084 5
472	17740		-	2.0E-05	2.0E-05 BE378471.1	EST_HUMAN	601236456F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3608663 5
29852	18943	32128	1.57	2.0E-05	2.0E-05 AJ011712.1	NT	Homo expiens TNNT1 gene, exons 1-11 (and joined CDS)
6024	19107		0.65	2.0E-05	2.0E-05 AF028308.1	Ę	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsthogen gene families
6082	19.82	\$7878	88.0	2 0F-05 0131R3	013183	SWISSPROT	RENAL SODIUMDICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
	ı	1					

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Single Exon Probes Expressed in Bone Marrow

	scriptor	ER (NA(+)/DICARBOXYLATE	Homo sepiens cDNA clone IMAGE:1715114 3'		te IMAGE:1238519 3'		ne IMAGE:2030003 3' similar to TR:002711	apiens cDNA clone IMAGE:2522077 3'	9), HaxA7 (HaxA7), HaxA6 (HaxA6), HaxA5 2), and HaxA1 (HaxA1) genes, complete cds	9), HoxA7 (HoxA7), HoxA6 (HoxA8), HoxA5 2), end HoxA1 (HoxA1) genes, complete cds	TT) mRNA, INMT-2 allele, complete cds	A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, lic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, 7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>	18 IMAGE:2108369 3	TCBAP2E1590 Pediatric pre-B cell acute lymphobiastic leukernia Baykor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1690	TCBAPZE1590 Pediatric pre-B cell acute lymphoblastic leukemia Baykor+KGSC project=TCBA Homo saplens cDNA clone TCBAP1590	නස)	<b>2</b> 055)		ne IMAGE:3340578 5'	Homo sepiens cDNA clone IMAGE-259570 5	Hamo sapiens cDNA cione IMAGE:269570 5
Ingle Exon Frones Expressed in Borre Mairow	Top Hit Descriptor	RENAL SODIUMDICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)	qc72a02.x1 Soares_placenta_8tx9weeks_2NbHP8tx9W Homo sepiers cDNA clone IMAGE:1715114.3 smiler to contains L1.13 L1 repetitive element;	CALCIUM-BINDING PROTEIN	nw06d12.s1 NCI_CGAP_SS1 Hamo septems cDNA clane IMAGE:1238519.3"	P.falciparum mRNA for AARP1 protein, partial	qz47b06x1 NG_CGAP_Kd11 Homo sepiens cDNA clone IMAGE:2030003 3' similer to TR:002711 O02711 PRO-POL-DUTPASE POLYPROTEIN;	w.1351/07.x1 Scares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA4), HoxA4 (HoxA4), HoxA3 (HoxA2), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds	Heterodontus francisci HaxA10 (HaxA10), HaxA9 (HaxA9), HaxA7 (HaxA7), HaxA6 (HaxA8), HaxA5 (HaxA5), HaxA3 (HaxA3), HaxA2 (HaxA2), end HaxA1 (HaxA1) genes, complete cds	Homo sapiens indolethylamine N-methyltransferase (II	Human germline T-cell receptor beta chein TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1P, TCRBV16S1, TCRBV16S1, TCRBV16S1, TCRBV16S1, TCRBV16S1, TCRBV4S1, TCRBV4S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2>	INZONO5x1 NCI_CGAP_CLL1 Homo sepiens cDNA done IMAGE:2108389 3	TCBAPZE1590 Pediatric pre-B cell acute lymphoblast cDNA clone TCBAP1690	TCBAPZE1590 Pediatric pre-B cell acute lymphoblassi cDNA clone TCBAP1590	COMPLEMENT DECAY ACCELERATING FACTOR (CD55)	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)	Homo sapiens chromosome 21 segment HS21C007	7775g09.y1 NCI_CGAP_Brn20 Homo sapiens cDNA clone IMAGE:3340576 5	yw91e08.r1 Soeres_placenta_8to9weeks_2NbHIP8to8W Homo sapiens cDNA clone IMAGE-259570 5	EST_HUMAN   yw91a08.r1 Soares_placerta_glo9weeks_2NbHP8tc9W Homo sapiens cDNA cione IMAGE:269570 5
ZOU FIODES D	Top Hit Detabase Source	SWISSPROT	EST_HUMAN	SWISSPROT	EST_HUMAN	¥	EST_HUMAN	EST_HUMAN	Į,	<b>7</b>	¥	ŢN	EST_HUMAN	EST HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	IN	EST_HUMAN	EST_HUMAN	EST HUMAN
Single	Top Hit Acession No.	Q13163	2.0E-05 AI149272.1	P35085	2.0E-05 AA714330.1	2.0E-05 Y08928.1	2.0E-05 AI482960.1	2.0E-05 A1991025.1	2.0E-05 AF224282.1	2.0E-05 AF224282.1	2.0E-05 AF128847.1	U68061.1	20E-05 AI381040.1	2.0E-05 BE244840.1	20E-05 BE244840.1	P49457	2.0E-05 P49457	AL163207.2	2.0E-05 BF055939.1	2.0E-05 N41751.1	2.0E-05 N41751.1
	Most Similer (Top) Hit BLAST E Veitue	2.0E-05 Q13183	2.0E-05	2.0E-05 P35085	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.05-05	2.0E-05	2.0E-05   U66061.1	20E-05	2.015-05	205-05	20E-05 P49457	20E-05	205-05	2.0E-05	2.0E-05	2.0E-05
	Expression Signal	0.86	0.68	0.49	232	1.52	76.0	8.62	2.22	22	0.81	0.5	1.25	0.52	0.62	0.57	0.57	0.67	0.87	21	2.1
	ORF SEQ ID NO:	32374		32667	33116	33322	33338		33679	33880		34484		35881	35882		_			37387	37388
	Exam SEQ ID NO:	19162		l		•	1		20330	20330	20553	21095	21186	2244	ł	L.		<u> </u>	L	23874	73874
	Probe SEO ID NO:	6082	8	8358	8778	2882	7089	7108	7360	7360	7592	8157	<b>6247</b>	7748	24,4	2288	8622	10283	10494	10954	10954

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Single Exon Probes Expressed in Bone Marrow

igie exon probes expressed in Bone Matrow	Top Hit Descriptor	WLSSN07.x1 Scares_Dieckgraefe_colon_NHCD Homo sepiens cDNA clone IMAGE:2522077 3*	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA	hw21803.x1 NCI_CGAP_KId11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832 Q12832 GLYCOPHORIN HEP2;	Homo sapiens ABCA1 (ABCA1) gene, complete cds	AU131513 NTZRP3 Hamo septens cDNA clane NTZRP3002707 5	Homo sapiens chromosome 21 segment HS21C082	Drosophila melanogaster strain Lamto 120 Suppressor of Hairless (Su(H)) gene, partial cds	Homo sepiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial ods, alternatively spited	MOSAIC PROTEIN LCN	Hamo sepiens chromosome 21 segment HS21C003	ZW69g04.r1 Scares_testis_INHT Homo sepiens cDNA clone IMAGE:781494 5	xy48g11x1 NCL_CGAP_Lu34.1 Hamo sapiens oDNA clone IMAGE:2866548 3'	H. saptens repeat region	Homo septiens Spest gene for spastin protein	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	rs19g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114.3' similar to contains L1.t1 L1 repositive element:	Hamo sepiens phospholipase A2, group X (PLA2G10) mRNA, and translated products	7p57d01x1 NCI_CGAP_Pr28 Homo sepiens cDNA done IMAGE:3649945 3' similar to contains MER10.b3 MER10 resolutive element:	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))	Homo sapiens chromosome 21 segment HS21C027	2235h12.s1 Soaras, total fetus, Nb24F8 9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb.102932 PEROXISOME PROLIFERATOR, ACTIVATED RECEPTOR ALPHA (HUMAN);	2805e11.r1 NCI_CGAP_GCB1 Homo septens cDNA done IMAGE:684332 5' stmiler to contains Atu		AV732180 H I F Homo septens cDNA ctone H I FBIHO1 5	hd41b02.x1 Soares_NR_T_GBC_S1 Homo sapients cDNA clone IMAGE:2912043 3' similar to contains OFR.t1 OFR repetitive element;	hd41b02x1 Sceres_NR_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2912043 3' similar to contains OFR.t1 OFR repetitive element;	UHHBIZ-egike-08-0-Ui.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
Stori Frodes E	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	N <sub>T</sub>	EST_HUMAN	N.	NT	Į.	SWISSPROT	Ę	EST_HUMAN	EST_HUMAN		LN.	SWISSPROT	EST HUMAN	ı	HIMAN	Т	N.	EST HUMAN		Т	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
albinc	Top Hit Acessian Na.	2.0E-06 A1991025.1	2.0E-05 BE175801.1	2.0E-06 BE348229.1	20E-05 AF275948.1	2.0E-05 AU131513.1	1.0E-05 AL163282.2	1.0E-05 AF088273.1	1.0E-06 AF223391.1	281274	2	1.0E-05 AA431119.1	+		1.1	208548	1.0E-05 AA641848.1	4505844 NT	1 0F.05 RF222848 1		1.0E-05 AL1632Z7.2	1.0E-05 AA452578.1	4 OE 04 A 220440 4	W230110.1	1.0E-05 AV732190.1	1.0E-05 AW510902.1	1.0E-05 AW 510802.1	W291521.1
	Most Similar (Top) Hit BLAST E Value	20E-05/	2.0E-05	2.0E-05	20E-05/	20E-05/	1.0E-05/	1.0E-05/	1.0E-05/	1.0E-05 P81274	1.0E-05/	1.0E-05/	1.0E-05/	1.0E-05 Z18943.1	1.0E-05/	1.0E-05 P08548	1.0E-05/	1.08.05	1 OF 05 P	1.0E-05 P19474	1.0E-05	1.0E-05/	20 00 4	100-10-1	1.0E-05/	1.0E-05	1.0E-05	1.0E-05
•	Expression Signal	2.01	1.9	6.5	1.54	1.49	3.2	1.88	1.17	10.43	1.52	1.77	1.82	96.0	1.03	0.52	3.02	8.81	990	1.5	2.45	2.22	2	3.4	0.82	0.79	0.79	1.11
ŀ	ORF SEQ ID NO:		37457			31759	28715	29621		28940	30119	30213	30798	30907	33262	31281	33370	33594	34252			35818	38	Conso	36201	36608	36610	36685
	SEQ ID	20042	23838	25740	25727		15902	16706	16866	170071	17232	17335	17804	18019	19987	18360	20063	20200	20864	20802	22232	22380	98966	8	22748	23123	23123	23201
	Probe SEQ ID NO:	11006	11781	12473	12626	12768	2705	3863	3828	888	4201	4306	4887	2005	6915	7028	7288	8872	ě	8057	8978 8	9415	58	200	हु	10198	10198	10278

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	Top Hit Descriptor	UI-H-BI2-egk-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sepiens cDNA clone IMAGE:2724398 31	he07c10.x1 NCI_CGAP_Kid12 Homo sepiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1 repetitive element;	Human hereditary hasmochromatosis region, histone 2A-life protein gene, hereditary hasmochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds	Human hereditary haemochromatosts region, histone 2A-life protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds	Hamo sapiens chromosoms 21 segment HS21C103	tt73406.x1 NCI_CGAP_HSC3 Hamo septens cDNA clane IMAGE:2246386 3'	qg11b08x1 Soares_placenta_8tc0wecks_2NbHP8tc0W Homo sepiens cDNA clone INAGE:1756191 3'	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2	Homo septens differentiation antigen CD20 gene, exons 5, 6	RC1-BT0313-110500-017-607 BT0313 Homo sepiens cDNA	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	ox20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656912.3' similar to contains Atu receitifie element.	Hamo sapiens chromosome 21 segment HS21C009	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED	BY V-SRC)	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED	BY V-SRC)	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C	RC3-CT0283-201199-011-h11 CT0283 Homo septems cDNA	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)	abs0710.s1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' stmilar to contains	MER20.tl MER20 repetitive element;	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA	qw18g09.x1 NG_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:1891296 3' similar to contains Atu repetitive element;
-	Top Hit Datebase Source	EST_HUMAN UI+	EST HUMAN 1920	H (H)	Htm (HL	NT Han	EST_HUMAN #73	EST_HUMAN qg1	NT Hu	NT Hon	EST_HUMAN RC	SWISSPROT LIN	EST HIMAN SON	T		SWISSPROT BY		SWISSPROT BY		SWISSPROT PU	EST_HUMAN RC		SWISSPROT FA		HUMAN		EST_HUMAN ela
	Top Hit Acession No.	1.0E-05 AW291521.1	1.0E-05 AW46895.1		_		9.0E-06 A1583811.1	F.			9.0E-06 BE065042.1		,			,			1		8.0E-06 AW362539.1				7.0E-06 AA669729.1	7882177 NT	7.0E-06 A1368252.1
-	Most Similar (Top) Hit BLAST E Value	1.0E-05/	1.0E-05	1.0E-05 U91328.1	1.0E-05 U91328.1	1.0E-05/	9.0E-06	9.0E-06	9.0E-06 M81755.1	9.0E-06 L23416.1	90E-08	9.0E-06 P08547	90 20 0	9.0E-06		9.0E-06 Q63769		9.0E-06 Q63769	90E-06	9.0E-06 Q10364	8.0E-06	8.0E-06 P34083	8.0E-06 P34083		7.0E-08	7.0E-06	7.0E-06
	Expression Signal	1.11	1.85	1.79	1.79	1.43	6.9	4.25	2.82	2.31	57.0	0.94	70 77	, ¢		251		2.51	4.44	3.65	223	19.0	0.64		214	3.05	7.94
}	ORF SEQ ID NO:	38888		37740	37741	31421		82082		32291				25.200		35728		35729	35990							27444	
	Edga SEQ ID NO:	23201			24216	25900	15676	16169	L		L			2477.4		22289		22299	22539	1	1	ı	1		14031	14467	1.
	Probe SEQ ID NO:	10276	10544	11284	11264	12941	2680	3112	3624	808	ğ	7674	2	300	3	8834		9334	1128	11286	2535	10898	1080		866	1433	2884

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Single Exon Probes Expressed in Bone Marrow

gie Exoli Ploues Expressed in Boile mairow	Top Hit Descriptor	П		y 1y65c07.r1 Soares_multiple_sclerosts_ZNIbHMSP Hamo sapiens cDNA clane IMAGE:278412.5	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF68S1E), mRNA	Г				OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)	0x08e02.x1 Soares_fetal_liver_spieen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:1655738 3' similar to contains MER8.t2 MER8 repetitive element;	Mus musculus E-cadherin binding protein E7 mRNA, complete cds	Г	Г	Homo sepiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA	Homo sepiens chromosome 21 segment HS210046	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds	Homo sapiens gene for LECT2, complete ods		Г				T	П	٦				Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
CAUI FIOUE	Top Hit Datebase Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	Ę	SWISSPROT	<b>EST_HUMAN</b>	EST_HUMAN	<b>EST_HUMAN</b>	SWISSPROT	EST HUMAN	N E	SWISSPROT	EST_HUMAN	노	TN.	Ę	¥	EST_HUMAN	<b>EST_HUMAN</b>	<b>EST_HUMAN</b>	SWISSPROT	<b>EST_HUMAN</b>	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	N.
Althie California	Top Hit Acession No.	7.0E-06 AA385542.1	7.0E-06 AW883141.1	7.0E-08 N98845.1	11420709 NT		7.0E-06 BF215972.1	8.0E-08 BE069189.1	6.0E-06 BE069189.1	Q01458	6.0E-06 Al040099.1	8.0E-06 AF167441.1	002040	6.0E-06 AW801912.1	11418157 NT	5.0E-06 AL163246.2	5.0E-06 U07561.1	5.0E-06 AB007548.1	5.0E-06 AW856972.1	5.0E-06 AW856972.1	5.0E-06 AA313620.1	0,28039	5.0E-08 A1065045.1	4.0E-06 R16267.1	4.0E-06 AW103354.1	4.0E-06 Al334928.1	4.0E-06 Al334928.1	4.0E-06 BF365612.1	4.0E-06 AW015401.1	4.0E-06 AF198349.1
	Most Similer (Top) Hit BLAST E Vaiue	7.0E-06	7.0E-08	7.0E-08	7.0E-06	7.0E-08 Q61147	7.0E-06	8.0E-08	8.0E-08	6.0E-06 Q01458	6.0E-06	8.0E-06	6.0E-06 Q02040	8.0E-08	8.0E-06	5.0E-06	5.0E-08	5.0E-06	5.0E-06	5.0E-06	5.0E-06	5.05-08 0.28039	5.0E-08	4.0E-06	4.0E-06	4.0E-06	4.0E-06	4.0E-06	4.0E-08	4.0E-06
	Expression Signal	0.78	5.16	0.81	0.7	0.54	2.83	127	1.08	2.35	2.54	1.41	1.05	1.52	1.74	3.86	3.96	41.1	0.49	0.49	7.1	2	2.14	6.59	6.33	4.22	4.22	2.58	3.05	0.94
	ORF SEQ ID NO:			32179	35533			28907	29664	28636	80208	31403	31495		31700	32487	32784	33762	35186	35196	28877			28835	26861	27340	27341	27477	28313	
	SEQ ID NO:	1	18872	18989	22107	23185	<u> </u>	15988	16749	16010	17811	18526	18583	1	26582	19254	19536	20410	21770	21770	23384	24972	25512	13714	13903	14371	14371	14503	15287	16133
	Probe SEQ ID NO:	3578	5780	6902	9141	10280	12202	2828	3706	4785	4784	5422	2488	10215	13041	6179	6471	744	8888	8803	10462	12101	12928	88	84	1337	1337	1470	2274	3076

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Table 4
Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor		KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)	AV657555 GLC Homo septens cDNA clone GLCFDB05 3"	2p02e05_r1 Strategene overten cancer (#637219) Homo sapiens cDNA clone IMAGE:565232 5	ULH-BIS-eky-6-05-0-ULs1 NCL_CGAP_Sub5 Hamo sepiens aDNA dane IMAGE:2736178 3"	Mus musculus gene for odorant receptor A16, complete cds	on34h01.s1 NCI_CGAP_Lu5 Homo sepiens cDNA clone IMAGE:1568609 3' strillar to contains Alu repestive element.	165/105.X1 Scares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2080241 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;	wj80b04.x1 NCI_CGAP_Lym12 Hamo septens aDNA dane IMAGE:2410063 3"	MR3-SN0067-1/20400-002-f02 SN0067 Homo septens dDNA	A447R Heart Homo sapiens cDNA clone A447	zh27c11.s1 Soares, pineal, gland, N3HPG Homo sapiens dDNA done IMAGE:413300 3' shrifar to TR:P70467 P70467 REVERSE TRANSCRIPTASE;	y437c04.11 Scenes overy tumor NbHOT Homo sepiens cDNA clone IMAGE:235974 5' shrifer to gb:X74929 KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);	Homo septems glyptican 3 (GPC3) gene, partial cds and flanking report regions	Homo septems glyptican 3 (GPC3) gene, partial cds and flanking repeat regions	#16g10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE-2141730 3'	yw68e03.s1 Soares_placenta_8to9weelss_2NbHP8to9W Homo saplens cDNA clone IMAGE:257212.3°	AV748989 NPC Hamo sepiens cDNA clane NPCAXD05 5	PYRIN (MARENOSTRIN)	PYRIN (MARENOSTRIN)	PROTEIN MOV-10	ORGANIC CATIONICARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH	AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)	Mus musculus DGWMSE protein (DGMm5e) mrtNA, complete cos	MEROZOITE SURFACE PROTEIN CMZ-8	Homo sapiens chromosome 21 segment HS21C078	zi08a12.s1 Soares_fetal_fiver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428882.3' similar to contains Alu repetitive element;	200812.s1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:428982 3' similar to contains Alu repetitive element.
Top Hit Database	Source	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Z	Ę	EST HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	SWISSPROT		SWISSPROT	노	SWISSPROT	보	EST_HUMAN	EST HUMAN
Top Hit Acession	<u> </u>	206719	2.0E-06 AV657555.1	2.0E-06 AA173518.1	1W450215.1	2.0E-06 AB030898.1	2 OF-06 AA974632 1	2.0E-06 AI53948.1	2.0E-06 AI819424.1	2.0E-06 AW869223.1	F12238.1	2.0E-06 AA772497.1	2.0E-06 H62051.1	2.0E-06 AF003529.1	2.0E-06 AF003529.1	2.0E-06 AI473450.1	2.0E-06 N30578.1	2.0E-06 AV748969.1	015553	015553	P23249		076082	1.0E-06 AF084364.1	P09125	1.0E-08 AL163278.2	1.0E-06 AA034141.1	1.0E-06 AA034141.1
Most Similar (Top) Hit	Vatue	2.0E-06 P06719	2.0E-08	2.0E-06	2.0E-06	2.0E-06	2.05.08	2.0E-06	2.0E-06	2.0E-06	20E-06 T12238.1	2.0E-06	2.0E-06	2.0E-06	20E-08	2.0E-06	2.0E-06	2.0E-06	2.0E-06 015553	2.0E-06 015553	2.0E-06 P23249		1.0E-06 O76082	1.05-06	1.0E-06 P09125	1.0E-08	1.0E-08	
Expression	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2.	62.1	1.56	0.67	1.74	a c	880	5.37	0.81	0.63	0.61	1.88	0.87	0.87	0.48	0.92	0.61	221	221	2.87		3.02	1.98			122	
ORF SEQ		28594	28500					32544			34806		36596	Į.		ļ	38454		38581	38582					27454			
Exan SEQ ID	ÿ	16674		<u></u>	L.	L		.l	19641	21219	L			1_		22553	<u> </u>			1	1	ı	13158		l	_		1
Probe SEQ ID	Ö	2573	3531	3774	3783	3789	anca	6241	6581	8250	8428	9188	8200	8671	9571	<u>8</u>	10059	10278	1211	1211	12545		88	858	1445	1527	1578	1576

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Top Hit Descriptor	ws84h05x1 NCI_CGAP_Cos Hamo septems cDNA clame IMAGE:2504697 3'	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exams 1-8	HISTONE DEACETYLASE 6 (HD5) (HISTONE DEACETYLASE MHDAT)	HISTONE DEACETYLASE & (HDS) (HISTONE DEACETYLASE MHDA1)	Homo saplens chromosome 21 segment HSZ10007	xy48g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2850048 3	601676748F1 NIH_MGC_21 Homo sepiens cDNA clone IMAGE:3969661 6	601676748F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:38595051 5	Homo explens chromosome 21 segment HS210018	wi81b08.x1 NCI_CGAP_Kdf12 Homo sapiens cDNA clone IMAGE::2389703 3	wi81b08.x1 NCI_CGAP_Kid12.Hamo sapiens cDNA clane IMAGE:2389703 3	PM1-BN0083-030300-003-e12 BN0083 Homo sepiens cDNA	Human microfibril-essociated glycoprotein (MFAP2) gene, putative promoter region and atternatively spiloed impensioned errors	Homo saplens Xq pseudosurbsomal region; segment 1/2	Himmen advancable microstratific DNA	numeri payring and permittee consect and 2 Visation 018 aliele	numar ign subject i gamme gare, cours i am 2, 1-25-10 i am 1, 1-15-10 i am 1,	n#56b09.s1 NCL_CGAP_Ov2 Homo septens cDNA clone IMAGE_3802225 smular to contents Au repairuve element,contains L1.t3 L1 repetitive element ;	Human polymorphic microsatellite DNA	NRO-BN0115-020300-001-111 BN0115 Homo saplens cDNA	MR0-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA	yd50f12.r1 Soares fetal liver spieon 1NFLS Homo sepiens cDNA clone IMAGE:111695 5	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR	OVOSTATIN PRECURSOR (OVCMACROGLOBULIN)	AVESO201 GLC Hamo sapiens aDNA dane GLCCCD01 3'	we86b12.x1 Soares_NR_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2347867 3"	yc14h09.s1 Stratagene lung (#037210) Homo sapiens cDNA clone IMAGE:80705 3' strritar to strritar to gb.M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)	ye14h09.s1 Stratagene lung (#637210) Homo sapiens cDNA clone IMAGE:80705 S' similar to similar to gb.M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)	WNT-14 PROTEIN PRECURSOR
Selon Top Hit Database Source	EST_HUMAN		SWISSPROT	/ISSPROT	Į			T_HUMAN	. ]			EST_HUMAN	Ę				Ž	EST HUMAN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	SWISSPROT	SWISSPROT
Top Hit Acession No.	4.0E-07 AW009602.1	4.0E-07 AJ272285.1			4.0E-07 AL163207.2	4.0E-07 AW419134.1	4.0E-07 BE901975.1	4.0E-07 BE901975.1	4.0E-07 AL163218.2	4,0E-07 AI765528.1	4.0E-07 AI765528.1	4.0E-07 BE001828.1	140740.4	3.0E-0/ 0 19/ 19.1	2004 40.4	M99149.1	W64857.1	3.0E-07 AA526763.1	3.0E-07 M99149.1	3.0E-07 BE005077.1	3.0E-07 BE005077.1	T84704.1	P38739	P20740	3.0E-07 AV650201.1	3.0E-07 AI797238.1	3.0E-07 T57850.1	3.0E-07 T57850.1	088807	042280
Most Similar (Top) Hit BLAST E Vatue	4.0E-07	4.0E-07	4.05-07 0922/6	4.0E-07 Q9Z2V6	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4,0E-07	4.0E-07	4.0E-07	2 0 00 0	3.0E-07	3.00-01	3.0E-07 M99149.1	3.0E-07 M64857.1	3.0E-07	3.0E-07	3.0E-07	3.0E-07	3.0E-07 T84704.1	3.0E-07 P38739	3.0E-07 P20740	3.0E-07	3.0E-07	3.0E-07	3.05-07		
Expression Signal	1.81	0.81	1.3	1.3	0.63	5.52	0.48	0.48	0.47	2.6	2.6	272	ļ	9.47	9.1	2.82	2.45	1.01	258	6.03	6.03	0.8	1.71	0.74		0.81				
ORF SEQ ID NO:	29984		33804	33805	34634	35806	36904	36905	37105		37764				/0007				28330						L	30706				
Exen SEQ ID NO:	17062	20354	20448	20448		22371	$\mathbf{l}_{-}$	23408	23610	24234	24234	_	<u>l</u>	13515			14683	15080	1	L	15481		1_	1_	1_	1	l			1 1
Probe SEQ ID NO:	4024	7382	7482	7482	8255	9408	10488	10486	10688	11284	11284	11555		4	8	1375	<u>88</u>	2062	2296	2477	2477	3047	3173	4708	4758	4796	5408	8408	6749	6085

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	Top Hit Descriptor		oc04c10.s1 NCI_CGAP_GCB1 Hamo saplens cDNA clane IMAGE:1338890 3'	QV1-UM0036-200300-115-g02 UM0036 Home sapiens cUNA	[WZ6f11.x1 NC]_CGAP_Ov35 Homo septens cDNA clone IMAGE:2261037 3' similar to contains Ature repetitive element contains element MSR1 MSR1 repetitive element;	Rettus norvegious mRNA for 45 kDa secretory protein, partial	Homo septens TRF2-interacting telomento RAP1 protein (RAP1) mRNA, complete cds	Homo sapiens Di George syndrame critical region, telomenic end	Homo sapiens DiGeorge syndrome critical region, telomenic end	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cas and itanking repeat regions	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;   ENDONUCLEASE]		zr08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' stmilar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN);contains Alu repetitive element;	vc15g04.srl Stratagene lung (#837210) Homo sepiens cDNA clone IMAGE:80790 3' similar to contains L1	repetifive element;	I/6 AUTOANTIGEN	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I	601818816F1 NIH_MGC_58 Hamo sepiens cDNA clone IMAGE:4044891 5	Hamo sepiens caveolin 1 (CAV1) gene, exon 3 and partial ods	WAZONO4.X1 NCI_CGAP_Lym12 Homo sapiens cDNA clone (MAGE:24128193'	RC3-NN0066-280400-021-g11 NN0066 Homo sapiens cDNA	UHHBI3-eite-b-01-0-UI,st NCI_CGAP_Sub5 Hamo sapiens cDNA ctare IMAGE:2734408 3	4g56d05x1 Scares_testis_NHT Hamo septems cLNA ctone IMAGET8391773	Infrase 6.51 NCI_CGAP_LIP2 Homo septens cUNA cione IMAGE: 1001836 similiar to contants Aufrichouvre	dement,	AV728390 HTC Homo saplens cDNA cone HTCAEC92 5	227g09.s1 Soares, pregnant uterus, NDHPU Horib sapens curvi cione invivor-171000 5	Hamo sepiens chranosome 21 segment HS21C103	CAA+NN0003-280300-124-e06 NN0003 Homo saplens GDNA	COMPLEMENT FACTOR B PRECURSOR (CA/OS CONVERTASE) (PROPERDIN FACTOR B)   (GLYCINE-RICH BETA CLYCOPROTEIN) (GBC) (PBF2)
	Top Hit Database	Source	EST_HUMAN	EST HUMAN	FST HIMAN	Z	Z	F	E	٤	ξŃ	Þ	SWISSPROT		EST HUMAN		EST_HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	L	<b>EST_HUMAN</b>	SWISSPROT
,	Top Hit Acession	ż	AA815175.1	3.0E-07 AW797168.1	3 DE 07 AISS1065 1	3.0F-07 AJ132352.1	2.0E-07 AF282988.1	77569.1	L77569.1	U38849.1	2.0E-07 AF003530.1	2.0E-07 AF003530.1	P11369		2 0F-07 AA223280.1		T83042.1	0,26768	Q09701	20E-07 BF131397.1	2.0E-07 AF125348.1	2.0E-07 AI873563.1	2.0E-07 AW898066.1	2.0E-07 AW448968.1	2.0E-07 Al208715.1		20E-07 AA572953.1	2.0E-07 AV729390.1	2.0E-07 AA035199.1	AL163303.2	20E-07 AW892507.1	P00751
-	Most Similar (Top) Hit	Vadue Vadue	3.0E-07	3.0E-07	9 DE 07	3.0E-07/	2.0E-07	20E-07 L77569.1	2.0E-07		2.0E-07	2.0E-07	2.0E-07 P11369	3	2.05-07		2.0E-07 T83042	2.0E-07 Q.26768	2.0E-07 Q09701	20E-07	2.0E-07	2.0E-07	2.0E-07	20E-07	2.0E-07		20E-07	2.0E-07	20E-07	20E-07	20E-07	2.0E-07 P00751
	<u> </u>		5.12	328	•	727	4.18	6.64	6.64	152.51	1.29	1.20	0.87	3	6		7.18	1.16	235	98.0	17.94	1.42	1.71	6.0	1.63		. 0.81	4.23	68'0	1.8	8.11	0.92
	ORF SEQ			34074			26051							1	24047				27013		29656						33178		35430		37052	
	Ean SEQ ID	ÿ	19914	L		25644	13461	13258	13258	13783	13810	13810	1982	13000	13005	L	13996	14208	14636	16876		]	<u> </u>	L	L		19885	21780		L	1.	1
	Probe SEO ID	Ö	6861	7752	1	19083	*	188	155	\$	748	748	787	3	8	5	25	1167	1604	3633	3700	4185	5417	6702	6820		6832	8813	8043	10119	10830	10856

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Top Hit Descriptor	AV734819 cdA Homo septems cONA clone cdABFB06 5'	wn30e07.x1 NG_CGAP_Gas4 Homo sapiens cDNA cone IMAGE:2446832 3' similer to contains OTK.12. OFR repetitive element;	Homo septens chromosome 21 segment HS21C101	Homo sapiens partial steerin-1 gene	wd16605.x1 Sceres_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2328273 3'	601590133F1 NIH_MGC_7 Hamo sapiens cDNA clane IMAGE:3843978 5	601660133F1 NIH_MGC_7 Hamo saplens cDNA clane IMAGE:3943878 5	on 15c02.x1 Normal Human Trabecular Bone Cells Homo sepiens cDNA clone NHTBC_on 15c02 random	cn15c02.x1 Normal Human Trabacular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random	EST382776 MAGE resequences, MAGK Homo sepiens cDNA	Homo sepiens jun dimerization protein gene, pertial cds; cfos gene, complete cds; and unknown gene	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cas	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)	Ret mRNA for ribosomal protein L31	DYNEIN HEAVY CHAIN (DYHC)	DYNEIN HEAVY CHAIN (DYHC)	IG KAPPA CHAIN V4 REGION OU	IG KAPPA CHAIN V-I REGION OU	cong3.P11.A5 conorm Hamo sapiens cDNA 3	Rattus norvegicus Munc13-1 mKNA, complete cas	DYNEIN HEAVY CHAIN (DYHC)	DYNEIN HEAVY CHAIN (DYHC)	Hamo septens SCL gene locus	Homo sapiens chromosome 21 segment HS21C048	Homo sapiens chromosome 21 segment HS210048	MR0-HT0168-191189-004-g09 HT0168 Homo sepiens cDNA	Hamo sapiens chranosame 21 segment HS210048	Hamo sapiens chrancsome X region from filamin (FLN) gene to glucose-6-phosphate denydrogenase (GGPD) gene, complete cds's	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
Top Hit Database Source	EST_HUMAN	EST_HUMAN	IN	ĿN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TA		SWISSPROT			SWISSPROT	SWISSPROT	SWISSPROT	T_HUMAN	NT.	SWISSPROT	SWISSPROT	NT	NT	N	EST_HUMAN	N	NT	SWISSPROT
Top Hit Acession No.	9.0E-08 AV734819.1	9.0E-08 A1891052.1	9.0E-08 AL 163301.2	9.0E-08 AJ251973.1	8.0E-08 AI911352.1	8.0E-08 BE795469.1	8.0E-08 BE795489.1	8.0E-08 AI762367.1.	8.0E-08 AI752367.1	8.0E-08 AW970693.1	8.0E-08 AF111167.2	8.0E-08 AF253417.1	Q02357	7.0E-08 X04809.1	P15305	P16306	P01606	P01606	7.0E-08 AI535743.1	7.0E-08 U24070.1	P15305	P15305	7.0E-08 AJ131016.1	6.0E-08 AL163248.2	6.0E-08 AL163248.2	6.0E-08 BE144398.1	6.0E-08 AL163248.2	8.0E-08 L44140.1	P08547
Most Stmilar (Top) Hit BLAST E Value	9.0E-08	9.05-08	9.0E-08	9.0E-08	8.0E-08	8.0E-08	8.0E-08	8.0E-08	8.0E-08	8.0E-08	8.0E-08	8.0E-08	7.0E-08 Q02357	7.0E-08	7.0E-08 P15305	7.0E-08 P15305	7.0E-08 P01606	7.0E-08 P01806	7.0E-08	7.0E-08	7.0E-08 P15305	7.0E-08 P15305	7.0E-08	6.0E-08	6.0E-08	8.0E-08	8.0E-08	8.0E-08	6.0E-08 P08547
Expression	2.18	1.46	232	3.51	2.97	0.77	207	3.38	3.38	2.8	0.46	2.63	4.07	17.17	0.7	0.7	6.0	6.0	2.33	4.32	1.55	1.65	1.9	4.23	423	2.72	1.28	0.49	0.74
ORF SEQ ID NO:	36661			<u> </u>				35482	35483		37363		28121								28563			26824			30184		Ш
SEO (D	23172	24456	24854	25212	15845		1	22057	22057	1_	23848		L				J	Ľ	L_	24859	16634	16834	_			L	1		H
Probe SEQ (D NO:	10247	11515	11977	12463	8	1052	3555	909	606	9985	10928	11575	8	1363	3589	3589	8	3948	11165	11982	12899	12899	12976	818	818	2371	4278	8162	8283

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Single Excit riones Expressed in Doilo manor	Top Hit Descriptor	obsects. 1 NCI_CGAP_GCB1 Homo septems cDNA clone IMAGE:1335368 3' similar to contains MER12.b3 MER12 repetitive element;	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCI.EASE]	Homo septens chromosome 21 segment HS21C103	nM03b09.s1 NCI_CGAP_Thy1 Homo septems cDNA clone IMA(3E:943193 similar to comains Au repoure element.	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)	QV0-CT0225-131089-034-412 CT0225 Hamo sapiens GJNA	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECONSON	RSAL-VEN I RAL PALLIERNING LOLLOID PROTEIN PRESONNESS.	oxidoe02x1 Soares fetal inversigheen invers of mains squares conventions inverse. To recover the contains Ab repetitive element,	Homo sepiens shox gene, etternatively spliced products, complete ods	URIDINE PHOSPHORYLASE (UDRPASE)	TRANSMEMBRANE PROTEASE, SERINE 2	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	o(78412.s.) Soares, total fetus, Nb2HF8, 9w Homo sapiens a.r.N. Gare Inv. C.	en 22410 x1 Gessler Wilms fumor Homo sepiens cDNA clone IMAGE:1694411 3' similar to contains Auu repetitive element contains element MER22 repetitive element ;	z/76b08.r/Socres_testis_NHT Hamo sepiens cDNA clone IMAGE:72X247 5 smitter to 11K.c3U378 G505679 NA/CA,K-EXCHANGER.;	2/70608.11 Sogres_testis_NHT Hamo saptens CONA clane IMAGE:728247 5' sámilar to TR:G605579	GS05579 NA/CA,K-EXCHANGER;	602248024F1 NIH MGC 62 Hamp septens alma dane invalor 4333300 5	2248024F1 NIH MGC 62 Homo septems curva done invalue 45555500 6	2065g0s.rf Sogres_feta_neart_NormT19W Frame septens curve water innocessors of commerce.	tassa11 x1 NCI_CGAP_Co16 Homo septens cDNA done IMAGE:2062076 3' similar to contains MER18.13	MER18 MER18 repetitive element;	Macaca hashoularis apolipoprobali A-1 gene, will processors of shinilar in TRO07158 092158	BP/98/10/3/1 NIH_M-SC_10 mano septens CANA CALIE INFOCESSORIOS COMMINES CANA SANTAXIN 17.;
אחוו דוטגפאנויו ווסג	Top Hit Dafabase Source	EST_HUMAN ME	RE SWISSPROT EN		EST HUMAN ele			T	SWISSPROT DC	EST HUMAN O	Т	ISSPROT	SWISSPROT TR	Г		EST_HUMAN   of	EST_HUMAN RE	FST HUMAN G	Ī	П		EST_HUMAN 80	EST HUMAN LA		T_HUMAN	¥ .	EST_HUMAN S
algale.	Top Hit Acession No.	6.0E-08 AA8Z7075.1		03.2	5.0E-08   AA493851.1	P06681	5.0E-08 AW851878.1	P25723	P25723	4 OF 08 A1078417.1	A OF OR I IRONS 1	P62824	015393	4.0E-08 L42571.1	P08547	4.0E-08 AI016342.1	4.0E-08 AI050027.1	4 n= na AA303607 1		4.0E-08 AA383827.1	4.0E-08 BF682483.1	4.0E-08 BF882483.1	4 0E-08 W78159.1		4.0E-08 AI343353.1	3.0E-08 M83242.1	3.0E-08 BE018348.1
	Most Similar (Top) Hit BLAST E	6.0E-08	6.0E-08 P11369	5.0E-08	5.05-08	5.0E-08 P06681	€.0E-08	4.0E-08 P25723	4.0E-08 P25728	4.05-08	80-30 4	4.0E-08 P52624	4.0E-08 015393	4,05-08	4.0E-08	4.0E-08	4.0E-08	4 05-08		4.0E-08	4.0E-08	4.0E-08	80-30 7				
	Expression Signal	25.0	181	322	200	10.16	1.63	1.07	1.07	500	2 S	200	90	1.32	0.82	0.65	3.67	3	2	1.61	3.11	3.11	4 98	B	1.84	0.94	3.06
	ORF SEQ ED NO:		88208	26125	38386		31814	27789	27790		00000	32868	28542	35898			37474		800/6	37890						29404	31958
	SEQ ID	22836	24670	13201	963	25032	25162		1	7000	10134	4060A	33448	L	1	22015		1	CCC347	24355		24370		ing:	26448	L	$oldsymbol{L}$
	Probe SEQ ID NO:	8	44744	38	mark.	12/85	12382	1775	1775	Log		3854	3 8	20/0	500	5	40752		וויוו	11411	11426	11428	8	12180	12830	3438	2882

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Probe SEQ ID NO: 7787 12157 207 230 497 1872 1346 1755 1872 322 322 322 322 4934 4434 4434 4434	Exan NO: NO: 18389 20740 20740 20740 13330 13727 14044 14881 14784 14881 17461 186009 18613	중 <sub>요</sub>	Signa Signa 1	AT 162737.1  No. 14.163246.2  AL 163246.2  AL 163246.2  AL 163246.3  AL 163247.2  AN 866438  BE 280477.7  AN 860216.1  CA2280  O42280   Top Hit Database Source Source Source Source EST_HUMAN NT EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN NT EST_HUMAN	Top Hit Descriptor  1	
5932 8337	19018	32213 34721	0.89	2.0E-08 AW088924.1 2.0E-08 P10272	SWISSPROT	MENTIS MENTIS INDOMINE GENERIT; POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8447		Ш		2.0E-08 AA490121.1 2.0E-08 AU139978.1	EST HUMAN	ab02g06.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 S' AU139978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

igie Exon Probes Expressed in Boire manow	Top Hit Descriptor	w72/02.rl Soares fetal liver spleen 1NFLS Homo saplens cONA clane IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element ;	yv72f02.rf Scares fetal tiver spleen 1NFLS Homo saplans cDNA clone IMAGE:248283 5' similiar to contains LTR1.b3 LTR1 repetitive element ;	Homo sepiens chromosome 21 segment HS210084	Homo septens hypothetical protein FLJ11342 (FLJ11342), mRNA	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]	Homo sapiens cavedin 1 (CAV1) gane, exon 3 and partial cds	PM2-HT0130-150989-001-f12 H10130 Homo sapiens cDNA	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baykor-HCSC project* i CBA Homo sepiens cDNA done TCBAP5232	TCBAP-ID6232 Pediatric pre-B cell acute lymphoblastic leukemia Beykor-HGSC project=TGBA Homo sentens cDNA ctone TCBAP5232	Lymn sarians hiverion data exams 1-30	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))	Homo seriens dromosome 21 segment HS21C102	Homo seniens mennosidese, beta A. hsosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3	(UBE2D3) genes, complete cds	Homo sepiens mannosidese, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme EZD 3	(UBE2D3) genes, complete cds	o(35g05.s1 Scares_testis_NHT Homo sapiens cuiva done invade::1016/30 3	S-ANTIGEN PROTEIN PRECURSOR	PN/2-BT0548-210100-004-dD2 BT0548 Homo sepiens cDNA	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CITY) (TRICARBOXYLATE CARRIER PROTEIN)	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)	Homo seniens mater histocompatibility locus class III region	RIPONI ICI FASE INHIBITOR	DONING FACE MUIDITOD		Human lambda-immunogicoulin constant region comprex (gentiume)	Human lambda-immunoglobulin constant region complex (germina)	Homo sapiens chromosome 21 segment HSZ1CJ/9	Homo septens chromosome 21 segment 1321 CU / 8	2008   2021   2021   102   102   114   124   103   104   105   105   105   105   105   105   105   105   105
XOII PIODES EX	Top Hit Detabase Source	EST_HUMAN L	EST_HUMAN L	NT H		SWISSPROT		EST_HUMAN P	EST_HUMAN 8	FEET LIMAN	1	/ISSPROT	Γ		<u> </u>		╗	1	7	EST_HUMAN F	TOGGSSIMS	1	Τ	TOGGGGG	T	ISSPROT				_	EST HOWAN
	Top Hit Acesston No.	2.0E-08 N78097.1	2.0E-08 N78097.1	2.0E-08 AL163284.2	11431676 NT			1.0E-08 BE141959.1	1.0E-08 BE246844.1	00046944.4	1.UE-06 DEZ40044.1	1.0E-08 AJUTU//U.1	4 OF 00 Al 403300 2	AL 1033022	1.0E-08 AF224669.1		1.0E-08 AF224689.1	1.0E-08 AI015304.1	1.0E-08 P09593	1.0E-08 BE072572.1	0300440	1.UE-00   7/91 10	1.0E-00   Scott	Arutanos. I	1.UE-06 F 285 15	1.0E-08 P28315	1.0E-08 X51755.1	1.0E-08 X51755.1	9.0E-09 AL163279.2	9.0E-09 AL163279.2	9.0E-09 T97950.1
	Most Similar (Top) Hit BLAST E Vætue	2.0E-08	2.0E-08	2.0E-08	2.0E-08	1.0E-08 P31792	1.0E-08	1.0E-08	1.0E-08	4 00	1.05-00	1.05-08	00 20 7	1.05-08	1.0E-08		1.05-08	1.0E-08	1.0E-08	1.0E-08	7 70	1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00	9 FO	١							9.0E-08
	Expression Signal	0.8	9.0	1.88	4.1	1.42	2.12	2.49	1.19	,	A.	4.0		0.47	990		0.56	1.89	0.46	99.0		18.0	0.07	3.4	T.5	1.5	3.12	1.68			0.53
	ORF SEQ ID NO:	37310				27613			28484			31947		34/48	34852		34853			35970				1	١	38603			30179	30180	
	Exam SEQ ID NO:	23808	l				1	15084	L	L	_1	18775	1	21338	21435		21435	21858	22521		ı			⅃		24998	25281	25520		1	
	Probe SEQ ID NO:	10886	10886	12472	12982	1510	1780	2067	3206		3208	5680	3	8388	8466		848	8892	8998	9998 8		10325	10821		12129	12129	12569	12940	4271	4271	10422

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Г	<del></del> T		Т	Т	Т		Т			Т	Т	1-		Т	T	7	T	Т	Т	آر	Т	Т	Т	T		٦
	Top Hit Descriptor	quaecti.xi NC_CGAP_Gas4 Homo sepiens cDNA clone IMAGE:1978984 3° shriber to contains L1.13 L1 repetitive element;	qd42e07.x1 Sceres_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.t1 MSR1 repetitive element;	CMO-NIN1004-100300-273-408 NIN1004 Homo sapiens cDNA	op74d08.s1 Sogres_NFL_T_GBC_S1 Hamo saplens cDNA clane IMACE:10625/0 3	Homo sepiens DNA for 3-ketoecyl-CoA thiclesse beta-subunit of mitochondrial trifunctional protein, exen 2, 3	Human familial Alzheimar's disease (STM2) gene, complete cds	7145e10.x1 Sogres_NSF_FB_9W_OT_PA_P_S1 Homo septems cDNA clone IMAGE3524443 3' samuer to contains MER29.b2 MER29 repetitive element;	280c05.r1 Soares_NhHMPu_S1 Homo sepiens cDNA clone IMAGE:681692 5' similiar to contains L1.12 L1	Limens becomes mentions absorption 2 (LAMP2) nens. 5 and flanking region	International literature by Mykrobian Z. Com. 2.) Born, C. Com. 2.] Born, C. Com. 2.	WITH INSTITUTION OF THE PROPERTY OF THE PROPER	258e07.s1 Scares retina N2D4HR Homo septens CDNA done IMACE.301150 5 British to Contest is L1.12.L1 repetitive element;	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:121918 3	DKFZp434C0514_rl 434 (synonym: htes3) Homo sapiens cDNA clane UNF2p434C0514_rl	nt17a11.st NCI_CGAP_HSC1 Hamo sapiens aDNA dane IMAGE::1040924 smillar to contains L1.IZ L1 repetitive element;	PMA-HT0527-160200-001-h05 HT0527 Homo septens CUNA	ARBSTACE AT SCARES NFL T GBC S1 Hamp capiens CLINA cane IMAGE:2/01311 3	MR3-HT0446-280300-201-h12 HT0448 Hamo sapiens CUNA	Homo sapiens fibrobiast growth factor receptor 3 (achondropiasia, thanstophoric dwarfism) (FGFR3) mRNA	Homo saptems testis-specific kinase substrate (TSKS) gene, complete cds	RC2-HT02552-120200-014-h10 HT0252 Homo sepiens cDNA	Hamo sapiens chromosame 21 segment HS21C084	EST66746 Fetal lung II Hamo saptens cDNA 6' end	Human germiline T-cell receptor beta chain Dopanine-beta-hydroxylesse-like, TRY1, TRY2, TRY3, TCRBV2751P, TCRBV2251A2N1T, TCRBV851A1T, TCRBV5751A1N2T, TCRBV551A1T, TCRBV13S3, TCRBV657P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV852A2PT, TCRBV7S2A1N4T,	TCRBV13S9/13S>
	Top Hit Detabase Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	M	M	EST HUMAN	MANI ILI POE	NAMOR I SE	Z	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	뉟	닏	EST_HUMAN	¥	EST_HUMAN		¥
	Top Hit Acession No.	8.0E-09 AIZ70615.1	8.0E-09 AI183500.1	8.0E-09 AW900159.1	8.0E-09 AAGG8892.1	) <del>9684</del> 2.1	J50871.1	7.0E-09 BF108755.1	1 00000	7.0E-09 AA236200.1	09709.1	7.0E-09 BE254850.1	7.0E-09 AA058626.1	7.0E-09 T97950.1	6.0E-09 ALO40439.1	6.0E-09 AA557940.1	6.0E-09 BE169421.1	6.0E-09 AW195784.1	8.0E-09 BE161653.1	4503710 NT	6.0E-09 AF200823.2		5.0E-09 AL 163284.2	5.0E-09 AA359454.1		5.0E-09 U66059.1
	Most Similar (Top) Hit BLAST E Vatue	8.0E-09/	8.0E-09	8.0E-09	8.0E-09	7.0E-09 D86842.1	7.0E-09 U50871.1	7.0E-09	1	7.0E-09	7.0E-09 [L09709.1	7.0E-09	7.05.09	7.0E-09	6.0E-09	6.0E-09	6.0E-09	6.0E-09	8.0E-09	6.0E-09	8.0E-09	5.0E-09	5.0E-09	5.0E-09		5.0E-09
	Expression Signal	88:	P8.7	3.04	2.64	1.91	1.22	0.56		0.91	3.06	1.17	0.50	3.65	96.0	0.96	5.44	9.56	0.88	2.12	4.42					0.59
	ORF SEQ ID NO:		33801								36008		<u> </u>			28890	30917		35315					32872		31277
	SEQ ID NO:	19888	20445	21302	22305	16864	17072	į.	1	- 1	22559	23465	22683	1_			[_	L.		i _				1	1	18357
	Probe SEQ ID NO:	8828	7479	8833	8340	3621	4034	8234		8382	9615	10543	40744	11032	2162	4059	5017	5454	8922	953	10639	1413	1870	6550		7025

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Single Exon Probes Expressed in Bone Marrow

Тор Hit Descriptor	OLFACTORY RECEPTOR-LIKE PROTEIN COR6	PM2-1 IMD053-240300-005-c09 UM0053 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C082	Dame combine Amount of comment HSM (2085)	TUIN SELECT IN CONTROL OF SELECT	ATIO SEPTIONS TRYOUGH (AT LOCAL) THE CO.	Homo sapiens eukayodic intitation factor 4AI (EIF4AI) gene, parua cos	Homo sapiens eukaryotic initiation tector 4AI (EIF4AI) gene, perua cus	EST58385 Infant brain Homo sapiens CLNA 5 end similar to similar to rica show protein, ov not	zw04c06.r1 Sogres_Nht1MP-u_S1 Homo sapiens culva carie inwalet. Pozzeo	yd11e07.s1 Soares fefai liver spieen 1NFLS Homo sapiens CUNA cione IMAGE: 20004-3	hu09e09.x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3166120 3's smiler to contains MEK16.to MER18 receitine element:	Parameter of No. 1924 House seriens cPNA clone INAGE 3168120 3' similar to contains MER18.13	nubscusti No. Com Luta mano equens com central management; MER18 repetitive element;	PROTEIN MOV-10	MU09609.X1 NCI_CGAP_LLI24 Homo sapiens cONA clone IMAGE:31661.2J 3' similar to contains mention.	MER18 repetitive element;	ZYS4804,71 Sogres, testis, NH1 Homo squars durva darie invace 137-122 o	H. saplene PADPRP4 gene for IVAD(+) AUP-4 mosty marster asset	Homo sepiens eulanyotic initiation factor 4AI (EII-4AI) gene, partial cas	258.1 KDA PROTEIN CZYORF6 (KJAA0833)	Homo sepiens DNA for 3-testoacy-CoA thiolesse befa-subunit of mitochondrial trifunctional protein, exon 2, 3	hasoloozii NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to 11k:055091 055091 IMPACT PROTEIN. ;	Hamo sepiens chramosame 21 segment HS21C047	72608.X1 Sogres NSF FB 9W_OT_PA_P_31 Homo sapiens dDNA clane IMAGE:3527030 3	7772508.x1 Sogres_NSF_F8_9W_OT_PA_P_S1 Homo saplans cDNA clane IMAGE:3527030 3'	sentens PADPRP-I gene for NAD(+) ADP-ribosyltransferass	Homo saciens chromosome 21 segment HS21C084	TKEZ-778181710 rt 761 (sworum: hamv2) Homo sapiens cDNA clone DKFZp76181710 5	258 4 KDA PROTEIN CHORFS (KIAA0833)	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR	mintellity of Sciences NH-IMPu S1 Homo seatiens CDNA clone IMAGE:1855783 3'	
ssion Top Hit Detechese Source	SWISSPROT	Γ	7				5	$\neg$	П	EST HUMAN z	EST_HUMAN Y	H NAME TO TOO	7	EST_HUMAN N	SWISSPROT		HUMAN	T HUMAN			SWISSPROT	Ę	EST HUMAN	Г	T HUMAN	F	1	İ	T LII IMAN	PANIOCODOT	Т	Т	٦.
Top Hit Acession No.	237074	F OF 00 A11/700007 4		I	4.0E-09 AL 163285.2	9558718 NT	4.0E-09 AF175325.1	AF175325.1	4.0E-09 AA350878.1	4.0E-09 AA485747.1	4.0E-09 T64942.1	1	3.0E-09 DE222239.1	3.0E-09 BE222239.1	P23240		3.0E-09 BE222239.1	3.0E-09 AA442272.1	3.0E-09 X16674.1	3.0E-09 AF175325.1	Q9Y3R5	3.0E-09   D86842.1	4 OE-100 BE-405780 1	3 0F-09 At 163247.2	3 0E-00 RE100043 1	A NE-NO RE4 NOOKS 1	V40074 4	20E-09 A10074.1	AL IOUGNA	20E-09 AL1185/3.1	2.0E-09 C813K3	20E-09 CO241	Alcoorto.
Most Similar (Top) Hit BLAST E Value	5 0F-09 P37071	201	80-00	1.01	4.0E-09	4.0E-09	4.0E-09	4.0E-09	4.0E-09	4.0E-09	4.0E-09	20.0	3.0E-08	3.0E-09	3.0E-09 P23240		3.0E-09	3.0E-09	3.0E-09	3.0E-09	3.0E-09		<u> </u>										
Expression Signel	20	25	7.03	0,	2.73	279	1.63	1.63	287	99.0	0.08	!	4.28	1.39	1.03		1.15	0.79	0.69	3.77	3.44	68'0	7	184	200			10.04	50.04		2.38		C9.L
ORF SEQ ID NO:	95228	2325	308/0			27472		28076	28461				28389	28579			28312			30371				STACK OF		37000			2/201				28977
Exon SEQ ID NO:	24606	21080	23877	13383	14018	14498	L	L	15443	21149	21834	1 _	15367	15561		L	1639A	16437		l_		1		2000	L	┙	┙		╛		L	_ 1	17077
Probe SEQ ID NO:	COOO	7000	10455	222	996	1465	2038	2038	2436	8173	8867		2359	2560	2859		3340	3388	4124	4457	4540	5225		7528		יפנין	<u>8</u>	833	1283	1667	2334	88	4039

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Abost Similar Top Hit Acession (Top) Hit Top Hit Acession Database Source Source		0.69 2.0E-09 A1004062.1 EST_HUMAN   0447b09.s1 Sogres_testis_NHT Homo septens cDNA clone IMAGE:1019897 3	2.0E-09 AL163249.2 NT	2.0E-09 AA357407.1 EST_HUMAN	SOF DO AAA81430 1 EST HUMAN	2 OF-09 W 28834.1 EST HUMAN	2.0E-09 AW862128.1 EST_HUMAN	NT	2.0E-09 X16674.1  NT	Т	2 0F-09  182868 1	1.0E-09 6031624 NT	1.0E-09 5031624 NT	1.0E-09 AJZ28041.1 NT	1.0E-09 AI356088.1   EST_HUMAN	1.0E-09 U80017.1 NT	4.07 1.0E-09 M28699.1 NT Homo expiens nucledar phosphoprotein B23 (NPM1) mRNA, complete cds	1.0E-09 M28639.1 NT	1.0E-09 BE635440.1 EST_HUMAN	1 EST HUMAN	0.84 1.0E-09 T60216.1 EST_HUMAN Inspetitive element, contains MER28 repetitive element;	0.82 1.0E-09 AL163283.2 NT Homo eaplens chromosome 21 segment HS2IC083	1.0E-09 U07000.1  NT	3.11 1.0E-09 P28694 SWISSPROT   CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)	45.1 EST_HUMAN	0.87 1.0E-09 AI688474.1 EST_HUMAN MER25.t1 MER25 repetitive element;
Expression (Top) Hit Signal BLASTE Value							Ì	l														[   				
Exam ORF SEQ SEQ ID NO:	18207 31081	18898 32081	18346	25174	34008			22028 35452		25975	26,00	14155 27105		l	15513	15959 28878			16108 28022		18171 31050	18677 31640			L	
Probe SEQ ID SI		L	8273	L	7607					12772	┸	1111	1111	1638		<u>l</u>	1_	2837		9889	5162	558	9836	2987	8113	8733

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	Top Hit Databese Source	Ā	¥	18127 NT	EST_HUMAN	740.1 EST_HUMAN MR0-SN0040-050600-002-c07 SN0040 Homo sapiens cLINA	EST_HUMAN	EST HUMAN	Ş	FCT HIMAN	4 EST HUMAN	1	706225 NT	110000	7706225 NI	SWISSPRO	SWISSPROT	보	2.1 EST_HUMAN	_	SWISSPROT	2 NT	2 N	¥		EST_HUMAN	1 EST HUMAN	SWISSPROT		SWISSPROT
סֿ 	Top Hit Acesston No.	1.0E-09 AL 163283.2	1.0E-09 AL163283.2	114	1.0E-09 TB3176.1	9.0E-10 AW867740.	9.0E-10 AI870071.1	0 0E-10 A1452082 1	9.0E 40   183830 2	OUE-10 DECENTAR	8.0E-10 DEVOO749.		1565308		7	7.0E-10 Q13342	P08547	7.0E-10 X00858.1	7.0E-10 AA345220	7.0E-10 BF352883.	7.0E-10 P35084	7.0E-10 AF029701.2	7.0E-10 AF029701	7.0E-10 L08895.1	8.0E-10 A.J400877.1	6.0E-10 AI424405.1	6.0E-10 AW853719	6.0E-10 P33730	6.0E-10 P33730	6.0E-10 P98073
	Most Similar (Top) Hit BLAST E Vatue	1.0E-09	1.05-09	1.0E-09	1.05-09	9.0E-10	9.0E-10	0.05.10	9.01	0.00-10	8.UE-10	0.05-10	8.0E-10	21-12:																
	Expression Signal	2.87	1.53	201	1.6	2.49	6.64	3	4.65	27.5	0.70	80.6	248	97,00	32.88	2.48	21.64	2.86	3.72	1.2	1.48	1.29	1.20	0.68		1.37	2.72	0.89		
	ORF SEQ ID NO:	<b>†</b>		31425		27314	28830	00770	2 2 2 2 2	20180	2222	30142	00000	98087	28899	27636		29072	32619	33973		34688	34689	37092		00282		35527		
ļ	SEO ID	23,599	24063	25.076	25418	14348	15905	3	3	13251	200	200	23248	13/64	13764	14659	16567	16161	19380	20607	20861	21277	21277	23595		15682		į .		1 1
	Probe SEO ID NO:	10877	286	12818	12781	1312	2845		3	<u>\$</u>		4228	10324	707	702	1626	2668	3104	8303	7647	7918	8308	8308	10673	914	2686	4768	8	9435	<b>B</b>

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO: 12221 781 9489 5026 5026 1111 1111 583 10833 10833 10833 10833 10833 10833 10833 6330 6337	Exan SEQ ID NO: 25058 13824 16535 152847 22847 22847 22847 22847 22847 23853 23853 23853 23853 23853 13970 14388 17588 17588 17588	g	Eggs	(Top) Hit Top Hit BLAST E	1-1252221-13818-12538 80-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1		EST384012 MACE resequences, MACL Home septems cDNA DKF2p434N219_J1 434 (synonym: https://dx.dc.home.septems.cDNA.chre.DKF2p434N219_S HYPOTHETICAL GENE 48 PROTEIN Home septems WRN (WRN) gene, complete cds GOTGS12947 INLAGG_T5 Home septems cDNA chre. IMAGE:4042413 \$\tilde{\text{T}}\$ HYPOTHETICAL GENE 48 PROTEIN TAKEN 12 MACL ITRA REPORTEIN ZK688.8 IN CHROMOSOME III RYPOTHETICAL 67.9 KD PROTEIN ZK698.8 IN CHROMOSOME ENDING CARDINER CDNA PMI-HTTOSC1-120200-001-688 HTTOSC1 HOME septems cDNA PMI-HTTOSC1-120200-001-688 HTTOSC1 HOME septems cDNA PMI-HTTOSC1-120200-001-688 HTTOSC1 HOME septems cDNA PMI-HTTOSC1-120200-001-688 HTTOSC1 HTOSC HOME SEPTEMS COMPARIAN COMPARIAN COMPARIAN COMPARIAN COMPARIAN COMPARIAN COMPARIAN COMPARIAN COMPARIAN COMPARIAN COMPARIAN COMPARIAN COMPARIAN
6486 8036	Ш	32801 34367		3.0E-10 3.0E-10	3.0E-10 BE302970.1 3.0E-10 AV743302.1	EST_HUMAN EST_HUMAN	ba76d08.y1 NIH_MGC_20 Home sapiens dDNA clone IMAGE:2906319 5' AV743302 CB Home sapiens dDNA clone CBFBGD08 5'
8036 8036 9404 9404	22048 22369 22369	35471 35803 35804	1.04	3.0E-10 3.0E-10 3.0E-10	3.0E-10 AV743302.1 3.0E-10 H87208.1 3.0E-10 AW850731.1 3.0E-10 AW850731.1	EST_HUMAN EST_HUMAN EST_HUMAN	AV743302 CB Homo septens cDNA clone CBFBGLX08 5 ys74bf2.s1 Scares retina N2b4HR Homo septens cDNA clone IMAGE:220511 3' similar to contains MER29 repositive element; IL3-CT0219-160200-064-B06 CT0219 Homo septens cDNA IL3-CT0219-160200-064-B06 CT0219 Homo septens cDNA

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Hamo sepiens FRA3B common fregile region, diadenosine triphosphate hydrolese (FHIT) gene, extn 5 Homo sepiens basic transcription factor 2 p44 (btt2p44) gene, pertial cds, neuronal epoptosis Inhibitory MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) yc11e12.r1 Stratagene lung (#837210) Homo sepiens cDNA clone IMAGE:80398 5 n238g03.s1 NCI\_CGAP\_GCB1 Hamo septens aDNA clane INAGE:1289908 3 protein (natp) and survival motor neuron protein (smn) genes, complete cds 602136840F1 NIH\_MGC\_83 Homo sapiens cDNA clone IMAGE-4273377 5 Top Hit Descriptor II.3-HT0618-110500-138-E07 HT0618 Homo sapiens cDNA Single Exon Probes Expressed in Bone Marrow EST HUMAN SWISSPROT EST HUMAN SWISSPROT EST\_HUMAN EST HUMAN SWISSPROT Top Hit Database Source 눌 Top Hit Acession 3.0E-10 AA766294.1 3.0E-10 BE178517.1 BF675047.1 3.0E-10 AF020503.1 ż 2.0E-10 U80017.1 2.0E-10 P48988 2.0E-10 P48988 3.0E-10 T65891.1 2.0E-10 (TOP) HIT BLAST E Value

\$30 BB		INT IDOVOEDIDE 5 (CYPSAS) GENE, DETUE CAS	2	-		
픠	Т	T HUMAN	FST HUMAN	Т	2.0E-10 AF-2010/.1	1.50 Z.O. 10 LOS 101 L
ᄩ		Т	SWISSPROT	SWISSPROT	SOC 40 Posson	SAL 20C 10 BEIGHT
-	Τ	Τ	TOGGGGGWG	TOGGGGGWG	TOGGGGIMO	TOGGGGIMO
	T	OW LOCATION TO THE PROPERTY OF	OWISSING	1	OWISSING	2.0E-10 P26809 SWISSTAU
		FST HUMAN repetitive element;	EST HUMAN		PORT 10 BEASABRE 1 EST HUMAN	PORT 10 BEASABRE 1 EST HUMAN
	T	Ť				Z.U10 10 10 10 10 10 10 10 10 10 10 10 10 1
	7	EST HUMAN MAKU-SMUUSO-28U	EST_HUMAN	7	EST_HUMAN	1.0E-10 AW867767.1   EST_HUMAN
		EST HUMAN AV652123 GLCH	EST HUMAN		1.0E-10 AV652123.1 EST HUMAN	1.0E-10 AV652123.1 EST HUMAN
	П	П	EST_HUMAN	П	EST_HUMAN	1,92 1.0E-10 AW852001.1 EST_HUMAN
<u> </u>		EST_HUMAN QV2-TT0003-16	EST_HUMAN		EST_HUMAN	1.0E-10 AW832912.1 EST_HUMAN
~''	$\neg$	$\neg$	EST HUMAN	$\neg$	EST HUMAN	0.81 1.0E-10 AL041685.1 EST HUMAN
_։լ	_	EST_HUMAN DKFZP434N131	EST HUMAN	_	EST HUMAN	1.0E-10 AL041685.1 EST_HUMAN
×	Homo septems nucleer factor of Keppa light polybeptice gaire or half and in 17-case 1 (14) 12-17 sent controlled					
- 17	88	NT Sd8	¥		¥	1.0E-10 AF213884.1 NT
<i>7</i>	Homo septiens X28 region neer ALD locus containing due spooting prospinates a (2004 s), incominal protein L18a (RPL188), Ca2+/Catmodutin-dependent protein kinase I (CAMKI), oreatine transporter (CRTR),	Homo sapiens X protein L18a (RF	Homo sapiens X protein L18a (RP	Homo sapiens X protein L18a (RF	Homo saplens X Home saplens X protein L18a (RF	Homo sapiens X protein L18a (RF
ᅵ	CDM protein (CDM), adrendeukodystrophy protein >	NT CDM protein (C	눌		눌	1.0E-10 U52111.2  NT
1 S 1	Homo sapiens X28 region near ALD tocus containing dual specificity phosphatases 9 (DUSP9), riboscomal Homo sapiens X28 region pear ALD tocus containing dual specificity phosphatases (CAMKI), creatine transporter (CRTR),					
ב ב	COM makin (COM) advandadodystrody protein >		ţ	<u> </u>		
	116 11 DCCX4 and A for renderin CXXC domain 1, complete cds		2	- 2	2	1.0E-10 USZTTIZEU 01-30.1
2	remore septents		-	7	TN + OBO3 TO V TO V	

Homo sepiens cytochrome P450 polypeptide 43 (CYP3A43) gene, pertial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450

(HPRG)

2.0E-10 Q28640

1.88 3.12

1.76 1.95 1.55

31728 26058 26069

25468 13157

23877

10957 12865 37 37

10828

13157

14937 16057 18988

1913

2999 5901

<del>1</del>.58

2.05

22649 23749

9696

Expression Signal

ORF SEO ÖNQ

EQ D

SEQ ID

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<u>0</u>

Probe

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Table 4
Single Exon Probes Expressed in Bone Marrow

Top Hit Acession Detabese Top Hit Descriptor	1.0E-10 M30829.1 NT Human pregnancy-specific dycoprotein beta-1 (SP1) mRNA, last exon	we82f04.x1 Sogres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347815 3' similer to contains 1.0E-10 AI797745.1 EST_HUMAN MER31.t1 MER31 repetitive element;	1.0E-10 AA631233.1 EST_HUMAN Ing81805.s1 NO_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1158704.3'	Homo sapiens X-linked arhidnoitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat 1.0E-10 AF003528.1 NT regions	SWISSPROT	Г	7:	1.0E-10 AI268340.1 EST_HUMAN repetitive element;	1.0E-10 AA081868.1 EST_HUMAN p.23g08.r1 Stratagene neuroepithelium NT2RAMI 837234 Homo sapiens oDNA clone IMAGE:548314 6	1.0E-10 A10382280.1 EST_HUMAN   0963h03.x1 Sogres_fetal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:1672881.3'	Ŋ	TEST HIMAN	1 EST HUMAN	1 EST HUMAN	9.0E-11 AL134395.1 EST_HUMAN DKFZp547D225_r1 547 (synonym: hfbr1) Homo saplens cDNA clone DKFZp547D225 57		9.0E-11 AA775885.1 EST_HUMAN   ae78f01.s1 Stratagene schizo brain S11 Homo sepiens cDNA clone IMAGE-970297.3'	9.0E-11 BE079780.1 EST_HUMAN RC8-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA		9.0E-11 AA324960.1 EST_HUMAN EST27872 Cerebellum II Homo sapiens cDNA 5' end	9.0E-11 C16835.1 EST_HUMAN   C16835 Cloritech human acrts polyA+ mRNA (#6572) Homo septems cDNA clone GEN-508908 6	EST_HUMAN	EST_HUMAN	8.0E-11 AW674316.1 EST_HUMAN ba60g04.x1 NIH_MGC_10 Homo sapients cDNA clone IMAGE 2200962.3'	EST_HUMAN	7.0E-11 AA330842.1 EST_HUMAN EST34392 Embryo, 6 week I Homo septems CDNA 6' end
196 H	M30626	AI79774	<b>AA6312</b>	AF0035	P08548	AU1285	AW408	AI2683	AA0818	A103822	XR7344	DE4456	AL1343	AL1343	AL 1343	AL1343	AA7758	BE0797	AA3249	AA3249	C16635	H19971	N23712	<b>AW674</b>	AW108	AA3306
Most Similar (Top) Hit BLAST E Value	1.0E-10			1.0E-10	1.0E-10	1.0E-10	1.0E-10	1.0E-10		1.0E-10	1.0F-10	0.05.44	9.0E-11	9.0E-11	9.0E-11	9.0E-11	9.0E-11	9.0E-11	9.0E-11	9.0E-11	9.0E-11	8.0E-11	8.0E-11	8.0E-11		
Expression Signal	263	0.92	0.61	0.49	0.56	0.63	1.11	1.1	3.95	3.25	2.46	2000	828 828	6.21	26	2.6	0.72	3.89	122	1.22	4.59	8.85	4.35	0.65	0.65	1.87
ORF SEQ ID NO:			33225	33543		34279	34988			37734		28200	28161	28152	28870	29371	30440		36634	36835	31809		30003	32170		27452
Econ SEQ ID NO:	17230	18221	19928	20214	20673	20888	21550	21968	23484	24211	18354	1	16131	15131	16443	16443	17552	18750	23438	23436	25289	1930	17109	18978	19883	14475
Probe SEQ ID NO:	4199	5212	6876	<b>689</b>	7716	7947	8582	8002	10562	11259	42468	300	2114	2114	3394	3394	4528	2654	10514	10514	12546	3133	4073	2860	6289	1442

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Single Exon Probes Expressed in Bone Marrow

ngie Exon Probes Expressed in Bone Marrow	Top Hit Descriptor	Homo sepiens WEE1 gene for protein kinase end partial ZNF143 gene for zinc finger transcription factor	Homo sepiens SNCA isoform (SNCA) gens, complete cds, atternativety spiloed	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]	Human matrix Gla protein (MGP) gene, complete cds	Human matrix Gla protein (MGP) gene, complete cds	Homo sepiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate defnydrogenase (GGPD) gene, complete cds's	LINE-I REVERSE TRANSCRIPTASE HOMOLOG	AV727859 HTC Hamo saptens dDNA dane HTCASC08 5	CM0-BT0281-031199-087-e03 BT0281 Homo sepiens cDNA	Hamo sapiens chromosome 21 segment HS210083	Hamo sapiens chromosome 21 segment HS210083	ALDIEHYDE OXIDASE	Homo sapiens chromosome 21 segment HS21C013	Homo sapiens protocadherin beta 3 (PCDHB3), mRNA	zu01b12.r1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:730559 5	601507631F1 NIH_MGC_71 Hamo sepiens cDNA clone IMAGE:3909235 5	Homo septens chromosome 21 segment HS21C047	HUMSUPY069 Human brain cDNA Homo sapiens cDNA done 069	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2	zy59f10.r1 Soares_testis_NHT Homo sepiens cDNA clone IMAGE:757983 5' similar to TR:G1055250 G1055250 PHEROMONE RECEPTOR VN4.;	Homo sapiens mannosidasa, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3	(UBE2D3) genes, complete ods	RC1-HT0256-210100-013-f08 HT0258 Homo saplens cDNA	ff82g12.x1 NCI_CGAP_Bm23 Homo sepiens cDNA clone IMAGE:2105630 3' similar to WP:ZK353.1  CE00385 :	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA	Mis musculus ecoressed in non-metastatic cells 2 protein (NM238) (Nme2), mRNA	FST180120 Liver herselnder carchima Homo sablens cDNA 5 end	gr38c04.x1 Sceres tests NHT Homo septens cDNA clone IMAGE:1752102.3' shriller to contains MER10.t3	MER10 repetitive element;
Xon Probes I	Top Hit Detabase Source	Į.	ᅜ	SWISSPROT	¥	NT	F	SWISSPROT	EST_HUMAN	EST_HUMAN	IN	NT	SWISSPROT	N	M	EST_HUMAN	EST_HUMAN	M	EST_HUMAN	SWISSPROT	EST_HUMAN		¥	EST_HUMAN	EST HIMAN	ĮΣ	Ę	EST LIMAN	1011	EST_HUMAN
Single	Top Hit Acession No.	7.0E-11 AJ277548.2	7.0E-11 AF163884.1	P11389	6.0E-11 M55270.1	6.0E-11 M55270.1	6.0E-11 L44140.1	P08547	6.0E-11 AV727859.1	6.0E-11 BE063509.1	5.0E-11 AL163283.2	5.0E-11 AL163283.2	P48034	5.0E-11 AL163213.2	11416799 NT	4.0E-11 AA436042.1	4.0E-11 BE885900.1	4.0E-11 AL163247.2	4.0E-11 D44668.1	P20095	4.0E-11 AA442830.1		4.0E-11 AF224669.1	4.0E-11 BE149425.1	4 OE-11 Alen9753 1	11545732 NT		4 4 9 0 0 0 0	MANAGE TO: 1	2.0E-11 AH50502.1
	Most Similar (Top) Hit BLAST E Vatue	7.0E-11	7.0E-11	7.0E-11 P11389	8.0F-11	6.0E-11	6.0E-11	6.0E-11 P08547	6.0E-11	6.0E-11	5.0E-11	5.0E-11	5.0E-11 P48034	5.0E-11	5.0E-11	4.0E-11	4.0E-11	4.0E-11	4.0E-11	4.0E-11 P20095	4.0E-11		4.0E-11	4.0E-11	4 OE-44	4 0E-11	9 00 4	0.0C-11	3.05-11	2.0E-11
	Expression Signal	1.11	2.79	1.19	6.97	6.97	0.88	3.22	7.37	0.42	0.75	1.31	1.51	1.91	11.91	1.68	7.63	0.92	1.24	3.27	0.54		3.97	1.68	o c	1 56	2 65	707	\c.1	1.48
	ORF SEQ ID NO:	2882	35228		28421			34294		38072	28030	28030	_,	32997	34099		28812	28962	30557	32957	33552					847E3				26967
	Exan SEQ ID NO:	16925	1	1	L			20898	21875	22621	13132	13132	17285	ļ			_			L	l		20581	22601	l	25369	١.	L	1/35	14014
•	Probe SEQ ID NO:	3885	8843	10590	412	412	6884	7957	8707	8988	12	3377	4258	9865	777.4	-46	2802	2984	4649	6621	7197		7600	9760		47724	2007	8	4303 COS	88

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Top Hit Descriptor		Г	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsiton-globin, and offactory receptor-like protein COR3 beta (COR3 beta) genes, complete cds	Gailus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and offactory receptor-like protein COR3 beta (COR3 beta) genes, complete cds	qc51c10.x1 Scares_pregnant_utarus_NM-IPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gb:L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);contains L1.t1 L recettive element:	Т	Г	N m54c09.X1 NCL_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2161836 3'	POLYPEPTIDE NACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDPACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC-POLYPEPTIDE, N-TACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1)	Homo sepiers FRA3B common fregile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5	N RC3-BT0316-170200-014-e05 BT0318 Homo sapiens cDNA	Homo sepiens chromosome 21 segment HS21C027					T OLFACTORY RECEPTOR-LIKE PROTEIN COR6	Homo sepiers chromosome 9 duplication of the T cell receptor beta locus and trypstnogen gene families							N RCO-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
Top Hit Detabese Source	EST_HUMAN	<b>EST_HUMAN</b>	F	Ę	EST HUMAN	Z	SWISSPROT	EST_HUMAN	SWISSPROT	¥	EST_HUMAN	IN	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	SWISSPROT	Ā	SWISSPROT	EST_HUMAN	<b>EST_HUMAN</b>	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	2.0E-11 R24807.1	2.0E-11 R24807.1	2.0E-11 L17432.1	20E-11 L17432.1	2 0F-11 Al128371 1	AF087913.1	2.0E-11 P10263	2.0E-11 AI478617.1	Q10473	2.0E-11 AF020503.1	2.0E-11 BE065537.1	2.0E-11 AL163227.2	2.0E-11 BE062558.1	2.0E-11 AW877806.1	2.0E-11 AA581028.1	2.0E-11 BF592945.1	P37072	20E-11 AF028308.1	Q13608	2.0E-11 AW885874.1	2.0E-11 AW885874.1	2.0E-11 AA035369.1	2.0E-11 AA035369.1	2.0E-11 AA261956.1	2.0E-11 AW842143.1
Most Similar (Top) Hit BLAST E Value	2.0E-11	2.0E-11	2.0E-11	20E-11	2 OF-11	2.0E-11	2.0E-11	2.0E-11	2.0E-11 Q10473	2.0E-11	2.0E-11	2.0E-11	2.0E-11	2.0E-11	2.0E-11	2.0E-11	2.0E-11 P37072	2.0E-11	2.0E-11 Q13608	2.0E-11	2.0E-11	2.0E-11	2.0E-11	2.0E-11	2.0E-11
Expression Signal	4.48	4.46	5.86	5.86	25	\$	8.7	-	0.77	1.09	1.24	96'0	238	-	1.71	0.82	0.51	1.31	4.42	0.85	0.85	1.54	1.54	214	4.12
ORF SEQ ID NO:	27186		27624			28787	29189	28309	28350					32562	32768	33722			37065	37305		37935	37836	Ш	
Exan SEQ ID NO:	14229		14649		1	1	1	_		16554	17498	17667	17988	18331	19508	20369	L_	22540		23802	L	l	24391	Ш	Ш
Probe SEQ ID NO:	1189	1189	1617	1617	, (%)	2775	3211	3337	3375	3508	4472	4636	4973	8228	8448	7401	8214	9678	10647	10882	10882	11448	11448	11477	12326

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Top Hit Descriptor	CM2-TN0140-070900-372-g01 TN0140 Homo saplens cDNA	Homo septens mRNA for KIAA0027 protein, partial cds	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	Homo sapiens SEC14 (S. cerevisias)-like 2 (SEC14L2), mRNA	Homo saplens SCL gene locus	Homo sepiens chromosome 21 segment HS210009	Homo sepiens chromosome 21 segment HS210079	Homo septems PRC3078 mRNA, complete cds	OXYSTEROL-BINDING PROTEIN	Homo sepiens homogentisete 1,2-diavygenese gene, complete ods	EST180186 Liver, hepatocellular carcinoma Homo sepiens cDNA 5 end similar to EST containing Alu repeat	CMO-BN0106-170300-292-d12 BN0105 Hamo sapiens cDNA	axistro6.s1 Soares_NhHMPu_S1 Homo sepiens cDNA clare IMAGE:1681243 3'	Homo sepiens chromosome 21 segment HS21C047	7p57d01.x1 NCI_CGAP_Pr28 Homo septens cDNA clone IMAGE:3646945 3' strnilar to contains MER10.b3	MER10 repetitive element;	Homo sapiens PTS gene for 6-pyruvoyftetratrydroptenth synthese, complete cds	Homo sapiens PHD finger protein 2 (PHF2) mRNA	y73d08_r1 Scares infant brain 1NIB Homo saplens cDNA clone IMAGE:28166 5	QV4-NN1149-250600-423-e03 NN1149 Homo septems cDNA	QV4-NIN1149-250600-423-603 NN1149 Homo sepiens cDNA	602154807F1 NIH_MGC_83 Hamo sapiens cDNA clone IMAGE:4285877 5	PREGNANCY ZONE PROTEIN PRECURSOR	Homo sepiens chromosome 21 segment HS21C100	Homo sepiens chromosome 21 segment HS21C100	OKFZp58610417_1 586 (synchym: huter) Homo septems cONA clone OKFZp58610417 5	IL 5-BT0578-130300-038-G12 BT0578 Hamo sepiens cDNA	Homo sapiens Xq pseudoautosomai region; segment 2/2	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)	223g01.s1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4511523'	AV730554 HTF Hamo sepiens cDNA clans HTFAW F08 5	nz8811.s1 NCI_CGAP_GCB1 Homo sapiens cDNA done IMAGE:1302573 3' similar to contains Alu	repenive evenent
Top Hit Database Source	EST HUMAN		SWISSPROT		NT				SWISSPROT	TN.	EST_HUMAN	EST_HUMAN	EST_HUMAN	Г		EST_HUMAN	NT		THUMAN	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	SWISSPROT	M	NT	EST_HUMAN	EST_HUMAN	F	SWISSPROT	<b>EST_HUMAN</b>	EST_HUMAN		EST_HUMAN
Top Hit Acessian · No.	2.0E-11 BF377859.1			11417988 NT	1.0E-11 AJ131016.1	1.0E-11 AL163209.2	1.0E-11 AL163279.2	1.0E-11 AF119914.1	16258	1.0E-11 AF000573.1	1.0E-11 AA308318.1	1.0E-11 BE004315.1	1.0E-11 AI168625.1	1.0E-11 AL163247.2		1.0E-11 BF222846.1	1.0E-11 AB042297.1	4885546 NT	1.0E-11 R13174.1	1.0E-11 BF365119.1	1.0E-11 BF365119.1	1.0E-11 BF680078.1	P20742	9.0E-12 AL163300.2	9.0E-12 AL163300.2	9.0E-12 AL046939.1	8.0E-12 BE074720.1	8.0E-12 AJZ71738.1	005904	7.0E-12 AA704736.1	6.0E-12 AV730554.1		6.0E-12 AA732516.1
Most Similar (Top) Hit BLAST E Value	2.0E-11	2.0E-11 D25217.2	2.0E-11 P08547	2.0E-11	1.0E-11	1.0E-11 /	1.0E-11	1.0E-11	1.0E-11 P16258	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11		1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	9.0E-12 P20742	9.0E-12	9.0E-12	9.0E-12	8.0E-12	8.0E-12	7.0E-12 Q05904	7.0E-12	6.0E-12		6.0E-12
Expression Signal	2.14	1.49	1.68	3.68	0.83	1.89	4.68	2.95	1.41	3.18	1.15	0.0	1.01	14.43		0.77	0.51	3.36	4.18	1.18	1.18	1.48	0.82	1.02	1.02	2.85	. 0.92	3.22	1.46	7.41	0.95		8730
ORF SEQ ID NO:	31854				26687			İ.	28091	28168	28207	Ĺ		1_		32212		34928	ĺ	L			28946	36558					30605			ĺ	30283
Excan SEQ ID NO:	25148	25313	25399	25604	13740	13844	14259	14531	15072	15153	15186	16556	17975	18508		19017	21049	21511	21894	22368	22368	24557	16021	23082	23082	24047	1_	L	L.	L			17403
Probe SEO ID NO:	12354	12617	12754	13070	229	Ş	1221	1498	2053	2136	2170	3540	6969	5405		5931	8112	8543	8828	9403	9433	11619	2963	10157	10157	12075	88	12407	4690	11677	3558		4375

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Top Hit Descriptor	Homo sepiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exan 5	Morone severalis myosin heavy chain FMSA (FMSA) mRNA, complete ods	od10g11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to conteins Mich23.02. MER29.repetitive element;	EST04462 Fetal brain, Stratagene (cat4836206) Homo sapiens cDNA clone HFBDV33	124/2005, yl N.C. CGAP_BIR52 Homo sapiens cDNA clone IMAGE:2291/217 6	Homo sepiens Xq pseudoautosomal region; segment 2/2	Homo sepiens chromosome 24 segment MSZ103/8	Homo sepiens chromosome 21 segment HS21C078	EST386850 MAGE resequences, MAGN Homo septems CUNA	DKFZp434B1615_s1 434 (synonym: mes3) Homo capiens CUNA come UNT 4p434B1615_s1	DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1616 s	ZO1912.s1 Sogree_fetal_heart_NbHH19W Homo septens CDNA clone IMAGE:375718 3' stimilar to contains	LIS LI repoulte certient;	RC1-010086-220300-011-007 0 10086 Hamo septems curve	DKFZp434.0428_r1 434 (syndrym: mess) mano seprens curvi dane uni spranaza a	Homo sepiens Xq pseudoautosomal region; segment 1/2	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPT OR LIKE PROTEIN HOMPOVE) (OLFACTORY RECEPTOR 17-4) (OR17-4)	Homo sepiens chromosome 21 segment HS21C103	Homo sapiens chromosome 21 segment HS21C102	2/74g11.s1 Scares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:4608/83	274g11.s1 Sogres_fetal_liver_spicen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:460676 3	bZGNO5X1 NCI_CGAP_LL24 Hamo septems cDNA done IMAGE:2270745 3' similiar to TR:Q13539 Q13539 MARINER TRANSPOSASE.;	ned21603_x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3366077 3' sanilar to contains MER7.b2	MER7 repetitive element;	Homo saptens S164 gane, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene,	partial cds	Bos taurus Mich2 mRNA for mitochondria carrier nomotog 2, compress cos	Homo saplens 959 to contig between AML1 and CBK1 on cromosome 21422, wgitten to 3	Homo sapiens Bruton's tyroshe kinase (BTK), apha-O-galactosidase A (GLA), L44-tike moseonia protein (L44L) and FTP3 (FTP3) genes, complete cds
Top Hit Detablese Source	Ŋ	NT	EST HUMAN	Г	EST_HUMAN			$\neg$	٦		EST_HUMAN		٦	П	EST HUMAN	INT	SWISSPROT	Ę	Ę	EST_HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN		Ę	NT	NT	TN.
Top Hit Acession No.	6.0E-12 AF020503.1	6.0E-12 AF003249.1	6.0E-12 AA847898.1	T06573.1	5.0E-12 BE047779.1	5.0E-12 A.1271736.1	5.0E-12 AL 163278.2	4L163278.2	5.0E-12 AW974760.1	5.0E-12 AL040739.1	5.0E-12 AL040739.1		5.0E-12 AA033745.1	5.0E-12 AW887037.1	5.0E-12 AL079581.1	5.0E-12 AJZ71735.1	28076	5 0F-12 At 183303.2	5.0E-12 AL 163302.2	AA700326.1	4.0E-12 AA700326.1	4.0E-12 AI68984.1		4.0E-12 BF445140.1		4.0E-12 AF109907.1	4.0E-12 AB042815.1	4.0E-12 AJ229043.1	4.0E-12 U78027.1
Most Similer (Top) Hit BLAST E Vatue	6.0E-12/	6.0E-12	6.0E-12	6.0E-12	5.0E-12	5.0E-12	5.0E-12	5.05-12	5.0E-12	5.0E-12	5.0E-12		5.0E-12	5.0E-12	5.0E-12	5.0E-12	5 0E-12   P34082	5 0F-12	5.0E-12	4.0E-12	4.0E-12	4.0E-12		4.0E-12					
Expression	0.65	0.98	188	3.67	1.17	6.8	4.99	4,89	9.52	-	1.8		1.14	7.0	95.0	2.78	90	414	0.84	4.17	5.51	0.74		0.72		2.92		3.26	282
ORF SEQ ID NO:	32851	35736		27043	29376	78887			32973	33274	33274		34960			36887		L	37144		19596	Ì		_			35422		
Exan SEQ ID NO:	19591	22312	23878	14080	16450	16782	19214	19214	19697	18977	18977		21539	21981	22311	22428	1	28680	2882	13342	13342		1	20825		21553	L	L	1.
Probe SEQ ID NO:	8538	8847	883	1044	260	3740	6137	6137	6839	7232	7242		8571	9015	9346	9464		0110		244	245	View.		788		8685	9835	11419	12658

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Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Delabase Source	Top Hit Descriptor
123	13231	28169	283		1.0E-12 AW627674.1	EST_HUMAN	hts0e09.x1 NC_CGAP_GU1 Homo septens cDNA done IMAGE:2970040 3' strailer to contains MER18.t1 MER18 repetitive element ;
2004	15025		1.46		1.0E-12 AI871726.1	EST_HUMAN	wm51f07.x1 NCI_CGAP_Ut2 Home septens cDNA clone IMAGE:2439463 3' similar to contains L1.b3 L1 repetitive element;
3086	l				1.0E-12 AF000991.1	NT	Homo septems testis-specific Testis Transcript Y 2 (TTY2) mRNA, pertial cds
3085	l				1.0E-12 AF000991.1	NT	Homo septems tastie-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3888	l		31.6		1.0E-12 AU132248.1	EST_HUMAN	AU132248 NT2RP3 Hamo septens aDNA dans NT2RP3004070 5"
3888	16928		31.6		1.0E-12 AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo septens cDNA clone NT2RP3004070 6"
8709	19158		2.05		1.0E-12 U82828.1	NT	Homo sepiens ataxia telangiectasia (ATM) gene, complete cds
6469	19234		1.65		1.0E-12 09Y2G7	SWISSPROT	HYPOTHETICAL ZING FINGER PROTEIN KIAA0961
6277	16340				1.0E-12 BF642800.1	EST HUMAN	EST00008 Sogres JNPL_T_GBC_S1 Homo, septens cDNA chare IMAGE:1847869 5
0277	18349		0.57		1.0E-12 BF642800.1	EST_HUMAN	EST00008 Soares_NRL_T_GBC_S1 Hamo septens cDNA clane IMAGE:1847869 5
							Mus musculus WNT-2 gene, partial cds; putative enkyrin-related protein and cystic fibrosis transmembrane
6882	19739	33014	0.78		1.0E-12 AF228843.1	Ŋ	conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unlocown gene
7323	1		1.9		1.0E-12 AF198864.1	NT	Homo sapiens putative BPES syndrome breekpoint region protein gene, complete ods
							qh88a04.x1 Soares_fetal_fiver_spieen_1NFLS_S1 Homo sepiens cDNA cione IMAGE:1849614 3' stinilar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.th MER10
7357	720227	33675	11.35		1.0E-12 AI248533.1	EST_HUMAN	repetitive element;
							qh88a04.x1 Soares_felai_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 S' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.th MER10
7357	20327	33676	11.35		1.0E-12 AI248533.1	EST_HUMAN	repetitive element;
							Human germiine T-cail receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3,
					·		TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1NZT, TCRBV5S1A1T, TCRBV13S3.
	200	06350			4 OE 42   188080 4	5	ICABV6S7P, ICABV7S3AZI, ICABV13SZATI, ICABV8SZAZPI, ICABV7SZATIN4I, ICABV13S9A3S>
8963					1.0E-12 AA782323.1	EST HUMAN	ac28d05.s1 Strategene oyary (#837217) Homo sapiens cDNA clone IMAGE:857577 3'
12213	}			Ĺ	1.0E-12/AW982164.1	EST HUMAN	EST374237 MAGE resequences, MAGG Homo sepiens cDNA
12434	1 .		2.54		1.0E-12 AI738592.1	EST HUMAN	wis3th08.x1 NCI_CGAP_Co16 Hamo saplens cDNA dane IMAGE:2382096 3'
12582	25881		251		1.0E-12 AL163268.2	TN	Homo saplens chromosome 21 segment HS21C088
	_						xb6/fi07.x1 Scares_NFL_T_GBC_S1 Hamo sapiens cDNA clone IMAGE:2580805 3' similar to contains
1054	14100	27050			9.0E-13 AW082714.1	EST_HUMAN	MER28.t3 MER28 repetitive element;
3643					9.0E-13 AJZ71735.1	LN.	Homo saplens Xq pseudoautosomal region; segment 1/2
3967	17007	29923	96.0		9.0E-13 AB029900.1	L L	Homo saplens CST gene for cerebroside sulforransferase, exon 1, 2, 3, 4, 5
							•

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Table 4
Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	za26508.s1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:283651 3'	Homo sapiens prion protein (PrP) gene, complete cots	Homo sapiens prion protein (PrP) gene, complete cds	Homo sepiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis tritibitory moden (near) and sundval motor neuron protein (smm) cenes, complete cds	WASHINGTON NCI CRAP LIM Homo seniers d'INA cione IMAGE:24376013	wm31h09x1 NCI_CGAP_U4 Homo septens dDNA clone IMAGE:2437601 3'	Homo sepiens Bruton's tyrostne kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein	(L44L) and FTP3 (FTP3) genes, complete cds	wm31h09x1 NCI_CGAP_Ut4 Homo sapiens cDNA cane IMAGE:2437601 3	wm31h09x1 NCL CGAP Ut4 Homo septems cDNA came IMAGE:2437001 3	OLFACTORY RECEPTORLINE PROTEIN OLFZ	601463285F1 NIH_MGC_67 Homo septens cDNA clone IMAGE-3868673 6	Homo saplens chromosome 21 segment HS21C007	y82604,r1 Scares placenta Nb2HP Homo septens cDNA clone IMAGE:145759 5	z77412.81 Soares_testis_NHT Homo sepiens cDNA done IMAGE:728350 3' similar to contains Alu Increditive element Contains element MER22 repetitive element;	CAP JI INCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)	INVOSINI KHT CHAIN KINASE SKELETAL MUSCLE (MLCK)	PAINTHT024.221094.001-414 HT0224 Homo seciens cDNA	1 manual and the Company of CDC3 man harded one and family mental molecus.	Truth Septembly Myndail 3 (34 Cd.) years, parties child child (35-795489 5)	PATTO TO TO TO THE TOTAL TO LITTLE HAVE CONTINUED AND A	PMS-FILLOSCI-230/200-00/2-000 TI TOUGO I MILID SEPARATO VATOR	FIGURE SEPTEMBER TO NATIONALIZE PRODUIT, POR CONTRACTOR 2004 BY Application for TD-CA457789	2W/8g12.rl Soares, testes, trains express curva carre invaces, focios o seitua de incorporado (2452763 COR1 MRNA.;	1y33g05.r1 Scares melanocyte ZNIHIM Homo saptens cONA clone IMAGE:273080 5' similar to PIR:A32895	A32995 t complex sterility protein - mouse;	DKFZp434A0128_r1 434 (synonym: https3) Hamo saplens cDNA clane DKr-zp434A0128 s	7B04H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B04H11	qn32d05.x1 NCI_CGAP_Kd5 Homo sepiens cDNA clone IMAGE:1899945 3' similar to contains Alu nerveitine element:	1-778-10 st Sogres testis NHT Homo septens cDNA clone IMAGE:728514 3'.	ATTRACTOR Somes testis NHT Homo seniens CDNA clone IMAGE:7285143	410g 10.01 Octave Common and the com
	Top Hit Database Source	EST_HUMAN	NT	NT	L.	NI FOT LIMAN	EST HUMAN		¥	EST_HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	TN.	EST_HUMAN	ECT LIMAN	CWISCODOT	GWISSERGI	NAN TOTAL	ביייים ביייים	NI TOT	ESI HOMAN	EST_HUMAN	Ž	EST HUMAN		EST HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	EST HIMAN	EST LITTAN	COT LINAN	ESI TOWAN
B	Top Hit Acession No.	N69653.1	J29185.1	J29185.1	7 17000	8.0E-13 U80017.1	8.0E-13 AI884398.1 8.0E-13 AI884398.1		8.0E-13 U78027.1	7.0E-13 AI884398.1	7.0E-13 AI884398.1	Q95155	7.0E-13 BE778223.1	8.0E-13 AL163207.2	5.0E-13 R78338.1	444957794	5.0C-13 AARBOUTS.	PU6963	FU/313	4.0E-13 AW3/8014.1	4.0E-13 AF003529.1	4.0E-13 AA454054.1	4.0E-13 BE169131.1	4.0E-13 AB037750.1	4.0E-13 AA431529.1		4.0E-13 N44291.1	4.0E-13 AL043810.1	4.0E-13 AA076907.1	4 66 4 1200034 4	A 405040 4	4.0E-13 AA433619.1	4.0E-13 AA435818.1
	Most Similar (Top) Hit BLAST E Vatue	9.0E-13 N69853.1	8.0E-13 U29185.1	8.0E-13 U29185.1		8.05-13	8.0F-13/	21	8.0E-13	7.0E-13	7.0E-13	7.0E-13 Q95155	7.0E-13	6.0E-13	5.0E-13	200	9.0E-13	0.0E-13 PUSSES	5.0E-13 PU/313	4.0E-T3	4.0E-13	4.0E-13	4.0E-13	4.0E-13	4.0E-13		4.0E-13	4.0E-13	4.0E-13				
	Expression Signal	259	6.78	6.78		3.1	0.75	2	4	0.58	0.58	0.49	5.56	3.56	0.74		06:1	0.7	20/	6.02	244	0.89	4.38	1.05	88		1.47	12	0.59		"		1.9
-	ORF SEQ ID NO:		28714	26715		1	34831	1_		34462	34463			28148					37693					33731	34100			35587			1	-	37996
	SEQ ID NO:	22887	13780	13780		14881	21418	21410	23427	21064	21084	2544	25350	15128	16384		1040	20082	24163	4908	15471	17798	18762	20380	AMAK	L	20828			l	1		24444
Ì	Probe SEQ ID NO:	88	18	7.18		1855	8 8	3	10505	8127	8127	8576	12682	714	3333		3	8	1200	# 88	2467	4778	5687	7413	07.87		7989	9183	0880		10380	11502	11502

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Top Hit Descriptor	Homo sepiens X-linked anhidrotitic ectodermal dysplasta protein gene (EDA), exan 2 and flanking repeat regions	zw68g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781406 5	Homo sepiens Xq pseudoautosomel region; segment 2/2	Homo saplens chromosome 21 segment HS21C010	CMS-FT0100-140700-242-h08 FT0100 Homo sapiens cDNA	ob 18d02 s1 NCI_CGAP_Kd5 Homo septens cDNA done IMAGE:1324035 3'	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)	zn88h10.r1 Stratagene lung carcinoma 837216 Homo sepiens cDNA clone IMAGE:565315 5' simiter to contains THR.t2 THR repetitive element ;	zn88h10.r1 Stratogene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR.t2 THR repetitive element;	wz88c02.x1 NCI_CGAP_Brn25 Homo saplens cDNA clone IMAGE:2565890 3' similar to TR:O75139 075139 KIAA0644 PROTEIN.;	Homo septiens X28 region near ALD locus containing duel specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Celmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrendeukodystrophy protein >	EST80487 Activated T-cells XX Homo sapiens cDNA 5 end similar to serine protesse P100, Re-	reactive factor	EST60487 Activated T-cells XX Homo saptens cDNA 5' end similar to similar to serine protesse P100, Raneactive factor	RC2-DT0007-110100-014-g10 DT0007 Hamo sepiens cDNA	HA0536 Human fetal liver cDNA library Homo sapiens cDNA	CMI0-BT0281-031199-087-e03 BT0281 Homo seplens cDNA	Hamo expiens chramosome 21 segment HS21CD48	Homo septens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Catmodulin-dependent protein lonase I (CAMKI), creatine transporter (CRTR),	CDM protein (CDM), adrenoleukodystrophy protein >	Hamo septens DNA polymerase deta small subunit (POLD2) gene, exons 1 through 11 and complete cds	nab76/05.x1 Scares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
Top Hit Databese Source	IN.	EST_HUMAN	NI	NT	EST_HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	EST HUMAN	EST_HUMAN	Į,		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT		Ę	NT	EST_HUMAN	Į.
Top Hit Acession No.	3.0E-13 AF003528.1	3.0E-13 AA430310.1	3.0E-13 A.1271736.1	3.0E-13 AL163210.2	3.0E-13 BF372962.1	3.0E-13 AA745844.1	P18616	P18616	3.0E-13 AA134017.1	3.0E-13 AA134017.1	3.0E-13 AW005639.1	3.0E-13 U52111.2		3.0E-13 AA352487.1	3.0E-13 AA352487.1	3.0E-13 AW835487.1	3.0E-13 AI064768.1	3.0E-13 BE063509.1	3.0E-13 AL163248.2		2.0E-13 U52111.2	2.0E-13 AF239710.1	2.0E-13 BF431899.1	2.0E-13 AF109907.1
Most Similar (Top) Hit BLAST E Value	3.0E-13	3.0E-13	3.0E-13	3.0E-13	3.0€-13	3.0E-13	3.0E-13 P18616	3.0E-13 P18616	3.0E-13	3.0E-13	3.0E-13	3.0E-13		3.0E-13	3.0E-13	3.0E-13	3.0E-13	3.0E-13	3.0E-13		2.0E-13	2.0E-13	2.0E-13	2.0E-13
Expression Signal	P.3.	3.35	1.65	211	25	2.19	8.0	6.0	0.64	0.64	0.71	8.24		0.51	0.61	0.48	2.68	3.32	15.		3.93	7.14	1.08	1.25
ORF SEQ ID NO:			28410		88987		20484	29485	31872			34594		34787	34788	30976			38338		26183	NZIZ		29489
Exan SEQ ID NO:	13284	13922	L	L _			16560		18714	L	<u> </u>	<u> </u>	1_	21381	21381	Ĺ.,	1		L		13254	14310		16564
Probe SEQ ID NO:	181	88	2378	2487	2873	3201	3514	3514	5618	5618	9106	8.24		8412	8412	10558	11036	11386	11924		151	1275	3284	3518

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	Top Hit Descriptor	Hamo sapiens chromosame 21 segment HS21C078	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)	Human PRKL gane for liver-type 6-phosphofnuctokinase (EC 2.7.1.11) extra 2	Homo sepiens N-myristoyfransferase 1 (NMT1), mRNA	Homo sapiens N-myristoyfarnsferase 1 (NMT1), mRNA	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA	CMO-NND001-100300-274-e11 NN0001 Homo septems cDNA	FGF-1=fbroblast growth factor 1 [human, kidney, Genomic, 342 fit, segment 2 of 2]	Homo sapiens LGMDZB gene	H.sepiens D.M.A., D.M.B., H.L.AZ1, IPP.2, L.M.P.2, T.A.P.1, L.M.P.7, T.A.P.2, DOB, D.Q.B.2 and R.ING-8, 13 and 14 demos	mw21g02.s1 NCI_CGAP_GCB0 Homo sepiens cDNA clone IMAGE:1241138 3' stmiler to contains THR.t3	THR repetitive element;	602038009F1 NCI_CGAP_Bm64 Hamo sapiens cDNA clane IMAGE:4185888 5	y1636, seq. F Humen fetal heart, Lambda ZAP Express Homo septens cDNA 5	m24d01.s1 NCI_CGAP_Gas1 Homo septens cDNA clone IMAGE:1084801 3' similar to contains Alu	repetitive element,contains element MER24 repetitive element;	m24d01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similer to contains Alu repositive element contains element MER24 repositive element ;	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)	Mus musculus estadesticular protein tyrosine phosphatase mRNA, complete cds	745er0.x1 Scares_NSF_F8_8W_OT_PA_P_S1 Homo sapiens cDNA clane IMAGE:3524443 3' similar to	contains MERZ9.b2 MERZ9 repetitive element;	AV715377 DCB Homo saplens cDNA done DCBAIEG3 5	Homo sepiens Xq pseudosutosomal region; segment 1/2	aj24c01.s1 Scenes_testis_NHT Homo sapiens cDNA clone 1391232 3 smiler to contains MEK18.t1 MEK18	repatitive element;	e/24001.s1 Scenes testis_NHT Homo sepients CLINA cione 1397/222 3 samilar di contentis micro e inicione	repetitive element;	RC4-CT0322-080100-013-d09 C10322 Hamo septens GUNA	Homo sepiens mRNA for sodium-glucose contensporter (SGL ( 2 gene)	Homo sepiens miRNA for sodium-glucose corransporter (SGL1 2 gene)	Hamo sapiens i FF gene guister for trefoi radial, complete das
	Top Hit Database Source	NT	SWISSPROT 1)	П				EST_HUMAN CA	NT	NT Ho	H E		EST_HUMAN TH	П	EST HUMAN M		EST HUMAN IN	EST HUMAN TER	Т	Τ	Г	П	L HUMAN	¥ LN		EST HUMAN 118		╗	T_HUMAN			Ť.
	Top Hit Acession No.	2.0E-13 AL163278.2		-	10835072 NT	10835072 NT	5031896 NT	2.0E-13 AW892155.1	1.0E-13 S74129.1	1.1	4 0E-43 YB7344 1		1.0E-13 AA720574.1	1.0E-13 BF340987.1	1.0E-13 AA090732.1		1.0E-13 AA577812.1	1 05 43 44577812 1	015481	1.0E-13 AF300701.1		1.0E-13 BF108756.1	1.0E-13 AV715377.1	1.0E-13 AJZ71735.1		9.0E-14 AA781159.1		9.0E-14 AA781159.1	9.0E-14 AW861577.1	9.0E-14 AJ133127.1	9.0E-14 AJ133127.1	9.0E-14 AB038162.1
	Most Similar (Top) Hit BLAST E Value	2.0E-13	2.0E-13 0.08652	2.0E-13	2.0E-13	2.0E-13	2.0E-13	- 20E-13	1.0E-13	1.0E-13	4 OF 43		1.0E-13	1.0E-13	1.0E-13		1.0E-13	1 05.43	4 OF-43 O15481	1.0E-13		1.0E-13	1.0E-13	1.0E-13		9.0E-14		9.0E-14	9.0E-14	9.0E-14	9.0E-14	9.0E-14
-	Expression Signal	1.61	471	6.40	0.50	0.50	4.63	5.43	1.49	4.85	7	3	2.43	22	0.61		0.78	g, c	0.00	0.49		10.13	2.34	3.21		3.14		237	4.8	1.03		6.94
	ORF SEQ ID NO:		32548						26312			2	28074				34616		1	37084		38240				26345		26346		28617		28777
	Exam SEQ ID NO:	17167	1	1_	1	ı		25165	13385	13944		2/24	15056				221		717			24672	L			13422		13423	L		L.	
	Probe SEQ ID NO:	4135	8246	2887	7255	7255	10824	12387	8	888	885	200	2037	4623	AS 78		8242	3	02/67	1088		11707	12206	12844		333		334	8833	2887	2897	2764

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Table 4
Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	xx64Hx65x1 NCI_CGAP_Utf Hamo capiens cDNA clane IMAGE:2707833 9'	e[24c01.s1 Sogres_testis_NHT Homo septens cDNA clone 1391232 3' straiter to contains MEK19.th MEK19 repetitive element :	Human DNA, SINE repetitive element	Seguinus cedipus gane for seminal veside secreted protein somenogean	hz71c08.x1 NCI_CGAP_Lu24 Homo septems cDNA clone IMAGE:3213424 3	y72e03.rf Sceres placenta Nb2HP Homo sapiens cDNA cone IMAGE:144/95 3	H.saplans DNA for endogenous retroviral like element	zq17c10.s1 Stratagene fetal retina 937202 Homo sapiens CDNA clone IMAGE:5628970 S	QV2-BT0258-261099-014-e01 BT0258 Homo sepiens cDNA	wc92h08.x1 NCJ_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:22/26143 3	x87e10.x1 NCL_CGAP_Gas4 Homo septens cONA clone IMAGE.2023146 3' similar to contains MEKTU.12 MEB40 receiffice element :	TO THE PROPERTY OF THE PROPERT	Homo sapiens officialisms at segment reactives	Homo sepiens FRA3B common fragile region, diadenosine triphosphate hydrolese (FHIT) gene, exon 5	Homo sepiens FRA3B common fregile region, diadenosine triphosphate hydrolese (FHIT) gene, exen 6	Homo saptens FRA3B common fregile region, diadenosine triphosphate hydrolese (FHIT) gene, exon 5	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)	Homo eaplens chromosome 21 segment HS21C047	xb03b05x1 NC _CGAP_GU1 Homo sepiens cDNA done IMAGE:2575185 3' similer to contains L1.1Z L1 repetitive element;	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	S-ANTIGEN PROTEIN PRECURSOR	Homo septems LGMD/2B gene	2467808.rf Scares_pregnant_uterus_NbHPU Homo sepiens cONA clone IMAGE:487838 5	y/73c12.s1 Soares_multiple_scierosis_2NbHMSP Homo sapiens cDNA clone IMAGE:279190 3' stratiar to contains L1.t3 L1 repetitive element ;	H. septiens DMA, DMB, HLA-21, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RINGS, 9, 13 and 14 nerves	
	Top Hit Detrabase Source	EST HUMAN	EST HUMAN	TM	NT.	EST_HUMAN	HUMAN			EST_HUMAN	EST HUMAN		NA CENT	Ę	Į.	Ę	NT	ISSPROT	K	EST HUMAN	SWISSPROT	SWISSPROT		EST_HUMAN	EST HUMAN	<u> </u>	
	Top Hit Acession No.	9.0E-14 AW513298.1	9.0E-14 AA781159.1	9.0E-14 D14547.1	9.0E-14 AJ002153.1	8.0E-14 BE468283.1	8.0E-14 R76289.1	8.0E-14 X88211.1	8.0E-14 AA218316.1	8.0E-14 BE062558.1	8.0E-14 AI688118.1	7 6202377	7.0E-14 AW1016/3.1	7.0E-14 AL163285.2	6.0E-14 AF020503.1	6.0E-14 AF020503.1	6.0E-14 AF020503.1	Q63120	5.0E-14 AL163247.2	5.0E-14 AW073791.1		P04928	4.0E-14 AJ007973.1	4.0E-14 AA046502.1	4.0E-14 N46328.1	7070X	4.0E-14 X8/344.1
	Most Similar (Top) Hit BLAST E Vætue	9.0E-14	9.0E-14	9.0E-14	9.0E-14	8.0E-14	8.0E-14	8.0E-14	8.0E-14	8.0E-14	8.0E-14	77 -00-	41-30:/	7.0E-14	6.0E-14	6.0E-14	6.0E-14	5.0E-14 Q63120	5.0E-14	5.0E-14	5.0E-14 P08547	4.0E-14 P04928	4.0E-14	4.0E-14	4.0E-14	100	4.0E-14
	Expression Signal	5.43	0.67	7.16	1.68	1.44	3.46	21.45	3.1	1.52	289		3.89	0.51	16.94	254	254	523	0.95	130	484	1.95	7	-	98.0		9.6
	ORF SEQ ID NO:	29094	26845	29759	30690			34630	36192		31783				26381	36587	36588			02002			27916		82028		
	SEQ ID	16185	19422	16851	17807	16555	17018	21128	22739	24690	26294		15873	22238	13453	23106	L	<u></u>	16726			1_	L.		<u></u>	1_	21280
Ī	Probe SEQ ID NO:	3128	3252	3811	4789	3509	3978	8803	8918	11782	12590		1633	2228	367	10181	10181	QZ9	3683	2002	2000 4000 4000 4000 4000 4000 4000 4000	1125	1895	378.F	3		88

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Single Exon Probes Expressed in Bone Marrow

ORF SEQ Expression (Top) Hit Top Hit Acession Database ID NO: Signal Vatue Vatue	36887 0.62 2.0E-14 AI978795.1 EST_HUMAN	37203 0.53 2.0E-14 AV741648.1 EST_HUMAN	37622 3.94 2.0E-14 AW139800.1 [EST_HUMAN	1.71 2.0E-14 AF008191.1 INT	27063 2.09 1.0E-14 AL163246.2 NT	27406 8.16 1.0E-14/AL163268.2 NT	27407 8.16 1.0E-14/AL163268.2 NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-8-phosphate dehydrogenase nose 15.42 1.0E-14 [44140.1 NT (G6PD) gene, complete cds's	28228 5.77 1.0E-14 AL163303.2 NT	28449 6.29 1.0E-14 AF001689.1 NT	28940 1.05 1.0E-14 P05227 SWISSPROT	29154 6.2 1.0E-14 BF335227.1 EST_HUMAN	29166 8.2 1.0E-14 BF335227.1 EST_HUMAN	28852 1.75 1.0E-14 AA682894.1 EST_HUMAN	30410 2.07 1.0E-14 AW275852.1 EST_HUMAN		32184 2.1 1.0E-14/AF128145.1 NT	33176 11.02 1.0E-14 11437150 NT	33177 11.02 1.0E-14 11437150 NT			1.37 9.0E-15 AF186779.1 NT	34056 4.28 9.0E-15 P21416 SWISSPROT	34733 1.17 9.0E-15 BE903559.1   EST_HUMAN	1.42 8.0E-15 BE281482.1 EST_HUMAN	33708 1.55 7.0E-15 BF035327.1   EST_HUMAN	2.45 7.0E-15 AW241958.1 EST HUMAN	27001 6.55 6.0E-16/AJZ71736.1 NT	32311 1.11 6.0E-16 X73462.1 NT	19/10 32312 1.11 6.0E-15 X73462.1 NT O.arles mRNA for hair keratiin cystelne-rich protein
									L													92								
D SEQ ED	10277 23202	L	Ł_			1405 14438	1405 14438	2017 15038	L		L.	3182 18237	3182 16237	3901 16941	4500 17525	L	5807 18993	831 25669	١	1579 14612	ı	 2183 15198	7738 20683	8350 21319	L.	7387 2035	10801 23722	996 14047	6027 19110	6027 1911
Probe SEQ ID NO:	۽ ا	2	F	12		Ť	۲		N	ñ	ă	က်	'n	క	4		Ø	g	8	Ĕ		Ö		86	N		후 -		Ø	Œ

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Single Exon Probes Expressed in Bone Marrow

gle Exon Probes Expressed in Borne Mariow	Top Hit Descriptor	Homo sapients chromosome 21 segment HS21C008	Human hereditary haemochromatosis region, histona 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphata transporter (NPTS) gene, complete cds	UIH-BW0-qfb-g-10-0-UI.s1 NCI_CGAP_Sub6 Homo sepiens cDNA done IMAGE:27312193	AV730058 HTF Homo saplens CDNA clone HTFAVE08 5	Homo sepiens diramosome 21 segment HS21C103	Homo sepiens mRNA, chromosome 1 specific transcript NIAAU301	Homo sapiens mRNA for transcription factor	Homo sepiens mRNA for transcription factor	LY1142F Human fetal heart, Lambda ZAP Express Homo saptens CUNA Gone LY1142 5 similar to ANF(CARD/ODILATIN)	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RT2D1)	Mus musculus ultra high suifur learatin gene, complete cds	Was musculus uitre high suifur keretin gene, complete eds	oc38a07.s1 NC_CGAP_GCB1 Homo sepiens cDNA clone IMAGE:1351764 3' stmilar to contains MEK19.t1 MFR10 receitive element :	Home services DNA DI ECH to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cos, attentiaevary	peoples	Homo sapiens calcium channel alpha1E subunit (CACANA1E) gene, exons 7-49, and parau ous, ausmauvay spitoed	Homo sepiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, atternativery	boiled	h09g01.x1 NCI_CGAP_Kid13 Hamo sapiens cDNA clone IMACIE.3140.200 3' similiar to contains microsus. MFR29 repetitive element :	Provot 4 NCI CSAP KH13 Home seniens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3	MER29 repetitive element;	xp28h01.x1 NCI_CGAP_HN10 Homo sapiens dDNA clone IMAGE2741521 3' strittat to contains L1.55 L1 prodettius element :	charte equal t
Xon Probes Ex	Top Hit Defebase Source	¥	Ę		T_HUMAN				±	EST HUMAN	Г	EST_HUMAN 7	SWISSPROT	Į.	Ę	OCT LIMAN	Τ	¥		¥	Ę.		۲	EST HIMAN	1	EST_HUMAN		EST HOMBIN
a eguis	Top Hit Acession No.	5.0E-15 AL163208.2	5.0E-15 U81328.1	5.0E-15 AW 296817.1	5.0E-15 AV730056.1	4.0E-15 AL163303.2			4.0E-15 AJ130894.1	3.0E-15.N89452.1	3.0E-15 AA078097.1	3.0E-15 AA078097.1	064625	3.0E-15 M27885.1	3.0E-15 MZ7685.1	10077004	3.UE-10 AMOU/120.1	3.0E-15 AB026898.1		2.0E-15 AF223391.1	20E-15 AF223391.1		2.0E-15 AF223391.1	0.00 45 05050477 4	DE300127.1	2.0E-15 BE350127.1		2.0E-15 AWZ38499.1
	Most Similar (Top) Hit BLAST E Veitue	5.0E-15	5.0E-15	5.0E-15	5.0E-15	4.0E-15	4.0E-15	4.0E-15	4.0E-15	3.0E-15	3.0E-15	3.0E-15	3.0E-15 Q64625	3.0E-15	3.0E-15	1000	3.05-10	3.05-15		2.0E-15	2.0E-15		2.0E-15	1000	205-10	20E-15		2.0E-13
	Expression Signal	5.24	2.05	1.08	227	3.54	0.98	1.78	1.79	8 54	0.67	0.67	127	3,66	3.68		7,00	3.42		4.45	4.01		4.01	3,	ZU.T	1.02		121
	ORF SEQ ID NO:	26418	28782			26020			ľ	i	30058				02883			37833		28273	Ĺ		26383		28413	28414		30023
	Exan SEQ ID NO:	13483	15783	18528	23999	13122	19876	21088	21088	47074	18077	18077	20200	20460	20460		23210	24106	1_	13347		Ι.	13454	<u> </u>	15388	15389	ł	17129
	Probe SEQ ID NO:	410	1	2482	11035	427	8822	1401	11401	104E	200	2909	8888	7485	7405		10285	11148		280	368		388		2381	7384		4095

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Top Hit Descriptor	wf07f06.x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2348923 3' similiar to TR:Q61043 Q61043 NINEIN: ;	601344253F1 NIH_MGC_8 Hamo sepiens aDNA dane IMAGE:3677268 5	601344253F1 NIH_MGC_8 Hamo septens cDNA dane IMAGE:3677268 5	Hamo sapiens ASCL3 gene, CEGP1 gene, C11 arf14 gene, C11 arf15 gene, C11 arf16 gene and C11 arf17	gene	2/7/ed3.s1 Scares feda [iver_spiesn_1NHLS_51 Homo septems curv. carre invivor	ze78d10.r1 Sceres_fetal_hung_NbHL19W Homo septens cDNA ctone IMAGE::288975 5' similar to WP:F44F4.8 CE02227 TRANSPOSASE;	Homo sepiens chromosome 21 segment HS210047	Human DNA, SINE repetitive element	2177g08.r1 Soares_testis_NHT Homo sapiens cONA clone IMAGE:728414 5	277g08.r1 Sceres_testis_NHT Homo sepiens cDNA clone IMAGE:728414 5	CMO-HT0244-201099-078-a12 HT0244 Homo sepiens cDNA	CM0-HT0244-201099-078-e12 HT0244 Homo sepiens cDNA	Homo sepiens Xq pseudosutosomal region; segment 1/2	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively	spliced	Homo sepiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cos, attemetively soliced	626H05.x1 NCI CGAP_LL24 Homo sepiens aDNA clane IMAGE-2270745 3' stmilar to TR.Q13539 Q13539	MARINER TRANSPOSASE.;	hika0e02 y1 NCI_CGAP_Ov84 Homo septens cDNA clone IMAGE:2899162 6	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	we8e04x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494590 3	ye40e10.s1 Scares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains	MER8 repetitive element;	QV3-BT0569-270100-074-g05 BT0569 Homo sepiens dDNA	DYNEIN BETA CHAIN, CILIARY	Homo saplens chromosome 21 segment HS21C080	qf88fn08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:17552273'	qf88h08.x1 Sogres_testis_NHT Hamo septens aDNA clone IMAGE:17562273	Homo septens chromosome 21 segment HS210007	Homo sapiens spermidine synthase (SRM) mRNA
Top Hit Database Source	EST HUMAN	EST_HUMAN	EST HUMAN		П	EST_HUMAN	EST_HUMAN		Z.	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	K		NT	IN		EST_HUMAN	EST HUMAN	SWISSPROT	EST_HUMAN		EST_HUMAN	EST_HUMAN	SWISSPROT	TN	EST_HUMAN	EST_HUMAN	M	ĮŅ.
Top Hit Acession No.	2.0E-15 Al806335.1	2.0E-15 BE582352.1	2.0E-15 BE682352.1			2.0E-15 AA704195.1	2.0E-15 W05084.1	20E-15 AL163247.2		2.0E-15 AA397758.1	2.0E-15 AA397758.1	2.0E-15 AW379465.1	2.0E-15 AW379465.1	20E-15 AJZ71735.1		2.0E-15 AF223391.1	9 0F-15 AF223391 1		1.0E-15 AI589984.1	3E043584.1	1.0E-15 P08547	1.0E-15 A1984928.1		1.0E-16 T96763.1	1.0E-15 BE074217.1	P39057	1.0E-15 AL163280.2	1.0E-15 AI200976.1	1.0E-15 AI200976.1	1.0E-15 AL163207.2	4507208 NT
Most Similar (Top) Hit BLAST E Value	2.0E-15/	2.0E-15	2.0E-15		2.0E-15/	2.0E-15	2.0E-15 \	2.0E-15	2.0E-15 D14547.1	2.0E-15	2.0E-15	20E-15	2.0E-15	20E-15		2.0E-15	2.05-45		1.0E-15	1.0E-15	1.0E-15	1.0E-15		1.0E-16	1.0E-15	1.0E-15 P39057	1.0E-15	1.0E-15	1.0E-15	1.0E-15	1.0E-15
Expression Signal	273	1.02	1.02		1.42	2.64	4.75	0.67	273	0.74	0.74	1.19	1.19	4.15		3.19	3.10		282	1.53	1.2	1.11		1.83	1.83	0.76	1.04	4.51	4.51	0.49	1.5
ORF SEQ ID NO:		32616				33810	33948		35653	35829	35830					31288		Ì		20002			L	32825		332772					Ш
Exan SEQ ID NO:	17674	18377	18877		20292	20451	20585	21054	22233	22394	22394	22700	22700	24143		18339			15777	L	L		L	19672	Ĺ	1	1	Ĺ.,	L	L	22362
Probe SEO ID NO:	4653	9089	9089		7321	7486	7625	8117	9257	9427	9427	9759	9769	11187		12884	13007		2785	3025	3158	5189		9020	L	7230	8574	8763	8783	8394	9397

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SEQ ID ORF NO: 10 Ph   NO: 52804			AAB62178.1 AAB62178.1 AAB62178.1 AAB62178.1 AAB62178.1 AAJ251164.1	TOP HIT DEBT HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN ES	TOP HIS SWITCH TODGE EXPLICATION IN MAILTON  TOP HIS SWITCH AND AND CHAIN, FLAGELLAR OUTER ARM SWISSPROT DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM GASTAGS at NO. CASA TOCK TOWN TO THE WORLD SWITCH AND THE SWITCH AND THE SWITCH TOWN TO THE WORLD SWITCH AND THE SWITCH TOWN TO THE WORLD SWITCH TOWN TO THE WORLD SWITCH TO THE SWITCH TOWN TO
- L 교ヴ도 1에 외에 이는[이는] 의 의미를 수 문제의의의를등등등등등의미의의의의	8 °	ORF SEQ Express  1D NO: Signification States  38055 38055 30443 377657 30443 377812 30443 377812 30443 377812 30443 377812 30863 33885 33885 33885 32800 33885 32800 33885 32800 33885 33885 32800 33885 33885 33885 33885 33885 33885 33885 33885 33885 338870 338870 338810 338810	ORF SEQ Expression (To Signal BU Sig	ORF SEQ Expression   Most Similar   Top Hit Ace	ORF SEQ Expression (Top) Htt Top Htt Ace (Top) Htt Ace (Top) Htt Ace (Top) Htt Ace (Top) Htt Ace (Top) Htt Top Htt Ace (Top) Htt A

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Ingle Exoli Flobes Expressed III Dolle Mailow	Top Hit Descriptor					ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]	EST08060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end	Homo sepiers FRA3B common fraglie region, diadenosine triphosphate hydrolese (FHIT) gene, exon 5	Human BXP20 gene	П	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions		602246538F1 NIH_MGC_62 Homo saplens cDNA clone IMAGE:4332032 5				П	Human SSAV-related endogenous retroviral LTR-like element	H.saplens DNA for endogenous retroviral like element	HISTIDINE-RICH PROTEIN KE4	#16e11.x1 NCI_CGAP_Ges4 Homo sepiens cDNA clane IMAGE:2141708 3' similar to contains element   MER33 repetitive element;		Г				Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA	Homo sepiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
EXOII FIODE	Top Hit Defebase Source	EST_HUMAN	EST_HUMAN	INT	SWISSPROT	SWISSPROT	EST_HUMAN	Ę	¥	EST_HUMAN	TN.	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	TN	EST_HUMAN	NT	M	SWISSPROT	EST_HUMAN	EST HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	<b>EST_HUMAN</b>	M	N
Alguic	Top Hit Acessian No.	3.0E-16 AW022862.1	3.0E-16 AL046445.1	3.0E-16 AF135446.1	3.0E-16 Q28983	P03200	3.0E-16 T08169.1	3.0E-16 AF020503.1	3.0E-16 U03887.1	3.0E-16 AA077225.1	3.0E-16 AF003529.1	3.0E-16 Al002836.1	3.0E-16 BF690617.1	3.0E-16 L.78810.1	3.0E-16 AL043268.2	2.0E-16 AL163279.2	2.0E-16 AA621761.1	2.0E-16 J03061.1	2.0E-16 X89211.1	2.0E-16 Q31125	2.0E-16 AI470723.1	2.0E-16 AI732837.1	2.0E-16 BE858028.1	2.0E-16 BE858028.1	2.0E-16 AW877214.1	2.0E-16 AW877214.1	6902145 NT	1.0E-16 AF200719.1
	Most Similar (Top) Hit BLAST E Value	3.0E-16	3.0E-16	3.0E-16	3.0E-16	3.0E-16 P03200	3.0E-16	3.0E-16	3.0E-16	3.0E-16	3.0E-16	3.0E-16	3.0E-16	3.0E-16	3.0E-16	2.0E-16	2.0E-16	2.0E-16	2.0E-16	2.0E-16	2.0E-16	2.0E-16	2.0E-18	2.0E-16	2.0E-16	2.0E-16	2.0E-16	1.0E-18
	Expression	1.24	1.91	3.08	1.53	3.94	0.96	0.77	1.06	1.11	12	4.92	6.0	577	1.4	1.04	1.32	1.25	1.14	0.83	1.4	1.86	0.73	0.73	0.75	0.75	1.58	2.57
	ORF SEQ ID NO:	26170			27455	28988	29909			-	31966	35392		36897	31317				30123	33254	34316	34681	34882					26210
	SEO ID	13238	13539	13548	14479	16046	16993	17020	17021	18455	18793	21971	23175	23400	25961	14025	15402	15695	17238	18967	20823	21269	21466	21466	_			13286
	Probe SEQ ID NO:	133	468	476	1446	888	3963	3980	3981	5350	8699	8008	10250	10478	13079	E	2395	<b>5888</b>	4207	<b>9089</b>	7884	0068	8488	8438	8872	8872	11274	186

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	Top Hit Acession Database Top Hit Descriptor No. Source	ar39g11.s1 Soares_total_fetus_Nb2HFB_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to	1 EST HUMAN		Z	MITOGEN ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN SWISSPROT KINASE MST)	Ę	.1 EST_HUMAN	.1 EST_HUMAN	122c11.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109524.5' similar to conteins MER28.t2 CS34.1 EST HUMAN MER28 repetitive element;	The state of the s	NA TOWAN	A FET HIMAN	NT	1 EST HUMAN	1 EST HUMAN	753851 NT		16850.1 NT Homo sapiens putative MTAP (MTAP) mRNA, partial cds, afternatively spitced	Į.	1.1 EST_HUMAN	EST HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	x22e64.x1 NCI_CGAP_Kid8 Home sapiens cDNA clone IMAGE:2816622 3' similar to contains Alu repetitive 129165.1   EST_HUMAN   element,contains MER19.b1 MER19 repetitive element;
	186 186 186 186 186 186 186 186 186 186	AAGOOG	RF327794	AF16388	U45983	002779	U45983	AW8756	AW9000	A139298		AW150Z	AWaan7	AI 16328	BE1720	AV7307			AF2166	AF22884	AW9838	8.0E-17 AW662772	P20138	6.0E-17 W92331.1	5.0E-17 T84110.1	5.0E-17 T81043.1	4.0E-17 AW129165
Most Similar	(Top) Hit BLAST E Value	4 05 40 44070607	4 0F-46 BP377942	1.0E-16 AF163884.			1.0E-18	1.0E-16 AW875661	9.0E-17 AW900048			9.0E-17 AW150257						7.0E-17	7.0E-17 AF216650.				L	Ĺ	1_		
	Expression Signal	21.00	200	0.68	25.8	90 8	6.75	1.06	277	235	1	5.47	250	207	3.24	182	0.54	263	3.14	7.34	6.62	8,1	0.54	0.46	3.22	1.78	1.24
	ORF SEQ ID NO:		28044	32083		33061		36031	29704						31927		34349	l		33183	ľ				28014		
	SEO ID NO:	1	13480	18900	19634	19782	19834	22582	16793	40078	3	21414	2000	14000	25842	20455	20856	14485	18489	19898	13305	19511	23577	23846	13116	20787	22745
	SEQ ID NO:	-	28 88	28.0	6574	87.78	7802	888	3751	88	3	8445	torn!	1020	1000	7480	8019	1452	2398	8845	ই	8448	10855	10926	424	£8€	9717

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Table 4
Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor	Hamo sepiens chromosome 21 segment HS210047	owi5e04.x1 Soares_bests_INHT Homo expiens cDNA clone INAGE:1640286 3' similar to TR-Q16530 Q16530 PMS3 MRNA ;contains MER10.t2 MER10 repetitive element;	Human DNA, SINE repetitive element	xd89c09.x1 Sceres_NFL_T_GBC_S1 Homo septems cDNA clone IMAGE:2804784 31	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG	Invotibot.x1 NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE:31818989 3	hwo5b04.x1 NCL_CGAP_Lu24 Hamo sepiens cDNA clone IMAGE:3181888 3	UI+HBI4-ed-0-08-0-UI.s1 NCI_CGAP_Sub8 Hamo sepiens cDNA clane IMAGE::3085043 3	za14b02.s1 Sogres fetal liver spiesn 1NFLS Homo sapiens cDNA clone IMAGE:222491 3' similar to comzans PTR5.t3 PTR5 repetitive element ;	Hamp sapiens DNA, DLEC1 to ORCTL4 gane region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	QV3-BN0047-270700-283-412 BN0047 Homo sepiens cDNA	QV3-BN0047-270700-283-er12 BN0047 Homo septems cDNA	Homo sapiens SEC14 (S. cerevistes)-like 2 (SEC14L2), mRNA	q163806 x1 NCI_CC3AP_Eso2 Homo sapiens cDNA clone IMAGE:1958922 3' similar to contains Afu	repetitive element,	qt63a08.x1 NCI_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1858822 3' similar to contains Atu	repatitive element.	2081dO4.81 Sogres fetal heart North 19W rights salvers carre inwest 301.3	ZONADHESIN PRECURSOR	ZONADHESIN PRECURSOR	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMEN I HEAVY POLYPEPTIDE) (NF-H)	Mus musculus ultra high sulfur keratin gene, complete cds	Mus musculus ultra high sulfur keratin gene, complete ods	Homo sepiens MHC class 1 region	DKFZp78210610_r1 782 (synanym: hmel2) Hamo sapiens aDNA dane DKFZp762J0610 5	Homo sepiens mRNA for KIAA1418 protein, partial cds	OLFACTORY RECEPTOR LIKE PROTEIN OLF3	EST13504 Testis tumor Homo septems CDNA 5' end strutter to simiter to glycogentin	600844680F1 NIH_MGC_17 Hamo sapiens cDNA clone IMAGE:2860615 5	Homo sepiens chromosome 21 segment HS21C047
Top Hit Databese Source	Į.	EST HUMAN		EST_HUMAN >	SWISSPROT	EST_HUMAN !		EST_HUMAN	EST HUMAN	1	¥	EST_HUMAN	EST HUMAN			EST_HUMAN (		٦	T	╗	SWISSPROT	SWISSPROT	Г	¥	Į.	T HUMAN		ISSPROT	EST HUMAN	П	
Top Hit Acession No.	4.0E-17 AL163247.2			3.1	>35410	3.0E-17 BE326522.1	3.0E-17 BE326622.1	3.0E-17 BF511286.1	3 0F-47 N68461.1		3.0E-17 AB026898.1	3.0E-17 BF327012.1	3.0E-17 BF327012.1	11417988 NT		2.0E-17 AIZ70080.1		2.0E-17 AI270080.1	2.0E-17 AA722882-1	0.28983	0,28983	P12038	2.0E-17 M27885.1	2 0E-17 M27685.1	2.0E-17 AF055086.1	20E-17 AL134881.1	20E-17 AB037839.1	Q95156	20E-17 AA300840.1	-	20E-17 AL163247.2
Most Similar (Top) Hit BLAST E Vatue	4.0E-17	4.0E-17	3.0E-17	3.0E-17	3.0E-17 P35410	3.0E-17	3.0E-17	3.0E-17	3.05-47		3.0E-17	3.0E-17	3.0E-17	3.0E-17		2.0E-17		2.0E-17	2.0E-17	2.0E-17 Q28983	2.0E-17 Q28983	2 0F-17 P12038	20E-17	2.0E-17	2.0E-17						
Expression	1.86	202	1.72	12	1.68	1.33	1.33	1.17	1 18	2	2	0.73	0.73	3.31		3.4		3.97	204	23	23	8			1.89	1.68	0.85				
ORF SEQ ID NO:	38286			28144			29615		9400A		38455					28367		26367		28479							34469			36643	Ш
SEQ ID	24704		L				16699	<u></u>	<u> </u>	ı	22987		L	L	L	13442	1	13442	14042	15458	15458		i	1	Ι.		L			1_	L
Probe SEQ ID NO:	11824	42203	1490	2108	3208	3656	3656	2068	7	8	10060	10748	10746	12268		353		354	088	2453	2453	770	2 2	200	805	8838	3	8420	S S	10228	10264

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igle Exon Probes Expressed in Bone Marrow	Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C047	Human CYP19 gene for aromatese cytochrome P-450, promoter region (containing two cis-acting	transcriptional regulatory elements)	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)	we94b04.x1 Soares_NFL_T_GBC_S1 Homb sepiens cDNA clone IMAGE:2348/193	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2348719.3	Homo sapiens nuclear factor of kappa light polypeptide gane enhancer in B-celis 1 (NFKB1) gene, complete	cds	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCUPROTEIN 1)	Homo sapiens Xq pseudoautosomal region; segment 2/2	Homo sepiens chromosome 21 segment HS210007	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR	Homo sepiens thrombospondin 2 (THBS2) gene, promoter region and exams 1A and 1B	Homo expiens mennosidase, beta A, Iysosomal (MANBA) gene, and ubiquith-conjugating enzyme E2D 3	(UBE2D3) genes, complete ods	y30e07.r1 Scares fetal liver spieeri 1NFLS Homo sepiens cDNA clone IMAGE:128388 5	he38e05.x1 NCI_CGAP_CMI.1 Homo septens cDNA clone IMAGE:2821312 3' similar to contains Alu	repetitive element;contains LTR8.t1 LTR8 repetitive element;	qe65b06.x1 Sozres fetal jung NbHL19W Hamo saplens cDNA clane IMAGE:1743826 3	qe65b05.x1 Soares_fetal_tung_NbHL19W Homo saplens cDNA clone IMAGE:1743825 3	URIDINE PHOSPHORYLASE (UDRPASE)	QV0-BT0283-101289-072-d07 BT0283 Homo sapiens dDNA	QV3-BN0046-220300-129-c10 BN0046 Homo septens cDNA	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCX) [CONTAINS: TELUNIN]	hiddeodaxi NCI_CGAP_Mel15 Homo saptens cDNA clone IMAGE:3171104 3' similar to contains MEX13.01	MER 13 repetitive element;	486d(03.x1 Scares_NSF_FB_9W_OT_PA_P_S1 Homo sapiens CLINA crone IMAGE_2140308 3	Hamo sepiens protein tyrosine phosphetase, non-receptor type substrate 1 (P.I.PNS1) mravA	POLYPEPTIDE NACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP	ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNACPOLYPEPTIDE, N-	ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-11)	xx10b04.x1 NG_CGAP_Pen1 Hamo saptens dDNA done IMAGE::2637071 3' samilar to go::L20636 ous RIBOSOMAL PROTEIN L4 (HUMAN);	
xon Probes E	Top Hit Database Source	Į.			SWISSPROT		EST_HUMAN	EST_HUMAN			ISSPROT	NT TA		SWISSPROT	Į.		Z	EST HUMAN	Г			EST_HUMAN	SWISSPROT	EST_HUMAN		SWISSPROT		EST_HUMAN	EST HUMAN	NT			SWISSPROT	EST HUMAN	
Single E	Top Hit Acesston No.	2.0E-17 AL163247.2		<b>313391.1</b>	59086	<b>98063</b>	2.0E-17 AI798902.1	2.0E-17 AI798902.1		2.0E-17 AF213884.1	POSTES	1.0E-17 AJZ71736.1	1.0E-17 AL163207.2	P02461	1.0E-17 U79410.1		1.0E-17 AF224689.1	1.0E-17 R09942.1		1.0E-17 AW468468.1	1.0E-17 AI185642.1	1.0E-17 Al185842.1	Q16831	1.0E-17 BE062744.1	1.0E-17 AW996538.1	Q28824		1.0E-17 BE221470.1	A1472167	4758977 NT			8.0E-18 Q07537	7 OF-48 AW316978.1	
	Most Similar (Top) Hit BLAST E Vatue	2.0E-17		2.0E-17 D13391.1	2.0E-17 P98063	2.0E-17 P98063	2.0E-17	2.0E-17		2.0E-17	1.0E-17 P08183	1.0E-17	1.0E-17	1.0E-17 P02461	1.0E-17		1.0E-17	1 OE-17		1.0E-17	1.0E-17	1.0E-17	1.0E-17 Q16831	1.0E-17	1.0E-17	1.0E-17 Q28824		1.0E-17	9.0E-18	8.0E-18					1
	Expression Signal	283		623	0.68	99.0	0.57	0.57		1.31	3.24	1.36	4.54	28,	243		1.05	8		99.0	1.73	1.7	96.0	1.7	0.87	101		1.83	2.96	1.87			3.75	22.45	31.8
	ORF SEQ ID NO:	36674		37044							28755		78772								33151									29747	Ĺ		29850		ı
	Exan SEQ ID NO:	23189		23544	23667	23667	23683	23693		26153	13812	14751				L.	16828	L		19660		L	1			<u> </u>	L		22732	<u>.</u>	L		16939	Í	13430
	Probe SEQ ID NO:	10284		10622	10746	10745	10772	10772		12366	761	172	1782	2124	2843		3584	4462	1	0099	6089	6089	788	8839	10368	11747		13104	9388	380			3800		3

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Single Exon Probes Expressed in Bone Marrow

Most Similar   Top Hit Acession   Top Hit	28362 23.15 7.0E-18 AW316976.1 EST_HUMAN RIBOSOMAL PROTEIN L4 (HUMAN);	33997 0.85 7.0E-18 AW887542.1   EST_HUMAN   RC3-OT0091-170300-011-403 OT0091 Homo septems cDNA	2.67 7.0E-18 AW316976.1 EST_HUMAN	2.67 7.0E-18 AW316976.1 EST_HUMAN	1.29 6.0E-18 X71791.2 NT	4.3 6.0E-18 P52181 SWISSPROT (TGASE C) (TGC)	Homo sepiens similar to high-mobility group (nontristone chromosomal) protein 4 (H. sepiens) (LOC63449), mRNA	6.0E-18 AL163210.2 NT	1.54 6.0E-18 AL163246.2 NT	8	Z	17.6 5.0E-18.AI280214.1 EST HUMAN	0.99 5.0E-18 AF087913.1 NT	6.63 5.0E-18 BE143312.1 EST_HUMAN	3.28 5.0E-18 10242378 NT	3.26 5.0E-18 10242378 NT	6.29 6.0E-18 AW887182.1 EST_HUMAN	EST_HUMAN	28160 1.04 4.0E-18 BE044078.1 EST HUMAN MER29 repetitive element;	4 OF -18 BEDADOTR 4 FST HIMAN	4 RK 4 NE-18 AARYS144 FST HIMAN	0.95 4.0E-18 AI738592.1 EST HUMAN	4.0E-18 Q06430 SWISSPROT
						4	72																
Exam ORF SEQ SEQ ID NO: NO:	13438					17707	21561	L			24085 30							25544				14930	
Probe E SEQ ID SE			L.,		<u>_</u>		Ĺ	L	1		1165/			L	L.	L		L.	<u>L</u>	<u> </u>	_ ـ ـ	1000	

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Single Exon Probes Expressed in Bone Marrow

Hit Descriptor			П	ouz3e06.x1 Soares_NFL_		nx64ex98.s1 NCI_CGAP_AM Homo sepiens cDNA clone IMAGE:1266698 similar to contains L1.t2 L1	T		Γ	7	٦	Homo seplens chromosome 21 segment HS21C047							ak53e07.s1 Soares_tests_NHT Hamo sapiens cDNA clare IMAGE:14096523' strailer to TR:014577 JMAN O14577 BAC CLONE RG114A08 FROM 7031, COMPLETE SEQUENCE.;	Human DNA, SINE repetitive element	Human DNA, SINE repetitive element			Human IFNAR gene for interferon alpha/beta receptor			aa89d11.r1 Stratagene fetal retina 937202 Homo sepiens cDNA clone IMAGE:838485 5' similar to JMAN TR:C81634 G61634 POLYPEPTIDE PR77;	JMAN HTM1-160F1 HTM1 Homo sepiens cDNA
Top Hit Database	Source	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	LINAMIN TOTAL		EST_HUMAN		EST_HUMAN	EST_HUMAN	MT	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	노	۲	<b>EST_HUMAN</b>	둗	뉟	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN
· • • • • • • • • • • • • • • • • • • •	OZ	208430	4.0E-18 AI581588.1	4.0E-18 AI017565.1	4.0E-18 AI017565.1	4 4 7 4004 4	*:UC-10 /W/40011.1	4.0E-18 AA371807.1		3.0E-18 AA814196.1	3.0E-18 BE089634.1	3.0E-18 AL163247.2	3.0E-18 BE001671.1	3.0E-18 BF218650.1	3.0E-18 AW022015.1	2.0E-18 AW836820.1	2.0E-18 BE256097.1	Q39575	2.0E-18 AA868610.1	2.0E-18 D14547.1	2.0E-18 D14547.1	2.0E-18 BF347229.1	2.0E-18 X80459.1	2.0E-18 X80459.1	2.0E-18 BF352940.1	2.0E-18 AW665853.1	2.0E-18 AA457819.1	20E-18 BE439624.1
Most Similar (Top) Hit	BLAST E Vatue	4.0E-18 Q08430	4.0E-18	4.0E-18	4.0E-18	1000	#.UC-10	4.0E-18		3.0E-18	3.0E-18	3.0E-18	3.0E-18	3.0€-18	3.0E-18	2.0E-18	2.0E-18	2.0E-18 Q39575	20E-18	2.0E-18	2.0E-18	2.0E-18	2.0E-18	2.0E-18	2.0E-18	2.0E-18	2.0E-18	20E-18
5	Signal Si	7.	0.78	220	229		0.0/	42		24.98	3.54	1.31	6.43	1.78	5.15	5.97	67.85	121	3.85	3.38	3.38	1.67	-	-	0.75	4.42	27.0	0.52
ORF SEQ	Ö Z Q	28248	29753	31447	31448		1	37826		26865	26936	29926	33444	37748		28274		28407	i	31844	31845		32598	32599	327724	32767		34872
Exen SEO ID	ë	15228	16846	18539	18539		27148	24298		13908	13983	17012	20129	24223	25412	13348	14197	16197	18585	18880	18880	19083	19361	19361	19477	19516	·	21455
Probe SFO ID		27.	3806	5437	5437		8/16	11348		850	88	3972	2002	11271	12774	251	1155	3140	5485	5584	5584	8265	6828	88738	6409	PAS1	E SE	8487

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	Top Hit Descriptor	Homo sepiens DEAD/H (Asp-Giu-Ale-Asp/His) box polypeptide 8 (RNA helicase, 54kD) (DDX8) mRNA	Rattus norvegicus cp151 mRNA, pertial cds	BETA CRYSTALLIN A2	tb01c08.x1 NCI_CGAP_Lu28 Homo septens cDNA clone IMAGE:2052302 3'	260b01.s1 Soares fetal liver splean 1NFLS S1 Hamo capiens dDNA clane IMAGE:435145 3	PMp-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA	OLFACTORY RECEPTOR 6 (M50)	OLFACTORY RECEPTOR 6 (M60)	Homo sapiens Xq pseudoautosomal region; segment 1/2	DKFZp762F182_r1 762 (synonym; hmel2) Homo saplens cDNA clone DKFZp762F192 5	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN 725 X (2005)	LETTHOS OF NOT COAD CITY Home services CONA chare IMAGE: 2969787 5	III/IDO. J. III/IDO. J. III/IDO. Oquan and and and and and and and and and a	Homo sepiens partial IL-12/051 gene for IL-12 receptor bean chain, excri 14	x/87702.x1 Scares_NFL_T_GBC_S1 Homo septens cUNA done IMAGE:2004171 & samiliar to contains element MSR1 repetitive element ;	Homo saplens mRNA, chromosome 1 specific transcript KIAA0501	ADVISORDET NIH MAC 58 Home series CDNA clone IMAGE 4287674 5	(NANIBA) serve and tribitition or the server of the server	Homo septens memostasse, best A, tystosuma (moutan) yend, and conjugated of the conj	BETA-2 ADRENERGIC RECEPTOR	BETA-2 ADRENERGIC RECEPTOR	LIM-ONLY PROTEIN 8 (TRIPLE LIM DOMAIN PROTEIN 8)	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)	AV708136 ADC Hamo sepiens aDNA dane ADCAMA11 5	Homo sepiens NPD008 protein (NPD008) mRNA, complete cds	Homo sapiens similar to ado-keto reductase family 1, member B11 (adose reductase-like) (H. sapiens)	(LOC83222), mRNA	M.musculus mRNA for TPCR33 protein	Homo sepiens phorbolin I protein (PBI) mRNA, complete cds	Hamo septens chiramosame 21 segment HS21C001	qog1e02.x1 NCI_CGAP_KId5 Homo sapiens CDNA clane IMAGE:1915898 3' smilar to 114:063388 Qessses POL/ENV GENE;
	Top Hit Defabase Source			SWISSPROT		П		П	SWISSPROT		EST_HUMAN [		Т	HOMAN	Ę	EST HUMAN	T	T LI BAARI		Į.	SWISSPROT	SWISSPROT	Γ	SWISSPROT	EST_HUMAN	IN				NT	FA.	EST_HUMAN
	Top Hit Acesslon No.	4758139 NT	7.0E-19 AF092090.1	28444	7.0E-19 AI344951.1	7.0E-19 AA705684.1	6.0E-19 AW852930.1	P34886	P34986	6.0E-19 AJZ71735.1	6.0E-19 AL120817.1		000193	5.0E-19 AW 663302.1	5.0E-19 AJ297689.1	5 OE-40 AW188726 4	4 of 40 ABANTOTA 4	4.0E-18/AD00/8/0.1	BF08/302.1	4.0E-19 AF224889.1	028997	028997	043900	043900	3.0E-19 AV708138.1	3.0E-19 AF223467.1		11432214 NT	3.0E-19 X89685.1	3.0E-19 AF165520.1	2.0E-19 AL163201.2	20E-19 AB11783.1
	Most Similar (Top) Hit BLAST E Vatue	7.0E-19	7.0E-19	7.0E-19 P26444	7.0E-19	7.0E-19	6.0E-19	6.0E-19 P3488	6.0E-19 P34986	6.0E-19	6.0E-19		5.0E-19 Q00193	5.0E-19	5.0E-19	A 10 A	100	4.0E-18	4.0E-19	4.0E-19	3.0E-19 0.28997	3.0E-19 028997	3.0E-19 043900	3.0E-19 O43900	3.0E-19	3.0E-19		3.0E-19	3.0E-19	3.0E-19	2.0E-19	2.05-19
	Expression Signal	1,43	1.86	1.02	0.43	3.28	1.6	1.44	1.44	1.47	1.28		4.88	0.69	0.78	07.4	2 2	0.83	1.69	1.05	7	7.	0.00	0.69	1.70	0.63		1.81	1.11	16.28	27.04	123
	ORF SEQ ID NO:	28296	32030	33845	36771			30403	30404		30954		32242	32652	37213		1	20544		31481									34539		28588	
	SEQ ID	15271	10658	28484	23295	26969	16833	17518	17516	17854	18074		19043	1941	23711				15687	18571		1		1	1.	Ĺ	L	20572		1_	L	oxdot
	Probe SEQ ID NO:	7257	g g	7519	10372	12313	3792	84	4480	4837	5064		6958	6342	10790		1000	28	<u>8</u>	5470	3868	3868	4315	4315	4475	5352		7612	9814	12552	2587	4474

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Top Hit Descriptor	AV731382 HTF Hamo septens cDNA clane HTFAZC06 5	Mus muscutus keratin-associated protein 9-1 (Krtap9-1), mRNA	2634c09.r1 Sceres refina N254HR Homo sapiens cDNA clone IMAGE:360880 5	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2	601304125F1 NIH_MGC_21 Hamp septens cDNA dane IMAGE:3638310 5	yo78g07.r.1 Soares adult brain N2b4HB65Y Homo eaplens cDNA clone IMAGE:184188 5' similar to contains	MER10 repetitive element;	Human gene for Ah-receptor, excn 7-9	Homo saplens profein fyrosine phosphatase, non-receptor type substrate 1 (P I PNS 1) mixtry	atabites a source jestis. NHT Homo sepiens on A clone IMAGE:1303631 3' similar to contains MEK37.2.  MEES 7 receittus element:	TODO CA LICENSTAND TO CA Licenstand Colored INACE-2804730 3' similar to contains			Info2d03.s1 NCI_CGAP_Pr1 Homo sepiens cDNA clone IMAGE:953093 strtillar to contains L1.f1 L1	repetitive element;	Orychologus curticulus Nat/glucose cotransporter-related protein mixivi, complete cus	Oryctolagus cuniculus Na+fglucosa cotransporter-related protein miCNA, complete cus	Homo septens pituitary tumor transforming gens protein (P I I G) gene, complete cas	Rabbit phosphorylase kinase beta subunit mRNA, complete cds	ye72b02.rf Soeres fetal liver spieen 1NFLS Homo septens CDNA crone IMAGE:123243 5 Similar to Commission	UTK (spourve evening)	Huffian Oysurgain (LAML) gairs, excite 7, o and 5, and parameters	INCLOSION STATE OF THE SECOND STATE OF THE SEC	Wolfedu Coares mesancoye Aranim rights earlies color cano invadir. Lore 1	di44(1) 1/1 Motion Fetal Cocilea Hono sapters and come invocation of	Mus musculus Kerelin-essociated protein 9-1 (Nagbe-1), mixin	Mus musculus keretin essociated protein 8-1 (Krape-1), mixNA	lgg86f09.x1 Sogres_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:1842089 3	log86f09.x1 Sozres_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:1842089 3'	PMA ANDOBE CEDBOD-003-e04 ANDOBE Homo septens cDNA	DKFZp547D092_r1 547 (synonym: hfbrt) Hamo sapiens cDNA clane DKFZp547D092 5	In46c04.st NCI_CGAP_P14 Hamo sepiens cDNA clone IMAGE:1043718 straifer to conteins MER29.b2 MER29 repetitive element;	
Top Hit Database Source	EST_HUMAN	노	EST HUMAN	SWISSPROT	EST HUMAN		EST_HUMAN	ᅜ	노	COT LIBRAN	NAMOU - CO	EST_HUMAN	토		EST_HUMAN	M	N	Z	N		EST HUMAN	LN	EST HUMAN	EST HUMAN	EST HUMAN	NT NT	SINT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	
Top Hit Acesslon No.	2.0E-19 AV731382.1	7657286 NT	2.0E-19 AA012854.1	395155	1.0E-19 BE408611.1		130795.1	338044.1	4758977 NT		1.UE-19 AABS4807.1	1.0E-19 AW117377.1			1.0E-19 AA595527.1	1.0E-19 U08813.1	1.0E-19 U08813.1	4F200719.1	1.0E-19 M84857.1		189820.1		1.0E-19 AW812259.1	1.0E-19 N44631.1	1.0E-19 AW023137.1	7657286 NT	7657286 NT	8.0E-20 A1221371.1	8.0E-20 At221371.1	7.0E-20 BF326455.1	7.0E-20 AL138120.1	7.0E-20 AA557657.1	
Most Similar (Top) Hit BLAST E Value	2.0E-19/	2.0E-19	20E-19/	2.0E-19 C95155	1.0E-19		1.0E-19 H30795.1	1.0E-19 D38044.1	1.0E-19		1.0E-19/	1.0E-19	1.0E-19		1.0E-19	1.0E-19	1.0E-19	1.05-19	1.0E-19		1.0E-19 T99820.1	1.0E-19	1.0E-19	1.0E-19	1.0E-19	8.0E-20	8.0E-20	8.0E-20	8.0E-20	7.0E-20	7.0E-20	7.0E-20	
Expression	0.64	22.0	935	880	211		1.66	248	4.28		1.18	0.0	2.73		0.63	0.99	0.89	0.71	1.72		2.74	0.97	27.33	21	3.69	2.45	2.45	1.31	1.31	0.72	5.56	9.11	
ORF SEQ ID NO:	32480						28211				29381		32502	L		34213			36182					36974		33143							
Eson SEQ ID NO:	19247	20524	24844	28404	13555		15190	15723	15920		16460	18195	1.		25995	2884	١_	L					23469	23479	24694	L			20714	L	1_	<u> </u>	⅃
Probe SEQ ID NO:	6472	75.54	E E	2 8	289		2174	2729	2860		3412	5486	3 8		6333	7890	2890	8085	8783		9083	10108	10547	10557	11809	888	803	7784	77.81	3280	7488	8841	

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Top Hit Descriptor		ni48c04.s1 NCI_CGAP_P14 Homo sepiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element ;	Homo sepiens ribosomal protein L13a (RPL13A), mRNA	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY	601441231F1 NIH_MGC_72 Homo septems cDNA clone IMAGE:3916231 5	AV725123 HTC Homo septens cDNA clone HTCBTA01 6	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250	Zh78d08.s1 Soares_fetal_liver_spieen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' stmilar to contains MER30.11 MER30 repetitive element;	zh78d08.s1 Soares_fetal_liver_splean_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to	contains MER30.H MER30 repetitive element;	MR3-HT0487-150200-113-g01 HT0487 Homo saplens cDNA	Mus musculus MMAN-g mRNA, complete cds	Mus musculus MMAN-g mRNA, complete ods	HYPOTHETICAL PROTEIN DJ845024.1	Homo sapiens chromosome 21 segment HS21C047	HISTONE H2B C (H2B/C)	t264g03.x1 NCI_CGAP_Ov35 Hamp saplens cDNA clone IMAGE:2283398 3	QV3-DT0043-090200-080-c04 DT0043 Homo seplens cDNA	Human BXP21 gene	OLFACTORY RECEPTOR-LIKE PROTEIN 114	zig8b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA cione IMAGE:484895 3' similiar to contains L1.63 £1 racetitive element :	Human DNA, SINE repetitive element	601843561F1 NIH_MGC_54 Homo seplens cDNA clone IMAGE:4064343 5	RETROVIRUS RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE;	ENDONUCLEASE	g/70d02.x1 NCL_CGAP_Kid3 Homo saplens cDNA clone IMAGE:1864803 3' stritter to contains Alu repetrive	element;	grodoz x1 NCI_CCAP_Kid3 Homo sepiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive]	element	601514180F1 NIH MGC 71 Homo sepiens CUNA done IMAGE:3913522 3	xx24e10.x1 NCI_CGAP_U4F Homo sepiens aDNA clone IMAGE:2761098 3' straiter to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5.;
Top Hit Database		T_HUMAN		/ISSPROT	EST_HUMAN	EST_HUMAN /	EST_HUMAN /	EST HUMAN	Т	EST_HUMAN	EST_HUMAN	ΤN	¥	SWISSPROT		SWISSPROT		EST_HUMAN		SWISSPROT	EST HIMAN	Т	T HUMAN		SWISSPROT		EST HUMAN			EST_HUMAN	EST_HUMAN
Top Hit Acessian	o X	7.0E-20 AA557667.1	12833		24.1	5.0E-20 AV725123.1				5.0E-20 W90525.1	5.0E-20 BE165980.1	5.0E-20 AB028174.1	6.0E-20 AB028174.1		17.2			4.0E-20 AW937469.1			,	Ī	=		711369		3.0E-20 AI284244.1		3.0E-20 AI284244.1	3.0E-20 BE888422.1	2.0E-20 AW303868.1
	BLAST E Value	7.0E-20/	7.0E-20	6.0E-20 P39188	6.0E-20	5.0E-20/	5.0E-20	5.05-20		5.0E-20	5.0E-20	5.0E-20	5.0E-20/	5.0E-20 O60809	4.0E-20/	4.0E-20 Q99880	4.0E-20	4.0E-20	3.05-20	3.0E-20 P23273	200	3.05-20	3.0E-20		3.0E-20 P11369		3.0E-20		3.0E-20	3.0E-20	2.0E-20
Expression	Signal	9.11	6.31	3.83	298	1.05	1.19	4		10	0.79	1.24	1.24	58:0	1.73	0.89	5.27	1.9	16.0	1.63	3	S 8	0.68		1.59		8.22		8.22	4.15	33.94
ORF SEQ	Ö Ö Ö	35228		29535	30210		33636			34658		l	35583		27635			37286		30153	L _	3	37099				38308		38309	31849	
Exon SEO E	Ö Ö Ö	21808	24899	18613	17330	17847	20283	ALCIC	CT-31.3	21248	21409	22153	L_	L	L		21227	23785	$L_{-}$	17266	<u>L.</u>	2775			23969		24723		24723	25130	
Probe	Ö Ž	8841	12023	3568	4301	4626	7322	8277	3	8277	8448	9187	9187	0086	1624	5732	8228	10865	2149	4237	2007	7800	10684		11024		11840		11840	12329	83.

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Table 4
Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor	ngGN09.s1 NCL_CGAP_Lip2 Hamo sapiens cDNA clane IMAGE:940097 similar to TR:G1224086 G1224086 ORF2 FUNCTION UNKNOWN. ;	ng68n09.s1 NG_CGAP_LID2 Hano sapiens dDNA dane IMAGE;940097 similar to TR:G1224068 G1224068 ORF2 FUNCTION UNKNOWN.;	x24e10.x1 NCI_CGAP_Ut4 Homo septens cDNA clone IMAGE:2761096 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5. ;	ZONADHESIN PRECURSOR	ZONADHESIN PRECURSOR	EST180328 Liver III Homo sapiens cDVA 5' end	Homo sapiens RGH1 gena, retrovirus-like element	Homo sapiens RGH1 gene, retrovfrus-like element	CHR220310 Chramosome 22 exam Hamo septens cDNA dane C22_391 5	ZI1408.r1 NG_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 6' similar to contains MER19.t2 MER19 renoffthin element :	ALL STANDS OF THE STANDS OF THE STANDS AND STANDS OF THE S	integations NCI_CASAP_Kitat 1 frame suprems curve cacre invalce; 5155155 5 sering to currents L.1.2. L.1 repetitive element;	AF049567 Human activated dendritic cell mRNA Homo sepiens cDNA clone GA05	Homo sepiens Autosomal Highly Conserved Protein (AHCP), mRNA	Homo sepiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7–49, and partial cds, alternatively spiced	nc60g08.rt NCI_CGAP_Pr1 Homp septens cDNA clone IMAGE:745694 stmiler to contains L1.t3 L1	repetitive element ;	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIpt12-8J21	RC3-NN0068-090500-021-b03 NN0068 Homo sepiens cDNA	b530s02.y1 NIH_MGC_10 Homo sepiens cDNA clone IMAGE:2884714 6' similer to SW:NAM_HUMAN 085169 NADH-UBIQUINONE OXIDOREDUCTASE ASHI SUBUNIT PRECURSOR;	ob71f06.s1 NCI_CGAP_GCB1 Homo septens cDNA clone IMAGE:1338835 3'	ATP SYNTHASE A CHAIN (PROTEIN 6)	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)	Homo sepiens chromosome 21 segment HS21C100	2/67/a08.11 Scares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487/858 5	Homo sepiens chromosome 21 segment HS21C018
Top Hit Database Source	EST_HUMAN G	EST_HUMAN C		SWISSPROT		EST_HUMAN E		NT	EST_HUMAN (	Z Z	T	EST_HUMAN I	EST_HUMAN /		<u>.</u>	T	EST_HUMAN r	EST_HUMAN /	EST_HUMAN F	EST HUMAN	Τ	SWISSPROT		/ISSPROT		EST HUMAN	7
Top Hit Acession No.	2.0E-20 AA616335.1	2.0E-20 AA516335.1				2.0E-20 AA309457.1			2.0E-20 H55371.1	A 204084 4	1.05-20/24261501.1	1.0E-20 BF115158.1		18491	1.0E-20 AF223391.1		1.0E-20 AA420453.1	9.0E-21 AJ003514.1	9.0E-21 AW898189.1	8.0E-21 AW674891.1	8.0E-21 AA809411.1	021330	P15800	P15800			7.0E-21 AL163218.2
Most Similar (Top) Hit BLAST E Value	2.0E-20	2.0E-20	2.0E-20	2.0E-20 Q28983	2.0E-20 Q28983	2.0E-20	2.0E-20	2.0E-20	2.0E-20	200	1,05-20.1	1.0E-20	1.0E-20	1.0E-20	1.0E-20		1.0E-20	9.0E-21	9.0E-21	8.0E-21	8.0E-21	8.0E-21 021330	7.0E-21 P15800	7.0E-21 P15800	7.0E-21	7.0E-21	7.05-24
Expression Signal	888	3.88	15.67	4.76	4.76	60	7.56	7.56	3.98	67	4.32	\$	<u>2</u> .	224	211		3.00	-	3.77	1.13	4.38	294	1.59	1.59	0.63	5.22	0.81
ORF SEQ ID NO:	27107	27108		30886		34840			L		28082	30380		L		L					38330		28115		17962		32900
Exan SEQ ID NO:	14157	L	l	17008	17998	21424		L	25714	l	1000	17493	1		L	L.	25215	L	L		1		L				19633
Probe SEQ ID NO:	113	1113	2828	4983	4983	8455	9545	9545	12703	8	2029	4487	6707	8518	11879		12458	2923	12175	9483	11868	12342	2082	2082	3716	4283	6573

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Table 4
Single Exon Probes Expressed in Bone Marrow

Single Exon Probes Expressed in Done Marrow	Top Hit Descriptor	Homo sepiens dNT-2 gene for mitochondrial 5(3)-decoyribonucleotidese (dNT-2 gene), exans 1-5	Human chromosomal protein HMG1 related gene	RC0-CT0301-271199-031-F03 CT0301 Homo sapiens cDNA	2073d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens dDNA clone IMAGE:398961 3' similar to gb-M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR.t3 OFR	repetitive element;	Homo septens PTD013 protein (PTD013), mRNA	601304125F1 NIH_MGC_21 Hamo saplens cDNA clone IMAGE:3638310 5	PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA	601649871F1 NIH_MGC_74 Hamo sepiens aDNA clone IMAGE:3863880 5	Homo sepiens melanoma antigen, family C, 1 (MAGEC1), mRNA	he05e10.x1 NCI_CGAP_CML1 Hamo sepiens cDNA dane IMAGE:29181543'	783d11.x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:3303573 3' similar to conteins OFR.th OFR receitifies element:	ZINC FINGER PROTEIN GL1 (GLL1)	ZINC FINGER PROTEIN GL11 (GLL1)	zt72c04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5	oo88608.s1 NCL_CGAP_Kid5 Homo sepiers cDNA clone IMAGE:1573094 3' similar to TR:Q16630 Q16530   PINS3 MFNA ;contains OFR.t1 OFR repetitive element;	Rattus norvegicus mRNA for rTiM, complete cds	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) ozne. RoRet ozne. and sodium phosohate transporter (NPT3) gene, complete ods	zq15d06.s1 Strategone fefal retina 937202 Homo sapiens cDNA clone IMAGE:629771 3'	Homo sapiens chromosome 21 segment HS21C001	Homo sepiens LCMDZB gene	Hamo sepiens dNT-2 gene for mitachandrial 5(3?)-deaxyribanucleotidase (dNT-2 gene), exans 1-5	Homo sepiens dNT-2 gene for mitochondrial 5(3)-decayribonucleotidase (dNT-2 gene), exons 1-5	AV661044 GLC Homo seplens cDNA dane GLCGOA10 3'	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064945 5	RC1-OT0083-100800-019-g08 OT0083 Homo septens cDNA
Exon Probes E	Top Hit Detrebese Source	TN	IN	EST_HUMAN		T_HUMAN		7	EST_HUMAN	T HUMAN		EST_HUMAN	NAMIN TRA	T	Т	T	EST HUMAN		Ž	T HUMAN		TN	NT	TN			EST HUMAN
eibuis	Top Hit Acession No.	7.0E-21 AJ277567.1	7.0E-21 D14718.1	7.0E-21 AW868922.1	,	7.0E-21 AA723404.1	7706668 NT	8.0E-21 BE408611.1	8.0E-21 BE162737.1	5.0E-21 BE968839.1	4885474 NT	5.0E-21 AW440864.1	5 OE-24 BE858505 4	Deffeor	091690	5.0E-21 AA393574.1	4.0E-21 AA970713.1	4.0E-21 AB019578.1	4 PF. 24   104   28 4	3.0E-21 AA218891.1	AL 163201.2	3.0E-21 AJ007973.1	3.0E-21 A.1277557.1	3.0E-21 AJZ77557.1	3.0E-21 AV661044.1	3.0E-21 BF184739.1	3.0E-21 BF361093.1
	Most Similar (Top) Hit BLAST E Value	7.0E-21	7.0E-21	7.0E-21		7.0E-21	7.0E-21	6.0E-21	6.0E-21	5.0E-21	5.05-21	5.0E-21	R 0E-24	5.0E-24 CO4600	5.0E-24   Q91690	5.0E-21	4.0E-24	4.0E-21	400	3.0E-21	3.0E-24	3.0E-21	3.0E-21	3.0E-21	3.0E-21	3.0E-21	3.0E-21
	Expression Signal	1.42	11.21	0.82		1.88	1.67	1.68	0.59	3.16	6.18	0.92	80	200	0.43	5.38	861	3.35	g	1.05	1.48	4.17	0.83	0.93	0.74	1.89	7.18
	ORF SEQ ID NO:	35124				37540	38094	30052		30302	30753		92870	37374	37376		27762	33386	3854	27876	28319	29066	31636	31637			33306
İ	SEQ ID	21699	21990	23394		24017	24537	17163	22455	17418	17856	20151	accoc	22050	23850	25081	14777	20077	20065	14880	<u> </u>			18673	L		20008
	Probe SEQ ID NO:	8731	9024	10472		11054	11599	4130	949	4390	4839	6927	7.240	1213	10030	12255	1748	7055	5	1854	2282	3096	5577	5577	2828	භාග	7271

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Table 4
Single Exon Probes Expressed in Bone Marrow

Igue Exoli Probes Expressed III Borie Mariow	Top Hit Descriptor	CA/1-NINDO63-280400-203-h08 NN0063 Homo sepiens cDNA	QV3-HT0458-170200-090-g12 HT0459 Homo sapiens cDNA	RC4-BTD311-141199-011-h08 BTD311 Homo saplens cDNA	ZONADHESIN PRECURSOR	ZONADHESIN PRECURSOR	ISSORO3.X1 NCI_CGAP_Part Home sapiens cDNA clone IMAGE:2230109 3' similar to TR:099854 Q89854 LIMBOTHETICAL EA 4 KD DECTEIN :	207424 Course fatel hand Nichtlide Home contare CINA days MAGE-28000 R	207212 1 Scare fetal heart NhHH10W Home seniors CNA chara IMAGE-365010 5	zc28h02.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone IMAGE:323667 5	Homo sapiens hyperion gene, exons 1-50	QV0-HT0103-091189-050-gr1 HT0103 Hamo sepiens cDNA	AU135779 PLACE1 Hamo sepiens cDNA done PLACE1005052 5	601680636F1 NIH_MGC_83 Hamo sapiens cDNA clone IMAGE:3951008 5	6016806336F1 NIH_MGC_83 Hamo septiens cDNA clone IMAGE:3851008 5'	Homo sapiens putative 8-hydraxyguanine DNA glycosylase gene, complete cds	nI48c04.s1 NCI_CGAP_Pr4 Homo sepiens cDNA clone IMAGE:1043718 similar to contains MER29.b2	MER29 repetitive element;	ar88d12x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'	DKFZp43410830_r1 434 (synonym: htse3) Homo sapiens cDNA done DKFZp43410830 5'	qg47e05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' strailar to glo:M84241 QM	PROTEIN (HUMAN);	Homo sapiens chromosome 21 segment HS21C003	Hamo sapiens chromosame 21 segment HS210003	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA	Homo sapiens chromosome Xp22 410-8	2294803.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:22962043' similar to TR:Q15408 Q15408	NEUTRAL PROTEASE LARGE SUBUNIT;	Homo sepiens chromosome 21 segment HS21C001	Homo sapiens chromosome 21 segment HS21C001	AV761874 MDS Hamo saplens cDNA clone MDSCCG05 57	CMO-HT0178-281099-076-h05 HT0179 Homo sapiens cDNA	zk67a08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487868 67	Homo sapiens chromosome 21 segment HS21C048
T SECOLUTION	Top Hit Detabase Source	EST_HUMAN (	EST_HUMAN (	EST_HUMAN F	SWISSPROT	SWISSPROT		EST CHANN	Т	Т	Т	EST_HUMAN	HUMAN	EST HUMAN	EST_HUMAN			EST_HUMAN N	EST_HUMAN 6	EST_HUMAN [		HOMAN				± F		EST_HUMAN	F	H H	EST_HUMAN /	EST_HUMAN (	T_HUMAN	П
	Top Hit Acession No.	+	20E-21 BE163247.1	10.1				20E-21 AI0240021			-				2.0E-21 BE973829.1			1.0E-21 AA557657.1	1.0E-21 AI601284.1	1.0E-21 AL079752.1			·	1.0E-21 AL163203.2	30038	1.0E-21 AF046133.1		9.0E-22 AI702438.1		9.0E-22 AL163201.2			8.0E-22 AA046502.1	7.0E-22 AL163246.2
	Most Similar (Top) Hit BLAST E Vetue	3.05-21	20E-21	20E-21	2.0E-21 Q28983	2.0E-21 Q28983	70 200	205-21	205.24	20E-24	2.0E-21	2.0E-21	20E-21/	2.0E-21	20E-21	2.0E-21		1.0E-21	1.0E-21	1.0E-21		1.0E-21	1.0E-21 /	1.0E-21	1.0E-21	1.0E-21		9.0E-22	9.0E-22	9.0E-22	9.0E-22	8.0E-22	8.0E-22	7.0E-22/
	Expression Signal	0.77	28.45	3.20	228	228	7	5.0	2	0.61	0.48	6.64	3.96	1.72	1.72	17.51		2.06	71.7	2.6		4.83	0.46	0.46	1.67	1.32		2.03	1.29	1.29	3.13	7.03	3.82	6.78
	ORF SEQ ID NO:	36445			28667	28668	78976	21004	21910	32454	34689	35099	35567	38152	38153	<u> </u>		27259		- 		33719	37021	37022				30355	35341	35342	37631			26656
	SEQ ID	22978	13250	14257	15643	15843	10050	10000	107.00	18224	21583	21674	22141	24584	24584	25279		14295	14435	19892		20366	23625	23525	23869	25514		17465	21917	21917	24104	14002	21197	13731
	Probe SEQ ID NO:	10051	147	1219	888	8848	7010	1000	333	848	8815	8706	9175	11647	11647	12560		1260	1402	<b>6634</b>		98 23 28	10603	10603	10949	12932		4439	8951	8951	11144	676	8228	989

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Top Hit Descriptor	Me Ald IA) door of an use of a second	ALPHA-Z-MACKOGLOBOLIN PREVONSON (ALPHA-Z-MACKOGLOBOLIN PREVONSON)	Homo explens gane for activity receptor type iib, continue cus	Hamo sapiens HSPC220 mRNA, complete cds	EST00738 Fetal brain, Strakegene (cathe36208) Homo septems CLAYA Gune Introving	Hamo saplens T cell receptor beta locus, TCRBV/S3A2 to 1 LABV12S2 regran	wx05g07.x1 NCI_CGAP_Gas4 Hamo sapiens cDNA clone IMAGE:2542812.3	Human DNA, SINE repeditive element	Homo sapiens chromosome 21 segment HSZIC/IO3	Human dystrophin (DMD) gene, excris 7, 8 end 8, and parted cos	negZ/b06.xf NCI_CGAP_PT28 Homo septens alina come invave=32.55086 5 suries to contains reconstitute element.	Incoming and in the second section and the second section and the second section and the second section and second section and	Homo septens /4 pseudostatochim paga, cognimin na	AV703223 ADB Hamo septens during AUDINUE IZ 3	Homo septens chromosome 21 segment noctious	601862813F1 NIH_MGC_67 Homo septiens CONA clone IMAGE: 4050434 3	Hamo sepiens chramosome 21 segment HS21C009	tm14h10x1 NCI_CGAP_Co14 Homo septens cDNA clane IMAGE:2156611 3' smillar to got L19053 HN4H	AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.t1 L1 repetitive element;	W68504 x1 NCI_CGAP_Bm25 Homo sapiens dDNA done IMAGE:2428839 3" stimitar to SW :rt_z1_nowwy	P46778 60S RIBOSOMAL PROTEIN L21.;	Human dromosoma protein rawo i release ye to	ph28c07.x1 Sogres_pregnant_uratus_nurity_nignes_septens_covin_come_no_no_no_no_no_no_no_no_no_no_no_no_no_	CONTRIBUTION MICHALIAN MICHAEL TO HATTERS HAMD SERVERS CANA	CAUCHT LOSGO-CASCA LAN BITATA LAnn samens cDNA	KCD-510/0/-100300-021-1110-510/0/1 halls captured on the control of the control o	KIRRIB NYACO IRIANA NO BOURING BURGARIA PROCES	Restricts RYZGS myANA for a potential upano-containing processing than the latest managed of	yc/3d/05.e1 Sogres melanocyte ZNDHM Homo sapiens dunka coure invace	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR	Homo sapiens protein kinase, AMP-echyanea, gamma a mar-dalaryus subulin (1 1457-57)	PN/1-ST0262-261199-001-012 ST0262 Homb septems GUNA	a:20f01.1 Scares_senescent_introllests_notice represe curv. Curs involved to get get y7z308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);	RC9-TN0079-160900-025-h12 TN0079 Homo sepiens cDNA	1
Top Hit Database Source	,	SWISSPROT	Z	TN	EST_HUMAN	F	EST_HUMAN	F	닐	N	MARKI II TOT	ESI HUMAN	¥	EST_HUMAN	Ę	EST HUMAN	¥		EST HUMAN		EST_HUMAN	Ę	1	EST HUMAN	EST HUMAN	EST HUMAN	토	노	EST_HUMAN	SWISSPROT	NT	EST_HUMAN	EST HUMAN	FST HIMAN	
Top Hit Acession No.		261838	7.0E-22 AB008681.1	7.0E-22 AF151054.1	7.0E-22 M78590.1	7.0E-22 AF009680.1	6.0E-22 AW029123.1	5.0E-22 D14647.1	5.0E-22 AL163303.2	5.0E-22 U60822.1		5.0E-22 BF476511.1	4.0E-22 AJZ71735.1	4.0E-22 AV703223.1	4.0E-22 AL163202.2	4.0E-22 BF218030.1	AL 163209.2		3 0E-22 AI469679.1		3.0E-22 AI859038.1	3.0E-22 D14718.1		3.0E-22 Al090125.1	3.0E-22 BE156813.1	3.0E-22 BE089841.1	3.0E-22 X60680.1	3.0E-22 X60660.1	2.0E-22 N24942.1	2.0E-22 P24916	8394043 NT	AW8177	2.0E-22 W39458.1	0 oc 22 BE002418 4	ו או ושפה וחו
2 ± 11	Agree	7.0E-22 Q81838	7.0E-22	7.0E-22	7.0E-22	7.0E-22	6.0E-22	5.0E-22	5.0E-22	5.0E-22		5.0E-22	4.0E-22	4.0E-22	4.0E-22	4.0E-22	4 OF-22		3 0E-22			3.05-22			3.0E-22	3.0E-22	3.0E-22	3.0E-22		<u> </u>		<u> </u>		ł	
Expression Signal		238	18.0	248	3.86	18	88	0.72	3.05	7.82		2.76	0.83	0.42	3.38	215	274		-		2.15	1.35		2.88	1.21	3.4	0.77	0.77	4.79		4.78		134		3.5/
ORF SEQ ED NO:		30221	30968		35578	36340	2		32988	37098				34824		37563					28596			30752		34964	35083			28552		30163			32611
SEQ ID	<u> </u>	17341	18088	22004	22450	33000	24 655	18204	19723	23604		25413		1	1_	1_	07000	1	44049	1	15577			17855	21540	21646	L	1_	1_	L		L	1 _	1	19372
Probe SEQ ID	į	4312	5078	888	78	2000	SEC 1	5284	9899	10682		12776	3850	8442	8758	41077	1000	200	8	3	2576	3686		4838	8572	8577	8703	8703	4970	25.2	3431	4263			8

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(Top) Hit Top Hit Acession Delabese BLAST E No. Source	2.0E-22 AIZ76522.1 EST_HUMAN	2.0E-22 AA715315.1   EST_HUMAN	2.0E-22 AA716315.1 EST_HUMAN	2.0E-22 R15209.1   EST_HUMAN	2.0E-22 AW418960.1 EST_HUMAN	2.0E-22 AL 163280.2 NT	1.0E-22 AW865517.1 EST_HUMAN	1.0E-22 U50871.1 NT	1.0E-22 D14547.1 NT		1.0E-22 AF003528.1 NT	1.0E-22[BE084687.1   EST_HUMAN		1.UE-22 Aladahaa. I	1.0E-22 Al365435.1 EST_HUMAN	9.0E-23 AW802801.1 EST_HUMAN	8.0E-23 AF198349.1 NT	7.0E-23 AV647246.1 EST_HUMAN	7.0E-23 5031952 NT	6.0E-23 AF199333.1 NT	6.0E-23 AL163249.2  NT		6.0E-23 AF224669.1 INT	Homo sapiens mannosidase, beta A, lysosomia (MANDA) gene, and unquim conjugating enzyme EZZ 3  (UBE2D3) genes, complete cds	B.0E-23 A1209130.1		(MAGEA12), melanoma antigen family A2b (WAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin	M	6.0E-23 AF179818.1 NT	25 5.0E-23 AF178918.1 NT Pongo pygmaeus oifactory receptor (PPY116) gene, partial cds
		П				Ţ		Hum	Hum	Hon	T			T		П	Gen Gen		Horr	Ratt	Hor	Hor	5 :			T	<u></u>	<u>₹</u>	£	P <sub>Q</sub>
	EST H	EST H	EST_H	EST H	EST H	5	EST_H	Þ	¥		Z	EST_H	- COT		EST_H	EST_H	¥	EST H	2 NT	Ŋ	¥	!	Ę	늏	EST H			노	Z	토
Top Hit Acession No.	AI278522.1	4A715315.1	AA716315.1	R15209.1	<b>1 2 1</b>	AL 163280.2	AW865517.1	U50871.1	D14547.1				A 100 E 40 E 4	41303455. I	Al365435.1		AF198349.1	AV647248.1	503195	AF199333.1	AL 163249.2		AF224669.1	AF224869.1	AI209130.1			U82671.2	AF179818.1	AF179818.1
Most Similar (Top) Hit BLAST E Value	2.0E-22	2.0E-22	2.0E-22	2.0E-22	2.0€-22	20E-22	1.0E-22	1.0E-22	1.0E-22	-	1.0E-22	1.0E-22	70 7	1.05-24	1.05-22	9.0E-23	8.0E-23	7.0E-23					6.0E-23	6.0F-28	8.0E-23			5.0E-23		Ш
Expression Signal	₽:	0.65	0.65	0.55	1.58	1.92	1.78	1.82	1.40		1.5	98.0		0.0	0.8	ľ	0.73	1.98	4.11	1.68			4.64	79 7						3.25
ORF SEQ ID NO:	36456		36557	37426		31705			29390			34347		3/304	37355		20548		37852		30206		31834	31835				31552		32679
SEQ ID	22888	23081	23081	23911	24927	25504	14921	15589	16470		18300	20963		23628	23838		16830	16373	24323	16494	17328		25099	00026	25778			18618		25659
Prabe SEQ ID NO:	10061	10156	10156	10991	12051	12139	1896	2588	3422		5295	8016		10918	10918	12891	3686	3322	11376	3447	4207		12281	13784	12480	32.5		5519	6367	7671

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ing in total Library Light Broad III Doried Walliam	Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C027	Homo saplens chromosome 21 segment HS21C027	zt35g09.r1 Soeres_pregnent_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503968 6' simitar to contains MER29.t2 MER29 repatitive element;	Human endogenous retroviral element HC2	Human endogenous retroviral element HC2	RC3-NN0066-270400-011-h01 NN0068 Homo sapiens cDNA	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTR.1 gene	Human matrix Gla protein (MGP) gene, complete cds	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)	9873711.x1 NCL CGAP_P728 Home septens dDNA clone IMAGE:1943767.3' similar to TR.Q13537 Q13537 MERAY TRANSPOSABLE ELEMENT POME ETE CONCENSIS SECUEDICE.	MENSY INVASOR CANADA ELEMENT, COMPLETE CONSENSOS SELECTORS,	write-in 1946/- 1946/- 1946/1 in 1946/ in 1946/ in 1946/ in 1946/- 1946/	uri Ratio et Source fatel liner endom 1NB S. Home endome et INA edges BAACE: 205418 R.	Human DNA. SINE reportition element		Homo septens cytochrome P450 polypeptide 43 (CYP3A43) gene, partiel cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450	polypeptide 5 (CYP3A5) gene, partial cds	Homo sepiens chromosome 21 segment HS21C103	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1	Homo sapiens T cell receptor beta facus, TCRBV7S3A2 to TCRBV12S2 region	Homo seplens chromosome 21 segment HS21C052	Homo sapiens chromosome 21 segment HS21C010	601236455F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3608663 57	2w82c08.r1 Source_testis_NHT Homo sepiens cDNA clone INAGE-782698 6' similar to contains PTR5.t2_PTR5 manifette element -	TEAD of Charles the Control of the C	RAY SEXOLE I SUBLINGUE FOR HOURS SO, ZUZ FIGURO SEPRENS CLIVA CICLIS INVANCE, COLZ, 700 S. SUTTINGUE TRE19822 E19822 CA PROTEIN;	OLFACTORY RECEPTOR-LIKE PROTEIN 13	OLFACTORY RECEPTOR-LIKE PROTEIN IS	Homo sepiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA	Homo sepiens capping protein (actin filament) muscle Z-line, atpha 2 (CAPZA2), mRNA
2	Top Hit Database Source	NT.	±V	EST_HUMAN o	¥		EST_HUMAN F	TN TN	NT	SWISSPROT 1	SWISSPROT	P TOTAL	T	EST HIMAN	T	T				H.	H TN	TN IN	上		EST_HUMAN 6	Z WIMAN	Ť	EST HUMAN T	Т	SWISSPROT		
J SIGNIO	Top Hit Acessian No.	3.0E-23 AL163227.2	3.0E-23 AL 163227.2	3.0E-23 AA130166.1			3.0E-23 AW897927.1	2.0E-23 AJ289880.1	2.0E-23 M35270.1		22105	2 0E 22 A 12014 4E8 4	Z.UE-Z.S AIZU1436.1	DE100800.1	2 OF 29 M50024 4	ĺ	İ		1	2		1	1.0E-23 AL 163252.2	2	1.0E-23 BE378471.1	1 0E-22   A 6.448007 4	T. PORTLAND	9.0E-24 AA683213.1			1	11422027 NT
	Most Similar (Top) Hit BLAST E Value	3.0E-23	3.0E-23	3.0E-23	3.0E-23 Z70664.1	3.0E-23	3.0E-23	2.0E-23	20E-23	2.0E-23 P22105	2.0E-23 P22105	20 20 0	2.0E-20.2	2.0E-23 BE16380	200	2.0E-28			. 20E-23/	2.0E-23	2.0E-23	2.05-23	1.0E-23	1.0E-23	1.0E-23	4.05.22	2001	9.0E-24	8.0E-24	8.0E-24 P23269	8.0E-24	8.0E-24
	Expression Signed	1.07	1.07	4.18	2.74	274	1.27	3.75	3.02	2.08	2.08	1.5	2 2	250	2 50	67 8			. 4.28	1.12	3.91	2.55	1.44	4.76	3.11	*		3.05	1.15	1.15	1.34	0.77
	ORF SEQ ID NO:		20628	34647	38058	36059		<b>2992</b>		28817			<u> </u>	20047		3050				35589			30472			oese.			30586	30587	32922	34492
	Exan SEQ ID NO:		19840	21141	22608		23602	13732	15817	15799	15789	46433	2000	17040	17040	18072			21175	22161	25088	25419	17581	17816	19934	24.0977		13624	17699	17699	19651	21083
	Probe SEQ ID NO:	9290	6580	8474	9604	9604	10880	299	1145	2807	2807	2997	5000	4004	Ž	202			8205	9185	12262	12787	4558	4789	6882	8600	3	38	4678	4678	6591	8155

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID	Exon SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E	Top Hit Acession No.	Top Hit Datebase Source	Top Hit Descriptor
:				Vatue			
3888	16926		1.36	7.0E-24	7.0E-24 AW937954.1	EST_HUMAN	QV0-DT0047-170200-122-e08 DT0047 Homo sepiens cDNA
707	13769		231	6.0E-24	6.0E-24 AB001421.1	IN	Macaca fuscata mRNA for Testis-Specific Protein Y (TSPY), complete cds
88		28851	15.68	8.0E-24	6.0E-24 AL163249.2	¥	Homo sepiens chromosome 21 segment HS21C049
3894			8.31	5.0E-24	5.0E-24 AJ229043.1	F	Homo sepiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
808	20971	34365	1.34	6.0E-24	6.0E-24 AF223391.1	ħ	Homo sepiens celclum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spiced
6039	19121	32326	3.63	4.0E-24	4.0E-24 AA594178.1	EST HUMAN	m31h05.s1 NCI_CGAP_Ges1 Homo septens cDNA done IMAGE:1085529 3' similer to SW:POL_MLVRK P31795 POL POLYPROTEIN;
9029				4.0E-24	4.0E-24 AW813711.1	EST_HUMAN	RC3-ST0197-130100-014-06 ST0197 Homo sapiens cDNA
11514		38005	1.62	4.0E-24	4.0E-24 BE544822.1	EST_HUMAN	601078812F1 NIH_MGC_12 Hamo sapiens cDNA clane IMAGE:3464468 5
12644			5.56	4.0E-24	1	NT	Homo sepiens mRNA for KIAA1083 protein, partial cds
12807	25718	31610	9.62	4.0E-24	4.0E-24 M20707.1	Į.	Human kappa-immunoglobulin germline psaudogene (Chr22.4) variable region (subgroup V kappa II)
12876	25509	31708	1.88	4.0E-24	11418318 NT	LN	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
7285	. 20062	33388	0.6	3.0E-24	3.0E-24 U68061.1	NT	Human garmiine T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV19S1P, TCRBV19S1P, TCRBV14S1, TCRBV14S1, TCRBV3S1, TCRBV4S1, TCRBV3S1, TCRBV4S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,
							Human germäine T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1P, TCRBV16S1, TCRBV14S1,
. 7285	20062	33369	9.0	3.0E-24	3.0E-24 U68061.1	K	TORBV3S1, TORBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TORBD1, TORBJ1S1, TORBJ1S2>
8788	24788		2.89	3.0E-24	3.0E-24 AW614871.1	EST_HUMAN	hh68c08.x1 NCI_CGAP_CU1 Homo sapiens cDNA clone IMAGE:2887950 3' similar to contains MER29.b2 MER29 repetitive element ;
8822	24789		1.25	3.0E-24	3.0E-24 AW962076.1	EST_HUMAN	EST374149 MAGE resequences, MAGG Hamo septens cDNA
8820		38126	4.11	3.0E-24	3.0E-24 AL163252.2	NT	Hamo sapiens chramosome 21 segment HS21C052
12715	25369	31772	2.18	3.0E-24	3.0E-24 BF127762.1	EST_HUMAN	601810449F1 NIH MGC_46 Hamo sapiens cDNA clane IMAGE:4053396 67
2354	<u> </u>		28	2.0E-24	2.0E-24 AA167539.1	EST_HUMAN	zp11f09_r1 Stratagene fetal retina 837202 Homo saplens cDNA clone IMAGE:609161 5
3812			0.89	2.0E-24	2.0E-24 AW898189.1	EST_HUMAN	RC3-NN0068-090500-021-b03 NN0068 Homo saplens cDNA
7588	26001		19.0	2.0E-24	2	IN	Homo septems chromosome 21 segment HS210009
7715	20872	34039	1.12	2.0E-24	1	NT	Mus musculus rhofrac-Interacting citron kinase (Crit) mRNA, complete cds
7720		34042	0.55	2.0E-24	2.0E-24 AJ003538.1	EST_HUMAN	AJ003536 Selected chromosome 21 cDNA library Homo septens cDNA clone MPIpt12-5H13
8082		35484	3.09	2.0E-24	2.0E-24 AL119158.1	EST_HUMAN	DKFZp781L1712_r1 761 (synonym: hamy2) Homo sepiens aDNA alone DKFZp761L1712 6"
-							

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	Top Hit Descriptor	ye2h09.r1 Soares fetal fiver spleen 1NRLS Homo sapiens cONA clone IMAGE:27/2729 5 struter to conterns MER28 repetitive element;	677a09x1 NCI CGAP Kkd11 Homo sapiens CUNA dane IMAGE: 21380v6 3	#77809.XI NCL CGAP KIDTH Hamp segnens GUNA Giane IMPACE 21.500.vo 3	Human O family dispersed repeat element	Homo sapiens CGI-127 protein (LOCo1646), minning	QVQ-STUZB4-TWAU-193-CTV 2010/294 TWIN SAMMIN SAMIN SAMMIN SAMMIN SAMMIN SAMMIN SAMMIN	Mus musculus mrays for rio! Naturi, pares too	Hamp sapara Files (Files) years, exert.	Mus musculus Natauli Culturas Ligaro Cas (1911) 111 111 111 111 111 111 111 111 11	Hamb sapars arounded in a beginner rock to recommend to the control of the contro	╗	7	Homo sepiers helicase-like procent (LOCS 170), illinus	Homo sepiens putative secreted protein (SIG11), minute.	ne82e10.81 NCL CCAP_KIQ1 HOMO SEPRES CLYNA CIGNE INVACE STITUS CONTINUES OF CONTINU	MERI repetitive element;	nedeado.s.1 NCI_CCSAP_Los riomo sapiens cuara cua in infract	PECHOR AND INC. COAP BY Home services (D)NA clone IMAGE:914843 similar to SW:R14A_YEAST		T	Mus musculus otogenii (Otog), neviva	T		П		7	П	╗	Homo sapiens nyposretical protein FL220414 (FL20441), in a con-	Home squeets hyboureducal process in Lazace 1 ( Case 1 ), man decertain channel MDEG mRVA, partial cds	יייייייייייייייייייייייייייייייייייייי
	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST HUMAN	Z	¥	EST_HUMAN	Ę	Ę	Ę	Ę	EST_HUMAN	EST_HUMAN	¥	¥		EST_HUMAN	NAM! HE		EST_HUMAN	EST HUMAN	Ę	EST HUMAN	EST_HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	Į.	EST_HUMAN	Ę!	Z !	ž
565	Top Hit Acession No.		.1		2.0E-24 M28877.1	706340	<del>1</del> .	۱	1.0E-24 AF143313.1	88			1.0E-24 AW901164.1	11420402 NT	T706707 NT		7.0E-25 AA483944.1	A 4 400048 4	/ UE-20 AAAOOOAO. I	7.0E-25 AA583540.1	W87623.	7305360 NT	5.0E-25 AW850271:1	5.0E-26 AA894228.1	5.0E-25 AW979107.1	4.0E-25 T98107.1	4.0E-25 AW887671.1	4.0E-25 AF000368.1	BE1709	8923324 NT		3.0E-25 U53212.1
	Most Similar (Top) Hit BLAST E Vatue	2.0E-24 H69214.1	2.0E-24	2.0E-24	2.0E-24	1.0E-24	1.0E-24	1.0E-24	1.0E-24	1.0E-24	1.0E-24	1.0E-24	1.0E-24	9.0E-25	9.0E-25		7.0E-25	10 10	7.UE-20	7.0E-25	8.0E-25	8.0E-25	5.0E-25	5.05-26	5.0E-25	4.0E-25		4.0E-25		3.0E-25		
	Expression Signal	980	88.0	9870	10.03	2.63	1.62	0.78	2	0.68	3.96	99.0	1.81	0.52	1.53		2.85		G, ES	3.24	4.41	10.26	1.67	60			2.68	0.83	3.13			0.64
	ORF SEQ ID NO:		36828	36627		71177		29009		32865	34123	L					30827	<u> </u>	34949	38486		34326				27451		29876	L	28303		32/157
	Ean SEQ ID NO:	22008	23,38	8,53	25047	14735	15877	16091	17328	19603	20748	20941	21245	19683	24885		18045		21529	24889	1_	Ŀ				L	L	1	L	1	ll	18968
	Probe SEQ ID	8	1073	10213	25,688	1385	2681	3033	4289	£ 54	138	8002	8278	8628	12008		5031		8561	12012	7184	7882	1659	870	11848	1441	3413	3923	\$55	3331	3331	5877

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Table 4
Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor	np27602.s1 NC_CGAP_P72 Homo septens cDNA clone IMAGE:1117515 \$' struiter to gb1M61866 ZINC FINGER PROTEIN 85 (HUMAN);	Hamp septems chramosome 21 segment HS21C010	Homo sepiens transducin (beta)-tike 1 (TBL1) mRNA	601611630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5	40S RIBOSOMAL PROTEIN S16	40S RIBOSOMAL PROTEIN S16	40S RIBOSOMAL PROTEIN S16	AL449573 Homo sepiens Testis (Stannides GS) Homo sepiens cumA	DKFZp434H0313_r1 434 (synonym: htes3) Hamo saplens CUNA clane UKFZp434H0313 o	Human endogenous retrovirus, complete genome	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNITION)	PM4-HT0454-080100-002-h09 HT0454 Homo sepiens cDNA	zq45b06.s1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632827 3' similar to	contains Alu repetitive element,	nn54h11.s1 NCI_CGAP_KId6 Homo septens cDNA clone IMACE::1087749 3	288g04.s1 Scares fetal heart NbHH19W Home sapiens cDNA clone IMAGE:384822 3' similar to contains	PTR6.13 PTR6 repetitive element;	R.rettus RY2G5 mRNA for a potential ligand-binding protein	R.reittus RY2G5 mRNA for a potentilal ligand-binding protein	Homo septens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1	(MAGE-B1) genes, complete cds	Human DNA, SINE repetitive element	Human DNA, SINE repetitive element	Human lambda-immunogidbulin constant region complex (germtine)	Homo sapiens chromosome 21 segment HS21C018	Human DNA, SINE repetitive element	Homo sapiens X-linked anhidroitic ectodermal dysplasta protain gene (EDA), exon 2 and franking repeat	regions	H.sapiens DNA for endogenous refroviral like element	Ind02e12x1 Sogree_NR_T_GBC_S1 Hamo sapiens cONA clane IMAGE:2308306 3	Hamo sapiens chramosome 21 segment HS21 C002	2x30d08.r1 Stratagene neuroepithelium NT2XAMI 837234 Homo saptens CUNA ctone IMAGE.546943 5 similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
Top Hit Detabese Source	EST_HUMAN	NT	NT	EST HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN	NT	SWISSPROT	EST_HUMAN		EST_HUMAN	EST HUMAN		EST HUMAN	F	Į		L	N.	IN	NT	ħ	NT		FN.	M	EST HUMAN	NT	EST HUMAN
Top Hit Acession No.	AA603590.1	3.0E-25 AL163210.2	5032158 NT	2.0E-25 BE888016.1	17008	17008	2.0E-25 P17008	L449573.1	1.0E-25 AL040229.1	9635487 NT		1.0E-26 BE162737.1		1.0E-25 AA189080.1	1.0E-26 AA582690.1		1.0E-25 AA709079.1	(60660.1	(60680.1		J93163.1	J14547.1	D14547.1	(51755.1	9.0E-28 AL163218.2	8.0E-28 D14547.1		7.0E-26 AF003528.1	X89211.1	AW340153.1	7.0E-26 AL163202.2	7.0E-26 AA115895.1
Most Similar (Top) Hit BLAST E Vatue	3.0E-25/A	3.0E-25	2.0E-25	2.0E-25	2.0E-25 P17008	2.0E-25 P17008	2.0E-25 F	2.0E-25	1.0E-25	1.0E-25	1.0E-25 Q06055	1.0E-26		1.0E-25	1.0E-25/		1.0E-25	1.0E-25 X60680.1	1.0E-25 X60680.1		1.0E-25 U93163.1	1.0E-25 D14547.1	1.0E-25 D14547.1	1.0E-25 X51755.1	9.0E-28	8.0E-26		7.0E-26	7.0E-26 X89211.1	7.0E-26		
Expression	99:0	4.08	2.8	7.52	3.35	1.98	1.88	203	1.4	1.34	2.5	233		0.83	3.22		4.36	890	0.68		2.91	1.47	1.47	1.83	1.47	1.58		2.88	1.21			8.08
ORF SEQ ID NO:	33107							36628	26378		28468				33516		34623		38318	ļ	37704		L		28519			27686			L	
SEQ ID	19824	21648	14385	15328	L		1	23049	13450	14289	15448	17912		19775	ı		21215	<u>:L</u>		L	24286		1_		L.	<u> </u>	L	14613		1	1_	t I
Prabe SEQ ID	62,680	888	1350	2317	2842	4218	4218	10123	క్ల	1283	2441	4895		6719	8985		8246	8	400		11316	12278	12278	13053	2491	5778		1580	4005	4188	5721	11978

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	Top Hit Descriptor	Homo sepiens chromosome 8 duplication of the T cell receptor beta locus and trypshogen gens families	zq52n04.nl Strakgene neuroepithelium (#837231) Homo sapiens cLNvA clone IMAGE:043271 3	Homo sapiens chromosome 21 segment HSZ1C010	es38h08.x1 Berstead eorta HPLRB6 Homo sapiens cDNA ctone IMAGE:2318519 3: smiller to WP:F49C12.11 CE03371;	as38408.X1 Barstsad acrta HPLRB6 Homo sapiens cDNA clone IMAGE:2319619 3' straitar to	WF.T. HWOLLET I CLUMO 1 .	S133446 Emitryo, 12 Week II from Sapitatis Cultur of the	Homo sepiens upstream proming transcriptor rates, have purposeed (1921), princes	601191345F1 NIH MGC / Homo saprens CUMA come invance: 35332 10 0	Human DNA, SINE repetitive element	DKFZp4341068_r1 434 (synonym: htse3) Hamo sapiens CLINA crans UNIT 2p4341060 3	zn30d08.rl Stratagene neuroepitheflum NTZRAMI 837234 Homo septens cLNA done IMACE:040643 o similer to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);	2030f10.r1 Stratagene ocion (#837204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G685374	G695374 THYROID RECEPTOR INTERACTOR;	2030/10.11 Stratagene coton (#837204) Hamo sapiens cDNA clone IMAGE;38842/5 smitter to 1 rc. cocosy4 G895374 THYROID RECEPTOR INTERACTOR;	801884983F1 NIH MGC 57 Hamo sepiens cDNA clone IMACE:4083278 57	QV2.PT0012-040400-124-e05 PT0012 Hano sepiens cDNA	QV2.PT0012-040400-124-e05 PT0012 Homo septens cDNA	m37do5.s1 NCI_CCAP_GC5 Homo eaplens cDNA clone INAGE:10880573' similar to contains OFR.t1	OFR repetitive element;	Homo sepiens pharbolin I protein (PBI) mRNA, complete cds	Homo sapiens chromosome 21 segment HS210082	DKFZp5661.171_s1 568 (synanym: hffd2) Hamo sepiens aDNA dane DNF-2p509.171 3	M.musculus mRNA for astrocytic phosphoprotein, PEA-15	Homo sepiens DNA for smykold precursor protein, complete cds	to89a01.x1 NCI_CQAP_Gae4 Homo sapiens cDNA clone INAGE:2185416 3' similar to contains Atu repetitive element;contains element MER20 MER20 repetitive element;	Homo septiens MHC class 1 region	Human endogenous retroviral element S71	Homo sapiens mRNA for KIAA1438 protein, partial cds
2011	Top Hit Database Source	-H	EST HUMAN Z	TA L	EST HUMAN V		1	HUMAN		T HUMAN		EST_HUMAN [	EST_HUMAN	2	EST_HUMAN	NAMILH TRE	Т	Г	Т	T	EST_HUMAN		NT	EST_HUMAN	LN TN	Ę	T HUMAN	Т		Į.
T DIRING	Top Hit Acession No.	6.0E-28 AF028308.1	6.0E-28 AA206131.1	8.0E-26 AL163210.2	5.0E-26/AI708235.1		5.0E-26 AI708235.1	4.0E-26 AA329548.1	TR57670 NT	4.0E-26 BE266187.1	3.0E-26 D14547.1	3.0E-26 AL045855.2	3.0E-26 AA115895.1		3.0E-26 AA152464.1	9 OC 39 A A 4 5 3 4 8 4 4	SOC-20 PAINTERS	S OF 28 AWRT5651 1	O NE DO AWRTERS 4		3.0E-28 AA583173.1	3.0E-26 AF165620.1	2.0E-26 AL163282.2	2.0E-26 AL038099.2	2.0E-26 X86694.1	2.0E-26 D87675.1	2 0E.38 A BB01 412 1	2 0F-26 AF055068 1	2.0E-26 M32788.1	2.0E-26 AB037859.1
	Most Similar (Top) Hit BLAST E Vætue	6.0E-26	8.0E-28	8.0E-26	5.0E-26		5.0E-26	4.0E-28	4.0E-26	4.0E-28	3.0E-26	3.0E-26	3.0E-26		3.0E-26	96,000	20 HO &	90.70	90.50	2000	3.0E-28	3.0E-28	2.0E-28	l						Ш
	Expression Signal	2.28	1.83	1,91	1.86		1.88	0.98	3.77	293	215	1.27	3.50		1.12		1.14	270	37	200	4.94	1.37	10.08	3.56	4.92	2.38	77.0	4 78	1.62	1.7
	ORF SEQ ID NO:	28272	28329	38462	87.7%		27179			37514	27787	28051			29738			10000		20202	38404		L		28025			aboos .	38565	Ш
	SEQ ID NO:	15248	16407	24867	14222		14222	14579	22708	23987	14802	15040	i		16832					C1147	24800		1_	L	1_	L			24068	
	Probe SEQ ID NO:	7226	3357	11990	187		1481	1546	2926	11022	1773	2019	2047	Š	978		3/91	960/	11684	100	11928	13101	689	188	3245	4 6 6			12007	12388

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Table 4
Single Exon Probes Expressed in Bone Marrow

D.	Top Hit Descriptor	QV4HT0538-020300-123-e02 HT0538 Homo sepiens cDNA	DKFZp434H1810_r1 434 (synonym: htes3) Homo septens cDNA clone DKFZp434H1910 5	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds	MR3-HT0487-150200-113-g01 HT0487 Homo saplens cDNA	DKFZp568C2146_r1 566 (synonym: hfldz) Homo sąpiens cDNA cione DKFZp688022146 5	CHR220032 Chromosome 22 evan Homo saplens cONA clane C22_46 5	RC8-FN0138-110800-022-A02 FN0138 Homo sepiens cDNA	Homo septiens MAGE-82 (MAGE-82), MAGE-83 (MAGE-83), MAGE-84 (MAGE-84), and MAGE-81 MAGE-81) censes, complete cds	PASS Homo serviers aDNA clane IMAGE:3263644 3' similar to contains OFR.H	OFR repetitive element;	wydoco4 x7 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2	I HK repetitive element;	Homo sapiens dromosome 21 segment HSZTWZ/	au87h08x1 Schreider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783285 3' simitar to gb1x00556 TUBULIN ALPHA-1 CHAIN (HUMAN);	aus71108.x1 Schmeider fetal brain 00004 Homo sepiens cDNA clone IMAGE:2783.296 3' similar to gb:1/C00558	TUBULIN ALPHA-1 CHAIN (HUMAN);	PM2-SN0018-220300-002-e07 SN0018 Homo sepiens cDNA	ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NLICLEOTIDE TRANSLOCATOR 3) (ANT 3)	Homo septems WRN (WRN) gene, complete cds	AV732214 HTF Homo sapiens cDNA clone HTFBC806 5	MR4-BT0398-250800-204-d06 BT0398 Homo sepiens cDNA	J1761F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' skullar to percentring of extent 14	ALL CONTRACT AND AND AND AND AND AND AND AND AND AND	CMI-CTUS19-091289-005-90/ CTUS19-homo suprems curva	CM1-CT0315-09/289-083-407 CT0315 Homo sapiens GUNA	Human endogenous retrovinal element HC2	h51h12x1 Scares_NFL_T_GBC_S1 Hamo sapiens cDNA clone IMAGE:2976879 3' similer to 1K:076040 076040 ORF2: FUNCTION UNKNOWN. ;	Human mRNA for KIAA0231 gene, partial cds	Homo sepiens Xq pseudoautosomal region; segment 1/2	AV723365 HTB Homo sapiens cDNA clone HTBAHE02 5
	Top Hit Database Source	EST_HUMAN (	EST_HUMAN [		EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	5		EST HUMAN		HOMAN	M	EST HUMAN	П		EST_HUMAN	SWISSPROT	Į.	EST_HUMAN	EST_HUMAN		Т		T HUMAN		EST_HUMAN	Г	NT	EST_HUMAN
	Top Hit Acession No.	1.0E-28 BE170371.1	1.0E-28 AL038363.2	1.0E-26 AF261085.1	1.0E-26 BE165980.1	1.0E-26 AL038487.1	155093.1	9.0E-27 BF371227.1			9.0E-27 BF445556.1		8.0E-27 Al831462.1	8.0E-27 AL163227.2	8 DE-27 AW182737.1		8.0E-27 AW162737.1	8.0E-27 AW864778.1	P12236	8.0E-27 AF181897.1	8.0E-27 AV732214.1	8.0E-27 BE926560.1		8.0E-Z7 N84970.1	8.0E-27 AW857579.1	8.0E-27 AW857579.1	7.0E-27 Z70664.1	7.0E-27 AW629172.1	7.0E-27 D86984.1	7.0E-27 AJ27:1735.1	7.0E-27 AV723365.1
	Most Similar (Top) Hit BLAST E Value	1.05-28	1.0E-28	1.0E-26	1.0E-28	1.0E-28	1.0E-26 H55083.1	9.0E-27	1 0004	9.05-27	9.0E-27		8.0E-27	8.0E-27	8.05-27		8.0E-27	8.0E-27	8.0E-27 P12238	8.0E-27	8.0E-27	8.0E-27		8.0E-Z7	8.0E-27	8.0E-27	7.0E-27	7.0E-27	7.0E-27	7.0E-27	7.0E-27
	Expression	37.48	133	11.4	279	2.12	2.65	1.24	,	5.	5.95		4.71	4.61	90 08		30.08	1.1	1.17	80	0.97	212		241	1.41	1.41	1.65	2.05	0.98	3.24	1.54
	ORF SEQ D NO:	28172	28100										28020		27410		27420				32053				35975	35976					
	Escan SEQ ID NO:	13242	15081	15693	20142	24192			1	CL927	25008	1	13131	13629	4447		14447	L		ı	ı	L	<u> </u>	19983	92525	L	13747		1	L	25402
r	Page SEQ ID NO:	137	2083	2697	2018	11239	12630	7837		83	12142		-	655	7777		1414	2177	3189	3364	82,29	7170		7248	9564	9564	88	23	8	11101	12759

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Table 4
Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	Human nucleater protein (B23) mRNA, complete cds	Homo sepiens chromosome 21 segment HS21C103	602/21491F1 NIH_MGC_56 Hamo saptens cDNA clane IMAGE:4278527 5	602121491F1 NIH_MGC_56 Hamo sapiens cDNA clane IMACE:4278527 5"	Mus musculus sperm tail associated protein (Stap), mRNA	Homo sepiens chromosome 21 segment HS21C009	Rattus norvegicus putative four repest ton channel mRNA, complete cds	QV0-OT70833-070300-152-b10 OT0033 Homo septens cDNA	H.sepiens DNA for endogenous retrovinal like element	Rrattus RYA3 mRNA for a potential ligand-binding protein	PM0-BT0527-090100-001-d11 BT0527 Hamo sapiens cDNA	7844008 Chromosome 7 Fetal Brain cDNA Library Homo saplens cDNA clone 7B44008	7633f02xf NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE:3284283 3'	601468531F1 NIH_MGC_68 Hamo septens aDNA clone IMAGE:3862086 67	Натто saptens atpha NAC mRNA, complete cds	nko1b10.s1 NCI_CGAP_Pr11 Homo septens cDNA clone IMAGE:1000699 strittar to glo:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);	histh12x1 Spares NFL T GBC S1 Hamp saplens cDNA clone (MAGE:2975879 3' shrifer to TR:078040	O76040 ORF2: FUNCTION UNKNOWN.;	Homo sepiens jun dimerization protein gene, pertial ods; cros gene, complete ods; and univnown gene	Homo sepiens jun dimerization protein gene, partial ods; cros gene, complete ods; and unknown gene	Y36e01.r1 Sogres placenta Nb24P Homo sapiens cDNA clone IMAGE:150840 5' straitar to SP:HMGC_MOUSE Q02591 HOMEOBOX PROTEIN ;	w/28g07.xf NCI_CGAP_Uff Hamp sepiens cDNA clone IMAGE:24282883'	nh08h05.s1 NCI_CGAP_Thy1 Homo septens cDNA done IMAGE:943737 similar to contains L1.13 L1	repetitive element :	R.rattus RYA3 mRNA for a potential ligand-binding protein	EST00738 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBCF07	EST00738 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBCF07	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000746 5'	nk01b10.s1 NCI_CGAP_Pr11 Homo sepiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
i i	Optimical Desiration Source	NT	NT	EST_HUMAN	EST_HUMAN	NT	NT	NT	EST_HUMAN	TN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	IN	EST HUMAN		EST_HUMAN	NT	F	EST HUMAN	EST HUMAN		EST_HUMAN	Z	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
	Top Hit Acession No.	M26897.1	5.0E-27 AL163303.2	5.0E-27 BF686614.1	5.0E-27 BF666614.1	B910569 NT	4.0E-27 AL163209.2	4.0E-27 AF078779.1	4.0E-27 AW880859.1	089211.1	<b>G0658.1</b>	3.0E-27 BE071924.1	_	3.0E-27 BE670351.1	3.0E-27 BF035327.1	2.0E-27 AF054187.1	2 0E-27 AA585345.1		2.0E-27 AW629172.1	2.0E-27 AF111167.2	2.0E-27 AF111167.2	H02655.1	20E-27 AI866347.1		AA551527.1	X80658.1	2.0E-27 M78590.1	2.0E-27 M78590.1	2.0E-27 AU121685.1	2.0E-27 AA565345.1
Most Similar	(Top) Hit BLAST E Vatue	8.0E-27 M26897.1	5.0E-27	5.0E-27	6.0E-27	4.0E-27	4.0E-27	4.0E-27	4.0E-27	4.0E-27 X89211.1	3.0E-27 X60658.1	3.0E-27	3.0E-27	3.0E-27	3.0E-27	2.0E-27	2 05-27		2.0E-27	2.0E-27	20E-27	2 OF-27 H02655 1	205-27		2.0E-27	2.0E-27 X60658.1	2.0E-27	2.05-27	2.0E-27	2.0E-27
	Expression Signal	10.71	6.79	3.37	3.37	1.72	122	1.26	0.72	1.98	4.38	1.08	5.66	0.67	4.46	9.25	24.32		10.81	1.61	1.61	22.0	144		2.61	0.78	1.32	1.32	297	19.93
	ORF SEQ ID NO:	37585		37010					36504		28096	30208								28215	29216					36552	36797	36798	37778	
,	SE CE No:	24042	20802	23519	23519	19960	21240	24285	23027	24810	15076	17329	18522	21026	22817	13163	14035		16183	16293	l	<u> </u>	L		22568	92082	23317	23317	24252	!J
	SEQ EQ.	11080	8055	10597	10697	8069	1/28	8316	10101	11929	. 2057	4300	5419	888	888	\$	ě		3128	3238	3238	8833	8477		9624	10151	10395	10395	11302	11816

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Top Hit Descriptor	Hamo sapiens chramosome 21 segment HS21,0046	Homo sepiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	Homo sapiens xykulokinasa (H. hrfluenzaa) homolog (XYLB) mRNA	htt/8g01.x1 NG_CGAP_Kld13 Homo sepiens cDNA clone IMAGE:3146256 3" similar to contains MER29.b3 MER29 repetitive element :	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA	HSPD20461 HM3 Hamo sapiens cDNA clone s4000085C10	HSPD20461 HM3 Hamo sepiens cDNA clane 94000096C10	Homo saplens mRNA for KIAA0454 protein, partial cds	RC8-BT0627-140200-011-E06 BT0627 Homo septens cDNA	Human mRNA for KIAA0280 gene, partial cds	Bos taurus latrophilin 3 spiice variant bbeh mRNA, complete cds	hw/16:11x1 NCI_CGAP_Lu24 Hamo sapiens cDNA clone IMAGE:3183188 3' similar to TR:007314 Q07314 SEGRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:007280 TR:007313 ;	AU128280 NTZRP1 Homo sepiens cDNA clone NTZRP1000443 6	ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 PROTEASE INHIBITOR) (ALPHA-1- ANTIPROTEINASE)	GM2-TN0140-070900-372-g01 TN0140 Homo espiens cDNA	autish08.x1 Schneider fetal brain 00004 Homo saptens cDNA clone IMAGE:2782911 3' shuiber to TR:060302 060302 KIAA0555 PROTEIN: ;contains element MER22 repetitive element;	AU142750 Y79AA1 Homo septens cDNA clone Y78AA1000824 5'	Homo sepiens gamma-glutamy/transferase-tike activity 1 (GGTLA1), mRNA	AV736348 CB Homo sepiens cDNA clone CBFAKA12 5	Homo sepiens zinc finger protein ZNF191 (ZNF191) gene, complete cas	aa60e03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA done IMAGE:825340 5 similar to contains Atu repetitive element;contains element PTR5 repetitive element;	wo18c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1 THR receitive element:	y899f10.r1 Sogres placenta Nb2HP Homo saplens cDNA clone IMAGE:148443 5	xx33c09.x1 NCI_CGAP_Kd11 Homo sepiens cDNA clone IMAGE-2895504 3' similar to SW:GG85_HUMAN	COSS/8 GOLGINASO, ;	HOMO Septens myosin prospinatese, target suburit 1 (mirril), linking	601300/UST1 NIFT MGC_Z1 riging sapiens gurer date invide_coccess o
Top 出 Detablese Source				HAM		T_HUMAN	T_HUMAN		EST_HUMAN ROSE			EST HUMAN SECR		SWISSPROT ANTIF	Π				T_HUMAN		EST HUMAN repedit		Т	T	7	Т	П.
Top Hit Acession No.	1.0E-27 AL168246.2 NT	1.0E-27 AB026898.1 NT	827059	BE950427 4 ES	005855			1.	1		7.	9.0E-28 BE348399.1 ES	-		- 95	-	7.0E-28 AU142750.1 ES	7866	7.0E-28 AV735348.1 ES	6.0E-28 AF016052.1 NT	6.0E-28 AA504562.1 ES				4W195066.1 (E.	4505316 N	4.0E-28 BE409100.1 EST HUMAN
Most Similar (Top) Hit BLAST E Vatue	1.0E-27	1.0E-27	1.0E-27	1 05.97	1.0E-27	1.0E-27 F30158.1	1.0E-27 F30158.1	1.0E-27	1.0E-27	1.0E-27 D87449.1	1.0E-27	9.05-28	9.0E-28/	9.0E-28 P50447	9 OF-28	8.0E-28	7.0E-28/	7.0E-28	7.0E-28	6.0E-28	6.0E-28	80 70 7	5.0E-28		4.0E-28	4.0E-28	4.0E-28
Expression Signal	228	88	0.85	8	524	201	201	0.71	233	27	3.73	2.18	264	1.08	274	1 8	8.98	243	2.98	1.09	382	6	4 50		1.48	1.18	3.
ORF SEQ ID NO:		27002	L		83028					36478			26320				27/182		<u> </u>				82000			28967	
Exan SEQ ID NO:	13510	14049	14738	27.7	19751	20076	20076	21823	22302	23007	24893	13245	13403	1784	OEOEO	25817			25029	72237	l		2 8 8		1		16182
Probe SEQ ID NO:	854	8	1707	90,7	70,00	250	7054	8957	7838	10080	12016	143	344	4847	1	12553	1185	11520	12181	9271	12808		910		2833	2989	3125

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Top Hit Acession Database No. Source	4.0E-28 A199941.1 EST_HUMAN REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);	4.0E-28 AP020308.1 NT Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families		EST_HUMAN	4.0E-28 AW864244.1 EST HUMAN RC3-CT0254-240400-210-110 C354 Homo septems conversed to the design (ADAM22) mRNA.	M	1.1 EST_HUMAN	M	1 EST_HUMAN	1 EST_HUMAN	4501912	2.0E-28 Y11107.3 NT HOMD SEQUENCE II COST STATE OF THE CONTRACT OF CONTRACT	EST_HUMAN	2.05-28 AL163209.2 NT Homo sapiens chromosome 21 segment FASTICAVE IN A CHARLES 134404.3' similar to contains LOR1.b1	HUMAN	EST_HUMAN	M	1 EST HUMAN	L	EST_HUMAN	E	3.1 EST_HUMAN	Z	EST HUMAN	29885 NT	
Most Similar (Top) Hit BLAST E Vatue	4.0E-28 A11	4.0E-28 AFC	4.0E-28 AB(	4.0E-28 A1	4.0E-28 AW	3.0E-28 AF	3.0E-28 BF	3.0E-28 US	3.0E-28 AI8	2.0E-28 BE	2.0E-28	2.0E-28 Y1	20E-28 AK	2.0E-28 AL	2.0E-28 BF	20E-28 BF	2.0E-28 AF	2.0E-28 AV	2 ME -20 A E	20E-28 HG						Ш
Expression Signal	2.45	3.61	38.65			261		214				1237	221	0.78	1.48			8.68								3.37
ORF SEQ ID NO:	33872			33872			35672			28123		27/164			307756	L	34760			4148	27.484		L	L		
Etan SEQ ID NO:	20514	24168	24280	20514	25301	14323	22145	24232		1	L	L	l	1_	40505				<u> L</u>	24517		.  _	┸	L	L	
Probe SEQ ID NO:	28	123	14340	41384	1258	4288	82	12%3	13636	3 8	\$	1169	2485	833	8440	SER SER	87.87	2 2		11988	1200	14/4	8 8	408E	8483	8352

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Top Hit Descriptor	EST179615 HCC cell line (matastasis to liver in mouse) (I Homo saptens cDNA 6' and similar to similar to retrovinal LTR	Homo sapiens gamma-glutramyfransferase-like activity 1 (GGTLA1), mRNA	Homo septens gamma-glutamytransferase-like activity 1 (GGTLA1), mRNA	2751c01.71 Scares retina N2b4HR Homo sapians cDNA clone IMAGE:380448 5	Homo sepiens chromosome 21 segment HS210047	hi78g06.x1 Soares_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:29/8206.3	HYPOTHETICAL GENE 50 PROTEIN	EST378521 MAGE resequences, MAGI Hamo septems cDNA	601114980F1 NIH_MGC_16 Homo sapiens cDNA done IMAGE:3355367 5	Rettus norvegicus mRNA for 45 kDa secretory protein, partia	wp69b01.x1 NCL_CGAP_Bm25 Homo sepiens cDNA clone IMAGE:2466965 3' shrifar to TR:015475 Ox5475 I INNAMED HERV-H PROTEIN combains LTR7.b1 LTR7 repetitive element :	RC3-UT0082-210800-021-c05 UT0082 Homo seplens cDNA	802184092F1 NIH MGC 42 Homo septens cDNA clone IMAGE:4300079 5	Homo sepiens chromosome 21 segment HS210003	RC3-0T0081-170300-011-c12 OT0091 Homo septems cDNA		on15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random	QV1-HT0471-280300-121-605 HT0471 Homo septens cDNA	wd35g06.x1 Sceres_NFL_T_GBC_S1 Homo septens cDNA ctone IMAGE:2330170 S' similiar to contains MER29.t2 MER29 repetitive element ;	wd35g08.x1 Soares_NR_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2330170 3' shnillar to conteins	MENZALZ MENZA repourte declinant,	Human SU RD need shook protein gene, complete ous	Human beta-galactoside alpha2,6-sialytransferase (SIA11) mKNA, exon U	Homo septens PTS gane for 6-pyruvoyitetrahydropterin synthese, complete cds	QV1-BT0821-120900-360-b03 BT0821 Homo sepiens cDNA	601152657F1 NIH_MGC_19 Homo septens cONA clone IMAGE:3508527 5	Human gene for Ah-receptor, exon 7-8	xv17f03.xf Scares_NR_T_GBC_S1 Homo sapiens cDNA cione IMAGE:2813405 3° similar to contains Atu repetitive element, contains MER19.t2 MER19 repetitive element;	Hamo septens chromosome 21 segment HS21C048
Top Hit Databese Source	EST_HUMAN			T_HUMAN				EST_HUMAN	T_HUMAN		COT LI IMAN	Т	Т	Т	T HIMAN	1		<b>EST_HUMAN</b>			EST HUMAN	Z	M	M	EST_HUMAN	EST HUMAN	NT	EST_HUMAN	NT
Top Hit Acessian No.	1.0E-28 AA308744.1	4758431 NT	4758431 NT	1.0E-28 AA054182.1	AL163247.2	9.0E-29 AW663987.1	200130	7.0E-29 AW968447.1	7.0E-29 BE254708.1	7.0E-29 AJ132352.1	20 CO CO CO CO CO CO CO CO CO CO CO CO CO	A ME DO DEDANASE 1	R AC. 20 BES 8007 4	5.0E-20 AI 163203 2	F OF 20 AW887544 4	11100101111	AI752367.1	4.0E-29 BE164930.1	4.0E-29 AI678101.1		4.0E-29 AI678101.1	JO4688.1	3.0E-29 U67847.1	3.0E-29 AB042207.1	3.0E-29 BF333238.1	3.0E-29 BE314018.1	3.0E-29 D38044.1	3.0E-29 AW 303317.1	3.0E-29 AL163246.2
Most Similar (Top) Hit BLAST E Veitue	1.0E-28/	1.0E-28	1.0E-28	1.0E-28	1.0E-28 AL163247	9.0E-29	8.0E-29 Q00130	7.0E-29	7.0E-29	7.0E-29	8	0.00-20	00.70	5 05 20	200	0.00-20	4.0E-29	4.0E-29	4.0E-29		4.0E-29	4.0E-29 J04888.1	3.0E-29	3.0E-29	3.0E-29	3.0E-29	3.0E-29	3.0E-29	3.0E-29
Expression Signal	4.47	6.47	8.47	4.36	2.58	3.46	3.12	40.1	6.0	9.37		0 42	7 07	187	30	o o	1.33	5.91	0.92		0.92	2.97	96.0	1.61	6.0	0.77	2.19	1.97	22
ORF SEQ ID NO:	38027			L		31302		27615				0/007		<u> </u>					34794			35488			L				
Exam SEQ ID NO:	22577	L	l.		L	25918		L	L		<u> </u>		2000		1	3	16301			1		22063		L	i.	L	L		1_
Pabe SEQ ID	883	10235	10235	12188	12831	13037	12713	1606	3564	13088		8		4/07	3 8	33	3246	6125	8417		8417	9097	2379	444	4784	8 8	9085	9855	6886

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Table 4
Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor	ht09g01.x1 NCI_CGAP_Kid13 Homo sepiens cDNA clone IMACE:3146256 3' similar to contains MER29.b3 MER29 receiftive element :	Human HsLIM15 mRNA for HsLim15, complete cds	Homo sepiens envelope protein RIC-6 (env) gene, complete cds	Homo sepiens envelope protein RIC-6 (env) gene, complete cds	wr65d10.x1 NCI_CGAP_Ut1 Homo sepiens cDNA done IMAGE:2492563 3' similer to TR:015549 016548 HERV-E ENVELOPE GLYCOPROTEIN;	w65d10.x1 NCI_CGAP_Ut1 Homo sepiens dNA done IMAGE:2482563 3° similar to TR:015549 015549 HERV-E ENVELOPE GLYCOPROTEIN ;	Homo sapiens chromosome 21 segment HS210068	POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE VA	os71e04x1 NCI_CGAP_GC2 Homo sepiens cDNA clone IMAGE:16108143' similar to contains L1.t2 L1 repetitive element;	wt27g07.xt Scares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element ;	wt27g07.xt Scenes_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:2356860 3' similar to contains	IGHERINE TO SELLEN CONTROL .	60144220811 NIH, MGC_60 Home suppers guina dome invicationed o	Homo sepiens DNA-binding protein (LOC66242), mKNA	Homo sepiens DNA-binding protein (LOC66242), mRNA	Homo sepiens chromosome 21 segment HS210048	Homo sepiens chromosome 21 segment HS210048	Hamo sepiens chromosome 21 segment HS21C048	Homo sapiens chromosome 21 segment HS210048	Homo sepiens splicing factor similar to dnaJ (SPF31), mRNA	QV0-OT0032-080300-155-d01 OT0032 Hamo sapiens cDNA	RC1+IN0003-220300-021-b04 HN0003 Hamo septens cDNA	R. rattus RYA3 mRNA for a potential ligand-binding protein	nz20c07.81 NCI_CGAP_GCB1 Homo sapiens cDNA done INAGE:1288332.3' similar to contains MERA.b1	MER4 repetitive element;	Homo sepiens zindiran regulated transporter-like (ZIRTL), mRNA	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA done c-23f05	EST97317 Thymus I Hamo septens cDNA 6' end similar to EST containing O femily repeat	PT2.1_13_B11.r tumor2 Homo sepiens cDNA 3'
Top Hit Datebase Source	EST HI IMAN				EST HUMAN		F	SWISSPROT	EST_HUMAN r	EST HUMAN		T	HUMAN			TN.	- LN	NT.	IN IN		EST_HUMAN (	EST HUMAN			HOMAN		EST_HUMAN		EST_HUMAN
Top Hit Acession No.		Ţ	-						9.1					10567821	10567821 NT	2.0E-29 AL 163248.2		2.0E-29 AL163248.2	2.0E-29 AL163248.2	25108	2.0E-29 AW880701.1	1.0E-29 AW983880.1			9.0E-30 AA761215.1	1422745		8.0E-30 AA383873.1	8.0E-30 AI557072.1
Most Similar (Top) Hit BLAST E Value	2 OE.20 RE350427	3.0E-29 D63882.1	2 OF-29 A	2.0E-29 A	2.0E-29 A	2.0E-29 A	2.0E-29	2.0E-29 054827	2.0E-29 A	2.0E-29 A		2.05-28	2.0E-29E	2.0E-29	2.0E-29	2.05-29	2.0E-29	2.05-29	2.0E-29	2.0E-29	2.0E-29	1.0E-29	1.0E-29 X60658.1		9.0€-30 /	9.0E-30	8.0E-30 F08688.1	8.0E-30/	8.0E-30/
Expression Signal	ğ	234	1689	1.68	7.19	7.19	24	0.99	1.08	122		1.18	1.04	0.ස	0.63	3.5	3.6	3.27	3.27	4.13	2.03	10.17			3.26	2.14	9.62	3.18	3.9
ORF SEQ ID NO:			28487								<u></u>		1		35318		l					35536			33070				35416
Exam SEQ ID NO:	22.42					L			J	l	<u>.</u>			,				ı	ı		ļ_		L	_	19790	25087			21997
Probe SEO ID NO:	1004	10010 4288	493	483	1535	1536	4308	5251	5924	8304		88	8309	8924	8924	9986	8888	10599	10589	11806	11844	914	10986		6734	12263	6452	8613	9031

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Single Exon Probes Expressed in Bone Marrow

ANGIE EXOIT PROBES EXPRESSED IN DOING MAINOW	Top Hit Descriptor Source	EST_HUMAN PM4-BT0724-150400-004-d11 BT0724 Homo saplens cDNA	NT Humen kembda-finnunoglobulin constant region complex (germiline)	NT Human mRNA for integrin alpha subunit, complete cds	EST_HUMAN QVO-BN0147-280400-214-f12 BN0147 Homo sepiens cDNA	EST_HUMAN   QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA	NT Homo septens CTCL tumor entigen sezo-10 mRNA, pertial ods	NT Human lambde-transmoglobulin constant region complex (germline)		HUMAN	NT Human aconitate hydratase (ACO2) gene, eaon 7	NT Homo septems chromosome 21 segment HS21C078	NT (Homo septens chromosome 21 segment HS21C010	NT Homo septens chromosome 21 segment HS21C010	EST_HUMAN QV3-DT0043-080200-080-008 DT0043 Homo septems aDNA	EST_HUMAN   QV3-DT0043-090200-080-c08 DT0043 Homo sepiens cDNA	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE; SWISSPROT   ENDONUCLEASE]	EST_HUMAN   CM1-ST0181-091199-035-f08 ST0181 Homo sapiens cDNA	qq83c05.x1 Soares_total_fetus_Nb2HFB_9w Homo sepiens cDNA clone IMAGE:1838920 3' similar to EST_HUMAN   contains MER29.b2 MER29 repetitive element;	NT Homo sepiens telomerase reverse transcriptase (TERT) gene, exons 1-6	EST_HUMAN   b12056t Tests 1 Homo saplens cDNA done b12056	NT Rattus norvegicus purative four repeat fon charmel mRNA, complete cds	NT Rattus norvegicus putative four repeat ion channel mRNA, complete cds	ht09g01x1 NCI_CGAP_Kid13 Home septens cDNA clone IMAGE:3146256 3' similar to contains MERZ9.b3	Т		SWISSPROT TRANSCRIPTION FACTOR AP-2	EST HUMAN CMO-CT0307-310100-158-h03 CT0307 Homo septems cDNA	EST_HUMAN HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05		EST_HUMAN ILZ-NT0101-280700-116-E04 NT0101 Homo septens cDNA	NT Homo saplens Y-linked zinc finger protein (ZFY) gene, complete cds
ed in Done Martow		724-150400-004-d11 BT072	mbda-immunoglobulin const	IRNA for integrin alpha subur	1147-290400-214-f12 BN014	147-290400-214-f12 BN014	olens CTCL tumor antigen se	mbda-immunoglobulin const	d NCI_CGAP_CLL1 Homos	element	conitate hydratase (ACO2) go	olens chromosome 21 segme	iens chromosome 21 segme	olens chromosome 21 segme	043-090200-080-006 DT004	043-090200-080-c08 DT004	IRUS-RELATED POL POLY ICLEASE]	181-091189-035-f08 ST018	xt Sogres, total fetus Nb2H VIER29.b2 MER29 repetitive	viens telomerase reverse tran	Tests 1 Homo sapiens cDNA	rvegicus putative four repeat	rvegicus putative four repeat	d NCL CGAP Kid13 Homo andition alement.	sieme mRNA for KIAA1143 pa	iens mRNA for KIAA1143 pr	RIPTION FACTOR AP-2	307-310100-158-has CT030	151 normalized infant brain of	582-110400-013-H08 HT058	01-280700-116-E04 NT0101	kens Y-linked zinc finger prot
CAPIESS		PM4-BT0	Human la	Human m	OVO-BNO	OVO-BNO	Homo sa	Human la	1082g03	repetitive	Human ax	Homo sex	Homo ser	Homo sar	QV3-DT0	QVS-DT0	RETROV ENDONU	CM1-ST0	qq83c05.x contains N	Homo ser	b12056t T	Rattus no	Rattus no	MER20 #	Homo sac	Homo sap	TRANSCI	CMOCTO	HSC23F0		7	7
XOII FIODES	Top Hit Deterberse Source	EST_HUMAN	LN	NT	<b>EST_HUMAN</b>	<b>EST HUMAN</b>	NT	K		EST_HUMAN	NT	M	M	¥	EST_HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	EST HUMAN	Þ	EST_HUMAN	M	M	EST LIMAN		<b>\</b>	SWISSPROT	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
	Top Hit Acession No.	7.0E-30 BE091133.1			6.0E-30 BE008028.1	6.0E-30 BE008028.1	.1	6.0E-30 X51755.1				2						188.1	_	3.0E-30 AF128893.1		1	3.0E-30 AF078779.1	3 NE 30 BE350477 4		-		5.1			4-	2.0E-30 AF114158.1
	Most Similiar (Top) Hit BLAST E Vatue	7.0E-30 F	6.0E-30 X51755.1	6.0E-30 D25303.1	6.0E-30	8.0E-30	6.0E-30/	6.0E-30		5.0E-30	5.0E-30 U87831.1	6.0E-30/	5.0E-30/	5.0E-30	4.0E-30/	4.0E-30/	4.0E-30 P11369	4.0E-30	3.0E-30 Al338551.	3.0E-30	3.0E-30 T18862.1	3.0E-30	3.0€-30/	3.05.30	305-307	3.0E-30 AB032989	3.0E-30 P34056	2.0€-30 /	2.0E-30 F08688.1	2.0E-30 E	2.0E-30	20E-30
	Expression Signal	1.02	1.4	1.8	2.61	1.02	0.74	4.35		32.98	4.98	221	203	203	1.79	1.79	0.65	2.5	4.51	1.83	0.5	0.52	0.44	2.40	0.62	0.52	5.69	1.67	3.03	5.36	11.19	8.11
	ORF SEQ ID NO:			Z7802	22478	22478	37337			228979			37981	37982	28185	28186	31254	35852		29721	33783			ACC07.8	37366	37367	38034	26666		27482	28738	28909
	SEQ ID	14550	14604	14817	16259			14604		13 20 20 20 20 20 20 20 20 20 20 20 20 20	25746	24186	24432	24432	15169	15169	18367	2222	14196	16812	20438	21253	21798	22724	23852	23852	24482	13739	14130	14508	15721	15988
	SEQ ID NO:	1518	1271	1788	3204	4791	10905	13054		4 -	5310	11233	11489	11489	2183	2153	7035	8258	1154	8778	7470	8284	8831	1000	10032	10982	11541	976	1088	1475	2727	2830

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Table 4
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Top Hit Descriptor	EST84555 Colon adenocarcinoma IV Homo sepiens cDNA 6' end	hw05e11x1 NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE:3182012.3'	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012.3'	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial ods	Homo sapiens V1-vescular vesopressin receptor AVPR1A gene, promoter region and partial cds	601304125F1 NIH_MGC_21 Hamo septens cDNA clane IMAGE:3838310 5	Human lambda-immunoglobulin constant region complex (germline)	Homo sepiens celclum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, afternatively soliced	Homo sapiens MHC class 1 region	ht08g01.x1 NCI_CGAP_Kid13 Homo sepiens cDNA clone IMAGE:3146256 3' similier to conteins MER29.b3 MER29 repetitive element ;	AU119106 HEMBA1 Homo septiens cDNA clone HEMBA1005050 5	RC5-BT0377-091289-031-D12 BT0377 Homo sepiens cDNA	601433087F1 NIH_MGC_72 Hamo septens cDNA clone IMAGE:3918524 5	Homo sapiens type I DNA topolsomerase gene, exon 8	Homo sapiens type I DNA topoisomerase gene, exon 8	7k06f04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13537 Q13537 SIMILAR TO POGO ELEMENT ; contains L1.ft L1 repetitive element;	Homo sepiens Xq pseudoautosomel region; segment 1/2	POLYPEPTIDE N.ACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP	ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC.POLYPEPTIDE, N- ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC.T1)	Hamp sepiens chramosome 21 segment HS21C080	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA	Rattus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds	Homo sepiens SEC83, endoplesmic reticulum translocon component (S. cerevisiae) like (SEC83L), mRNA	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASHI) (NDUFB8) mRNA	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA	Hamo sepiens chromosome 21 segment HS21C006	Horse mRNA for ferritin L-chain, complete ods	ZU06004, rl Sogres, testis_NHT Homo sapiens CUNA done IMAGE: 731047 5
Top Hit Database Source	EST_HUMAN E	EST_HUMAN I	EST_HUMAN I	TN.	TA IN	EST_HUMAN	¥	<u></u>		EST HUMAN	Τ	Γ.	EST_HUMAN	Į.	ᅜ	EST HUMAN	Г		SWISSPROT	Г		IN						EST_HUMAN
Top Hit Acessian No.	7.0E-31 AA372637.1	7.0E-31 BE326517.1	7.0E-31 BE326517.1					AF222304 4		8 0F-31 BE350127.1		Ļ				5.0E-31 BF056540.1				802	30038	4.0E-31 AF084464.1	6005871 NT	- - - - - - - - - - - - - - - - - - -	11420329 NT	12		3.0E-31 AA421242.1
Most Similar (Top) Hit BLAST E Value	7.0E-31	7.0E-31	7.0E-31	7.0E-31	7.0E-31	7.0E-31	7.0E-31 X51755.1	8.0F-34	6.0E-31/	8.0F.31.E	6.0E-31	6.0E-31	6.0E-31	5.0E-31 M60694.1	5.0E-31 M60694.1	5.0E-31	4.0E-31		4.0E-31 Q 10473	4.0E-31	4.0E-31	4.0E-31	3.0E-31	3.05-31	3.0E-31	3.0E-31	3.0E-31 D14523.1	3.0E-31
Expression	1.89	2.38	2.38	0.99	0.89	0.82	5.66	82.6	7.57	7.0	1.86	227	208	283	283	1.46	3.45		101	200	1.98	0.43	0.98	6.73	1.28	2.35	4.66	0.52
ORF SEQ ID NO:		28691	28692				31771			35067					28223	j			27622			37329	28625		L		36328	
SEQ ID	13774	15672	l	L_	ı	ı	l		21461	<u>.</u>		25127	1_		13295	21755			14647		1_	L	15803		Ĭ			Ш
Probe SEQ ID NO:	712	2878	2676	8744	8744	1208	12711	ğ	8483	8674	11090	12325	12458	호	휼	8788	888		1615	1834	2800	10900	2603	7562	7736	8501	9939	10961

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Single Exon Probes Expressed in Bone Marrow

		Ι. Τ			HUMAN [1244g05.x1 Source_NFL_T_GBC_S1 Homo septems cDNA clone IMAGE:21116723'					<b>1</b>	Т	Γ	Т		UMAN 601304125F1 NIH_MGC_21 Homo sapiens cDNA done IMAGE:3638310 6	Homo sapiens hexoldnase II gene, promoter region		Homo septens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds	T.		П				Homo sapiens minisatelifite ceb1 repeat region	Bos taurus xenobiotichnedium-chain fatty acid: CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds		Homo sepiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
	Top Hit Databass Source	SWISSPROT	EST_HUMAN	EST_HU	EST_HU	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HIMAN	Ę	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	NT	<b>EST_HUMAN</b>	Ę	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	<u>H</u>	토	EST_HUMAN	눌
	Top Hit Acession No.	P11174	3.0E-31 BF035327.1	2.0E-31 AW838171.1	2.0E-31 Al393388.1	2.0E-31 AL119245.1	2.0E-31 AA458824.1	2.0E-31 AW444498.1	2.0E-31 BE350127.1	2 NE. 24 A A ST7784 4	7881535 NT	2 0F-31 AV710948.1	2.0E-31 AV710948.1	2.0E-31 BE408611.1	2.0E-31 BE408611.1	2.0E-31 AF148512.1	2.0E-31 AI114527.1	4 OE-34   1923463-1	096371	095371	095371	1.0E-31 AL134376.1	1.0E-31 AL134376.1	1.0E-31 AW391679.1	1.0E-31 AF048727.1	1.0E-31 AF126145.1	1.0E-31 BE972818.1	1.0E-31 U83163.1
	Most Similar (Top) Hit BLAST E Vatue	3.0E-31 P11174	3.0E-31	2.0E-31	2.0E-31	2.0E-31	2.0E-31	2.0E-31	2.0E-31	205.24	20E-31	20E-31	20531	20E-31	2.0E-31	2.0E-31	20E-31	4.0E-34	1.0E-31 096374	1.0E-31 095371	1.0E-31	1.0E-31	1.0E-31	1.0E-31	1.0E-31	1.0E-31	1.0E-31	1.0E-31
}	Expression Signal	3.17	6.84	1.33	96.0	2.63	5.67	0.72	288	27.0	4.13	1 13	1 13	2.57	2.57	1.91	3.94	7, 63	3.34	3.34	3.34	1.35	1.35	3.75	231	1.08	0.76	0.68
-	ORF SEQ ID NO:	37486		27953	28262	28379	28473	31323	32072		35973	36677	36678	36844	36845			28728	27878	27679	27680	30571	30572	31341	32559	33831	34468	
	SEO ED	23961	24430	14956	15238	15356	15452	18452	1889	2000	2252	8	340	23357	23357	25195	25987	43467	4788	1478	14703	17687	178871	18470	18329	20471	21069	1 1
	Probe SEQ ID NO:	10996	11487	1932	7222	2347	2447	5347	886	300	2 29	- 10268	10269	10435	10435	12427	12568	ţ	1671	1671	1871	4686	889	2388	9928	7506	8132	10596

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	SEQ IS	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Volue	Top Hiit Aceeston No.	Top Hit Defeabese Source	Top Hit Descriptor
11261	24213	37737	4.68	1.0E-31	1.0E-31 Al086434.1	EST_HUMAN	qf21h03.x1 NCI_CGAP_Brit25 Homo sepiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595 Q16595 FRATAXIN.;
12103	24974	38571	, IÚ		1.0E-31 [U88081.1	Ę	Human germitne T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV34S1, TCRBV34S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
6795	١.		2.13		9.0E-32 AV723978.1	EST_HUMAN	AV723976 HTB Homo sepiens cDNA clone HTBAAG01 5
7598	ı	33919	0.63	9.0E-32	9.0E-32 1.31770.1	NT	Bos taurus vacuolar H+-A TPase subunit mRNA, complete ods
7848	'		0.85	9.0E-32	11430822 NT	Į,	Homo sepiens hypothetical protein FLJ11294 (FLJ11294), mRNA
2080	15107		3.05		8.0E-32 A1056770.1	EST HUMAN	oz15e09.x1 Scenes_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1676384.31
9999	18856	31601	0.89		8.0E-32 AW997214.1	EST_HUMAN	RCZ-BN0048-200300-015-e04 BN0048 Homo septens cDNA
888	17943	30803	1.16	7.0E-32 P62591	P62591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)
12405	1		7.66	7.0E-32	7.0E-32 X17283.1	Į.	Human chromosome 22 immunoglobulin V(K)I gene, part. with 6' breakpoint between orphon and neighbouring non-emplified region
2742	L.	28762	12	L	6.0E-32 AI478104.1	EST_HUMAN	tm34a10x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2169994 3' similar to contains MER29.13 MER29 repetitive element;
7697	20662		1.20		6.0E-32 BE888016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo saptens cDNA clone IMAGE:3913087 5
1035	14081	27032	17.73	5.0E-32	5.0E-32 AF116827.1	M	Hamo sapiens PRO1181 mRNA, camplete cds
831	13984		1.85	4.0E-32	AL163248.2	۲	Homo seplens chromosome 21 segment HS21C048
7861	20805	34181	3.03	4.0E-32		IN	Homo sepiens AT-binding transcription factor 1 (ATBF1), mRNA
7861		34182	3.03	4.0E-32	32574	Į,	Homo sepiens AT-binding transcription factor 1 (ATBF1), mRNA
8702	21670		1	4.0E-32	1.	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo septens cDNA
466	13529	26469	3.32	3.0E-32		Z	Homo sepiens FLL-1 gene, partial
1448	14481		9.76		3.0E-32 AV731500.1	EST HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAKCO7 5
9749	22690	36147	19.67	3.0E-32	3.0E-32 AV758634.1	EST_HUMAN	AV758634 BM Homo sepiens cDNA done BMFBBH12 5
9749	22890	36148	19.67	3.0E-32	3.0E-32 AV758634.1	EST_HUMAN	AV758634 BM Homo sepiens cDNA clone BMFBBH12 5"
				100		NALULU TOTAL	zi95e07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:448500 3' similar to
מיצוו	$\perp$	3//4/	7.01		3.0E-32 AM / /021.1	LONG TOWNS	CALLED THE WITH THE WORLD.
11550	24491		1.48		3.0E-32 BF035327.1	EST HUMAN	6014-0003171 NIT MICC OF HOME SEPTEMBER CONTRACTOR INVITED SECTION OF THE WAS CONTRACTOR
12430			5.4	3.05-32	3.0E-32 BE279086.1	ESI HOMAN	001100Z5571 NID MCC_Z1 rights square myst_s 157/01 0
12786	18336	31283	3.46	3.0E-32	5174574 NT	¥	Homo sepiens myeloid/lymphoid or mbeck-lineage leukemia (trithorax (Drosophua) homolog); translocated to, 4 (MILT4) mRNA

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Single Extil Flores Explessed in Doile Iwaner	Top Hit Acession Databese Top Hit Descriptor No. Source	Homo sapiens myeloid/fymphold or mixed-lineage leukennia (triffnorax (Drosophila) homolog); translocated to, 4  6/174574 NT (MLLT4) mRNA	3.0E-32 BE278086.1 EST_HUMAN   601156285F1 NIH_MGC_21 Homo sepiens cDNA done IMAGE:3139701 5	3.1 EST_HUMAN	Į.	28133.1 NT	238133.1 NT	AA114294.1 EST_HUMAN	1 EST_HUMAN		2.0E-32 AV736449.1 EST_HUMAN AV736449 CB Homo expients cDNA clone CBFBIA08 5	1.0E-32 BE743299.1 EST HUMAN   601573207F1 NIH_MGC_9 Homo sapiens cDNA done IMAGE:3834433 5	439789 NT	1.0E-32/AA720674.1 EST_HUMAN THR repetitive element;	hw07c05x1 NCI_CGAP_LL24 Homo sepiens cDNA clone IMAGE:3182216 3' stmiller to 1 R:088539 U88539 U885399 U885399		9.0E-33 AF223391.1 NT spliced	1 EST_HUMAN		031736 NT		7.0E-33 A1600116.1   EST_HUMAN   repetitive element;	EST HUMAN	1 EST_HUMAN	7.0E-S3 AW971307.1 [EST_HUMAN   EST38S396 MAGE resequences, MAGL Homo saptens cDNA	!	Z	.1 EST_HUMAN	7.0E-33 AW971568.1 EST HUMAN EST383657 MAGE resequences, MAGL Homo sapiens cuna	not6th01.s1 NCL_CGAP_Phe1 Homo sepiens cDNA clone IMAGE:1100881 3' similar to contains L1.f1 L1 repetitive element;	
	Top Hit.		BE27906	BE29661	M35418.	238133.	Z38133.	AA1142	AA1142	AV7364	AV7364	BE7432		AA7205	RE3771		AF2233(	BF347Z	AL1632			A159011	AV7300	AV7300	AW971:		X34890	BF3472	AW971	AA6014	
	Most Similar (Top) Hit BLAST E. Veitue	3.0€-32	3.0E-32	20E-32	2.0E-32 M35418.1	2.0E-32 Z38133.1	2.0E-32	2.0E-32	2.0E-32	2.0E-32	2.0E-32	1.0E-32	1.0E-32	1.0E-32	0.05-33		9.0E-33	9.0E-33	9.0E-33	7.0E-33	7.0E-33	7.0E-33	7.0E-33	7.0E-33	7.0E-33		7.0E-33				١
	Expression Signal	3.48	4.33	78.0	0.87	6.86	6.86	219	219	4.17	4.17	1.07	6.73	6.78	7.4	3	3.43	1.82	4.08	2.4	2.4	2.43	7.82	1.62	16.32		1.07	2.89	2.65	3.85	
	ORF SEQ ID NO:	31284		30827	32690	32959	32960	35006	35007	31683	31684		33289	35334				35532		20098		28206		27719				37684	38071		İ
	SEQ ID	1838	25517	17935	19449	19682	19682	21589	21589	25589	25589	16167	19991	21809	40540	3	19820	22106	24110	13182	13182	15185	15654	14737	16310		22284	24134	24516	1	1
	SEQ ID	12786	12837	4918	6381	9824	8824	228	1288 128	13049	58,0	3110	7256	8943	ļ.	3	0929	9	11150	8	8	2169	2867	284	3258		86208	11178	11578	12400	1

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Top Hit Descriptor Source	qb67g03.x1 Scares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:17052043' similar to EST_HUMAN contains OFR.t1 OFR repetitive element;	qb67g03.x1 Scenes_fetal_heart_NbHH19W Home sapiens cDNA ctone IMACE:170524-3 smiller to EST_HUMAN   contains OFR.t1 OFR repetitive element;	EST_HUMAN   MR0-HT0405-160300-202-408 HT0405 Homo septems cDNA	HUMAN			EST_HUMAN   qi88d01.x1 Soares_NhHMPu_S1 Homo sepiens cDNA clone IMAGE:1880161 3	HUMAN		Homo sepiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA	Homo sepiens X-finked enhidrottic ectodermal dysplasia protein gene (EDA), excn 2 and tranking repest	Homo sapiens F-box protein FBL4 (FBL4) mRNA, complete cds	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete ods		T	EST HUMAN QV3-BN0047-230200-102-box BN0047 Homo septems cunk	NT Internal operation (CMA) gene, example, care of any parties of the IMAGE:24624103	Т	regons	HUMAN			EST_HUMAN MR4-8T0389-200100-001-h03 B10389 Homo septens cunva	HUMAN	EST_HUMAN   yd15605.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE::108320 5	T_HUMAN		NT Human G2 protein mRNA, partial cds
<b>E</b>	Scares_fetal_heart_NDHH19W Ho R.t1 OFR repetitive element;	Scares_fetal_heart_NbHH19W Ho R.t1 OFR repetitive element;	5-160300-202-d08 HT0405 Homo	Strategene lung carcinoma 837218 cds1 TUBULIN BETA-6 CHAIN (H	ns hypothetical protein SIRP-b2 (Si	ns hypothetical protein SIRP-b2 (SI	Soares_NhHMPu_S1 Homo sepien	Scares_fetal_liver_spicen_1NFLS_ TRANSLATIONAL INITIATION FA	ns hypothetical protein SIRP-b2 (S	ns hypothetical protetn SIRP-b2 (SI	ns X-linked enhidroitio ectodermal o	ns F-box protein FBL4 (FBL4) mRt	ns protein kinase C beta-II type (PF	rophin (DMD) gene, exons 7, 8 and	CB Homo sapiens CDNA clone CB(	17-230200-102-503 BN0047 Homo	NCI CGAP Kid11 Homo saciens	rs X-linked antidroitic ectodermal		52-181199-001-D02 HT0352 Home	ms Xq pseudoeutosomal region; se	ins hypothetical protein FLJ10900 (	99-200100-001-h03 BT0399 Hamo	Sceres fetal liver spieen 1NFLS Ho	Soares fetal liver spleen 1NFLS Ho	Soares placents Nb2HP Homo sap	protein mRNA, partial cds	protein mRNA, partial cds
·	ab67g03.x1 contains OFI	ocritains OF	MRO-HT040	ab51g11.r1 gb:X00734	Homo sapler	Homo sapler	q196d01.x1	gb:M29636	Homo saple	Homo seple	Homo sapie	Homo sapie	Homo saple	Human dyst	AV744220	QV3-BN00	MOSSCOR Y	Homo sacie	regions	PN4-HT03	Homo saple	Homo saple	MR4-BT03	yd15e05.rt	yd15e05.rl	y14c10.r1 \	Human G2	Human G2
Top Hit Detrabese Source	HUMAN	HUMAN	T HUMAN	T HUMAN			T HUMAN	HUMAN							HOMAN	HOMAN	MAN			HUMAN			HUMAN	T_HUMMN	ST_HUMAN	ST HUMAN	Ę	F
	ES	EST	留	🖁	E	뉟	ES	EST		Þ	Ļ	ZZ	5	Į	ន		뒫	3	뉟	EST	호	호	EST	EST	三	9	-	-
Top Hit Acession No.				AA626883.1 ES	11421332 NT	11421332 NT			21332 NT	11421332 NT												8922751 NT						
Most Similar (Top) Hit Top Hit Acession BLAST E No.	2.0E.33 A1160189.1 EST	2.0E-33 A1160180.1 EST		2.0F-cg AA626883.1 ES	114	2.0E-33 11421332 NT	A1277492.1		21332 NT			1.0E-33 AF003528.1	1.0E-33 M13975.1	1.0E-33 U60822.1	1.0E-33 AV744220.1	1.0E-33 AW996818.1	1.0E-33 U60822.1	1.0E-33 AI8Z/191.1	1.0E-33 AF003528.1	9.0E-34 BE155575.1 EST	9.0E-34 AJZ71735.1	8.0E-34 8922751	8.0E-34 BE069882.1	7.0E-34 T70845.1	7.0E-34 T70845.1	7.0E-34 H12868.1	6.0E-34 U10991.1	6.0E-34 U10991.1
		2.0E-33 A1160189.1	2.0E-33 BE159039.1	2 0F-cc   AA626883.1	2.0E-33 114	2.0E-33	2.0E-33 AI277492.1		11421332 NT	2.0E-33			1.0E-33 M13975.1	1.0E-33 U60822.1		1.0E-33 AW996818.1	1.0E-33 U60822.1				9.0E-34 AJ271735.1	0.83 8.0E-34 8922751	0.49 8.0E-34 BE069882.1	2.93 7.0E-34 T70845.1	0.6 7.0E-34 T70845.1	1.69 7.0E-34 H12866.1	2.11 8.0E-34 U10991.1	2.11 6.0E-34 U10991.1
Most Similar (Top) Hit BLAST E Value	2.0E-33 A160189.1	2.0E-33 A1160189.1	2.0E-33 BE159039.1	2 0F-ce   AA626883.1	2.58 2.0E-33 114/	2.58 2.0E-33	1 2.0E-33 AI277492.1	2.29 2.0E-33 A1052256.1	37411 0.9 2.0E-33 11421332 NT	37412 0.9 2.0E-33		2.05 1.0E-33 AF003528.1	33961 1.18 1.0E-33 M13975.1	0.73 1.05-33 U60822.1	1.0E-33 AV744220.1	1.79 1.0E-33 AW996818.1	38448 2.69 1.05-33 U60822.1	1.88 1.0E-33 AI8Z/191.1	3.4 1.0E-33 AF003528.1	1.17 9.0E-34 BE155575.1	3.44 9.0E-34 AJZ71735.1	28216 0.93 8.0E-34 8922751	34414 0.49 8.0E-34 BE069882.1	27449 2.83 7.0E-34 T70845.1	27449 0.6 7.0E-34 T70845.1	1,69 7.0E-34 H12866.1	26471 2.11 8.0E-34 U10991.1	26472 2.11 6.0E-34 U10991.1
Most Similar Expression (Top) Hit Signal BLAST E	2.0E-33 A160189.1	2.08 2.0E-33 A160189.1	17475 4.22 2.0E-33 BE159039.1	1000 D R2 2 DE-33 AA628883.1	31015 2.58 2.0E-33 114	18138 31016 2.58 2.0E-33	32888 1 2.0E-33 AI277492.1	2.29 2.0E-33 A1052256.1	37411 0.9 2.0E-33 11421332 NT	0.9 2.05-33		13129 2.05 1.0E-33 AF003528.1	33961 1.18 1.0E-33 M13975.1	28010 0.73 1.0E-33 U60822.1	1.72 1.0E-33 AV744220.1	24587 38157 1.79 1.0E-33 AW999818.1	24851 38448 2.59 1.0E-33 U60822.1	1.0E-33 AI9Z/191.1	1.0E-33 AF003528.1	17865 1.17 9.0E-34 BE155575.1	25603 3.44 9.0E-34 AJZ71735.1	15196 28216 0.93 8.0E-34 8922751	21014 34414 0.49 8.0E-34 BE069882.1	14472 27449 2.83 7.0E-34 T70845.1	14472) 27449) 0.6  7.0E-34 T70845.1	26227 1.69 7.0E-34 H12868.1	13543 28471 2.11 8.0E-34 U10991.1	13543 26472 2.11 6.0E-34 U10991.1

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 	Т	7	Т	Т	Т	┱	_	7	т	7	т		┌┈	$\neg$	T	┪		_		~7	7	Т	T	╗	7	٦	┑	Т	7		$\neg$
Top Hit Descriptor	Mus musculus DAB/2J hair-specific (hacl-1) gene	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA	Human spilicing factor SRp55-1 (SRp-55) mRNA, complete cds	Rattus norvegicus putetive four repeat kon channel mRNA, complete cots	Homo sapiens mRNA for KIAA1435 protein, partial cds	Homo sepiens chromosome 21 segment HS210009	1894c08.x1 NCI_CGAP_Pr28 Hamo sepiens aDNA dane IMAGE:22491943"	RC5-0T0078-280300-022-D02 OT0078 Homo saplens cDNA	601874950F1 NIH_MGC_54 Homo sepiens cDNA clone IMAGE:4102213 5	Human ig germline H-chain D-region genes, pertial ods	601458531F1 NIH_MGC_66 Hamo septems cDNA dane IMAGE:3862086 5	wd35g08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' stritier to contaîns MER29.t2 MER29 repetitive element ;	writtents vt Scenes NFL T GBC S1 Homo seciens cDNA clone IMAGE:2330170 3' struitar to contains	MER29.t2 MER29 repetitive element;	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)	ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)	Homo serviens X-linked enhidrottic ectodermal dysplasia protein gene (EDA), exch 2 and flanking repeat	enclars	Homo septiens WNT3 precursor (WNT3) mRNA, complete cds	Homo sepiens WNT3 precursor (WNT3) mRNA, complete cds	RC2-BT0506-240400-016-H08 BT0506 Homo septens cDNA	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886899 5	601484430F1 NIH_MGC_69 Hamo capiens cDNA clane IMAGE:3886899 5	OLFACTORY RECEPTOR-LIKE PROTEIN F5	DKFZp584A1563_11 564 (synonym: htbr2) Homo sapiens cDNA clone DKFZp584A1563 5	601470592F1 NIH_MGC_67 Hamo sapiens cONA clane IMACE:3873478 5	801470582F1 NIH_MGC_67 Homo sapiens cDNA clone IMACE:3873478 5	Homo saplens nucleobindin 2 (NUCB2), mRNA	ocs1c11.s1 NCI_CGAP_GCB1 Homo capiens cDNA clone IMAGE:1351316 3' similar to gb:XBBZ03 TYROSINE-PROTEIN KINASE RECEPTOR PLT4 PRECURSOR (HUMAN);	Homo saplens chromosome 21 segment HS21C010
Top Hit Detabase Source	MT	¥	M	NT	IN	K	<b>EST_HUMAN</b>	EST_HUMAN	EST HUMAN	IN	<b>EST_HUMAN</b>	EST HUMAN		EST_HUMAN	SWISSPROT	SWISSPROT	SWISSPROT		Ę	N.	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	¥	EST_HUMAN	TN.
Top Hit Acession No.	J03686.1	T706500 NT	J30883.1	5.0E-34 AF078779.1	5.0E-34 AB037856.1	5.0E-34 AL163209.2	4.0E-34 AI804687.1		4.0E-34 BF209778.1	3.0E-34 M37277.1	3.0E-34 BF035327.1	2 OF 34 AI678101 1	10000	2.0E-34 AI678101.1	51805	251805	712238		1.0E-34 AF003528.1	1.0E-34 AY008397.1	1.0E-34 AY008397.1	1.0E-34 BE071414.1	1.0E-34 BE874052.1	1.0E-34 BE874052.1		1.0E-34 AL036635.1	1.0E-34 BE781790.1	1.0E-34 BE781780.1	11430599 NT	<u>-</u>	7
Most Similar (Top) Hit BLAST E Vatue	6.0E-34 U03686.1	5.0E-34	5.0E-34 U30883.1	5.0E-34	5.0E-34/	5.0E-34	4.0E-34	4.0E-34	4.0E-34	3.0E-34	3.0E-34	2 OF-34		20E-34	2.0E-34 P51805	2.0E-34 P51805	1 0F-34 P12238		1.0E-34	1.0E-34	1.0E-34	1.0E-34	1.0E-34	1.0E-34	1.0E-34 P23288	1.0E-34	1.0E-34	1.0E-34	1.0E-34	1.0E-34	1.0E-34
Expression Signal	1.86	2.36	4.68	1.17	2.03	1.49	1.71	0.64	1.07	0.74	3.18	8	<u> </u>	1.83	1.57	1.57	8.53		1.35	0.81	0.81	6.11	1.98	1.98	0.48	14.47	1.71	1.71	328	4.1	4.01
ORF SEQ ID NO:	31836		30983	35617	37506		28046	31106	35788	32671	-	00535	ORDO	35688	37987	37988	<u> </u>		29641	30025	30026	-	32565	32568	38080	38450	38007	38008	38022		
Estan SEQ ID NO:	25103	14922	18111	22184	23980	24521	15035	18231	22358	10428	24429	aaccc	00777	22268	24439	1_			16730	17132	17132	17531	18334	19334	22634	22882	l_	L	1		
Probe SEQ ID NO:	12287	1897	5101	9218	11015	11583	2014	6223	8383	6359	11488	8	302	8303	11496	11486	1505		3687	4088	4088	4506	583	6261	9681	10055	11518	11516	11530	12864	12874

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Most Similar (Top Hit Acession Database BLASTE No. Source		AW663302.1 EST_HUMAN	8.0E.35 6031190 NT Home saplens prohibitin (PHB) mRNA	8.0E-35 BF589837.1 EST HUMAN 075912 DIACYLCLYCEROL KINASE 10TA.;	EST HUMAN	EST_HUMAN	EST_HUMAN	T_HUMAN	25417 NT	AA757115.1 EST HUMAN	5676 NT	AW297191.1 EST HUMAN	35921 NT		TN	4.1 NT	N	5.0E.35]X83392.1 INT H.septers immunoglobulin kappa light chain variable region L14	3.2 NT	12639 NT		_!	5.0E-35/AF023288.1 NI cos	EST_HUMAN	5.0E.35 BE800982.1 EST HUMAN 601431984F1 NIH MGC_72 Hamo sapiens cDNA cione IMANEE3917229 0		EST HIMAN	EST HIMAN	EST HIMAN	T COLUMNIA
	Value		13.21 8.0E-	4.47 8.05			L		1.85 7.0E	0.93 6.0E	2.85 6.0E	0.76 6.0E		0.61 6.0E		30'9 89'0.							205 5.0E	 0.99 5.0E	4.74 5.0E	2.2 5.0E				19.86
ORF SEQ Expression ID NO: Signal		29617		27765	37768	30811	37537		32968	27416	28009	30012	34605	35447	35448	36420	36672	27737	28805	28000			30354	30656		680%	l	OH545		27440
SEO ID	į	16702	L	ł	1	L	ł.	Ĺ	L	L	15006	1_	L	1_	L	L		上	1.	L	↓_		17464	17762	21493	1	1	L	200	
Probe SEQ ID	ÿ	3659	722	4754	77.	4907	110%	12402	6831	1411	1985	4083	8238	8028	8028	10025	10283	472	77.05	302			4438	4742	8526	8552		200	ZIGIL	1429

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	Top Hit Descriptor	yu98a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMACE:241236 6' similar to contains PTR5 repetitive element ;	Homo sepiens X-linked antituotiic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat recions	601300705F1 NIH_MGC_21 Homo sepiens cDNA done IMAGE;3635401 5	ht09g01.xf NCI_CGAP_Kid13 Homo saplens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3 MER29 repetitive element;	DKFZp434L148_r1 434 (synonym: htes3) Homo septens cDNA clane DKFZp434L148 5	601125260F1 NIH_MGC_8 Homo septens cDNA clone IMAGE:3345063 5	Homo sepiens phospholipid scramblase 1 gene, complete cds	7n25a09.x1 NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE:3565361 3's similar to TR:090,ZH7 090,ZH7 F-BOX PROTEIN FBL2;	7n25a09x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone INAGE:3565361 3' similar to TR:090ZH7 Q90ZH7 F-BOX PROTEIN FBL2.;	Homo sepiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively soliced	W03605X1 NCL_CGAP_GC6 Homo sepiens dDNA clone IMAGE:2480432 3' similer to SW:POL1_HUMAN P10266 RETROVIRUS-REI ATED POI, POI, YPROTEIN ICONTAINS: REVERSE TRANSCRIPTASE:	K6832F Human fetal heart, Lambda ZAP Express Homo sapians cDNA done K6932 5' similar to REPETITIVE ELEMENT	A971F Heart Homo sepiens cDNA clone A971	Homo sepiens mRNA for Gab2, complete cds	hi86a12.x1 Soares_NR_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2979168 3' similer to SW:TR12_HUMAN Q14669 THYROID RECEPTOR INTERACTING PROTEIN 12;	Homo sepiens Grb2-essociated binder 2 (KIAA0571), mRNA	Hamo sepiens Grb2-essociated binder 2 (KIAA0671), mRNA	Homo sapiens mRNA for KIAA0895 protein, partial ods	TC8APZE4328 Pediatric pre-B cell acute lymphoblastic laukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328	TCBAPZE4328 Pediatric pre-B cell acute lymphoblastic laukemia Baykor-HGSC project=TCBA Homo sapiems cDNA clone TCBAP4328	yq18a12.r1 Soares fetal liver spleen 1NFLS Hamo sapiens cDNA clans IMAGE:274079 5	QV0-BT0701-210400-199-b04 BT0701 Homo sapiens cDNA
	Top Hit Database Source	EST_HUMAN F	<u></u>	T_HUMAN	EST HUMAN A	Г	Г	П	EST_HUMAN C			. NAM		Т	Г	T_HUMAN				EST_HUMAN o	EST_HUMAN o	П	EST_HUMAN C
,	Top Hit Acession No.	191193.1	4 NE.35 AF003528 1		4.0E-35 BE350127.1	_	-				3.0E-35.AF223391.1				2.0E-35 AB018413.1	5	6912459 NT	6912459 NT	2.0E-35 AB020702.1	2.0E-35 BE247575.1	_		2.0E-35 BF332417.1
	Most Similar (Top) Hit BLAST E Vætue	4.0E-35 H91193.1	4 05.35 /	4.0E-35	4.0E-35	4.0E-35/	3.0E-35	3.0E-35/	3.0E-35	3.05-35	3.05-35/	2000	2.0E-35 N88965.1	2.0E-35 T11909.1	2.0E-35/	2.0E-35/	2.0E-35	2.0E-35	2.0E-35/	2.0E-35	2.0E-36	2.0E-35 H49239.1	2.0E-35
	Expression	7.51	8	0.83	1.81	8.37	21.76	3.36	27.0	27.9	17.4	8	88	1.39	5.04	-	0.83	0.83	1.06	1.42	1.42	2.65	1.8
-	ORF SEQ ID NO:	27859				35253	27688		31303			280E4		l	28266	28706	29294	29295		29883	2984		31926
	SEQ ID	14862	17861	1	20383	ł	14615	15349	18516	18516	22780	<u> </u>	L		15241	15689	16374	16374	16615	16970	16970	17718	18758
	Probe SEQ ID NO:	1835	7877	5145	7416	888	1582	2338	6413	5413	9844	40595	100	1182	1222	2883	3823	3323	3570	3930	3930	4697	2995

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	Most Similar Top Hit Aceesion Top Hit Descriptor Signal BLAST E No. Source	0.63 1.0E-35 BF689594.1 EST_HUMAN	1.72 1.0E-35 AB028980.1 NT	1.72 1.0E-35 AB028980.1  NT	1.59 1.0E-35 A1525119.1 EST_HUMAN	1.0E-35 11418274 NT		11418110 NT	1.0E-35 BE782832.1 EST_HUMAN	2.35 9.0E.36 AW821707.1 EST_HUMAN	0.75 8.0E-36 X78479.1 NT B.bowis BBSc mRNA for schröderin	0.61 8.0E-36 AA348480.1 EST_HUMAN	0.45 8.0E-36 7708259 NT	1.68 7.0E-36 AW 857579.1 EST_HUMAN	4.05 7.0E-36 4557498 NT	MT	8.21 7.0E-36 U06672.1  NT	2.01 7.0E-36/AF052051.1 NT	4.16 6.0E-36 7706822 NT	6.0E-36 AB035346.1 NT	1.88 6.0E-36 BF615101.1 EST_HUMAN	5.08 6.0E-36/Al436169.1 EST_HUMAN	3.48	2.51 6.0E:36/AF208161.1 NT	0.6 6.0E-36 C16927.1   EST HUMAN	TABLE TO THE PARTY OF THE PARTY	3.61 6.0E-36/AI380469.1 EST HUMAN	1.9 6.0E-36 BE737154.1 EST_HUMAN	12.88 5.0E-36 AJ271735.1 NT	12.8 6.0E-36 BE388436.1 EST_HUMAN	1.32) 5.0E-36 AL163209.2
	Expression Signal	870	1.72	1.72	68:-		1.42			2.35	0.75	19:0	0.45	1.88	4.05	6.21	6.21	2.01	4.16		1.88	5.66	3.48	2.51	0.6		3.61	1.9	12.88	12.8	1.32
	SEQ ID ORF SEQ NO:	23882 37378				25887	15550 28571	25177	25396	17050 29966	19201 32425	22647 35998		16000 28923	16192	20859 34247	20859 34248	L		15434	16696 29611	18507 31384							13243 26173		16669 29581
+	Probe SEQ ID SI	10942	12052	12052	12057	12/88	12320	12404	12747	4011	6423	9896	10516	2842	3136	7916	7816	12668	1202	2427	3653	404	7316	8	10585		11874	12963	138	2761	3626

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Ingle Exoll Flobes Expressed in Dolle Mailow	Top Hit Descriptor	Hamo sepiens AP16-like 1 (AP16L1), mRNA	Homo sepiens API5-tike 1 (API5L1), mRNA	Homo sapiens N-ethylmaleimide-sensitive factor (NSF), mRNA	Homo sepiens Xq pseudoautosomal region; segment 1/2	Homo sepiens celcineum binding protein 1 (KIAA0330), mRNA	PM3-BN0176-100400-001-g04 BN0176 Hamo septems aDNA	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]	601298574F1 NIH_MGC_19 Hamo septens cDNA clane IMAGE:3628386 5"	2820020. Eprime NIH_MGC_7 Homo sepiens cDNA clone IMAGE:2820020 5	601282266F1 NIH_MGC_44 Homo sepiens cDNA clone IMAGE:3604168 5	601282286F1 NIH_MGC_44 Hamo septens cDNA clane IMAGE:3604168 5	Homo sepiens chromosome 21 segment HS21C004	y19705.r.1 Soares placenta NbZHP Homo sapiens cDNA clone IMAGE:139713 5'	Homo sepiens a distribegin and metalloproteinase domain 22 (ADAM22), trancript variant 3, mRNA	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29	Homo sepiens DNA for amyloid precursor protein, complete cds	Homo sepiens DNA for emylobid precursor protein, complete ods	2169c10.r1 Sceree_bedts_NHT Homo sepiens cDNA done IMAGE:743250 S	Homo sepiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA	AV753629 TP Homo septens cDNA clone TPGABH01 5"	Homo sapiens neurean III-abha gene, partial ods	Homo sepiens celctum/celmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial ods	Homo sepiens calotum/calmodulin-etimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds	Mus musculus junctophilin 1 (Jp1-pending), mRWA	601106343F1 NIH_MGC_18 Hamo septiens aDNA dane IMAGE:3342706 5	QV0-OT0030-240300-174-h04 OT0030 Homo saplens cDNA	Mus musculus p47-phox gene, complete cds	EST06648 Infant Brain, Bento Soeres Homo saplens cDNA clone HIBBJ28 5' end	yc4a07.rf Stratagene liver (#837224) Homo sepiens cDNA clone IMAGE:83508 5	UHHBW1-emu-e-11-0-UI.s1 NCI_CGAP_Sub7 Homo septens cDNA done IMAGE:3071132 S'	Homo sapiens ubiquifin specific protease 13 (isopeptidase T-3) (USP13) mRNA
XOII FIODES L	Top Hit Datebase Source	NT	¥	Ŋ	NT	NT	EST_HUMAN	SWISSPROT	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	NT	N	M	NT	EST_HUMAN	M	EST_HUMAN	¥	N	LN	Z	EST_HUMAN	EST_HUMAN	Z	EST_HUMAN	<b>EST HUMAN</b>	EST_HUMAN	NT
Sirigie	Top Hit Acession No.	5729729 NT	5729729 NT	11079227 NT	AJZ71735.1	11417862 NT	4.0E-36 BE010038.1	710288	4.0E-36 BE382574.1	4.0E-36/AW247772.1	4.0E-36 BE389239.1	4.0E-36 BE386299.1	AL163204.2	364023.1	11497041 NT				4.0E-36 AA400370.1	11420516 NT	-	3.0E-36 AF099810.1	3.0E-36 AF110239.1	3.0E-36 AF110239.1	10181139 NT	2.0E-36 BE259287.1	20E-36 AW880378.1	2.0E-36 AF267747.1	T08756.1	T69629.1		4507848 NT
	Most Similar (Top) Hit BLAST E Vatue	5.0E-36	5.0E-38	6.0E-38	€.0E-36	5.0E-36	4.0E-36	4.0E-36 P10266	4.0E-36	4.0E-36/	4.0E-36	4.0E-36	4.0E-36/	4.0E-36 R64023.1	4.0E-36	4.0E-36 M33320.1	4.0E-36 D87675.1	4.0E-36 D87675.1	4.0E-36/	4.0E-36	4.0E-36/	3.0E-36/	3.0E-36	3.0E-36/	3.0E-36	2.0E-36	20E-36/	205-36	20E-36	2.0E-36 T69629.1	2.0E-36	2.0E-36
Ī	Expression Signal	1.21	1.21	0.77	2.97	3.03	1.24	0.99	1.63	18.	0.65	0.65	0.71	96.0	2.48	1.74	1.2	1.2	1.8	1.86	8.26	3.9	76.0	0.97	6.81	2.17	8.63	252	3.80	124	0.82	0.57
}	ORF SEQ ID NO:	30743	30744	34405	20173	31832	27223	77447	27658		28340	28341	30696	-	32481	34246	35290	35291	37806	-		20691	27502	27503	30442				İ_	33063		38184
	SEQ ID NO:	17844	17844	21007	13243	25214	14266	14469	14884	15245	16415	16415	17804	18895	19248	20858	21867	21867	24282	25220	25768	13759	14530	14530	17554	16239	18011	18660	L	L		22728
	Probe SEQ ID NO:	4827	4827	8878	12156	12455	1228	1436	1662	233	3365	3366	4786	5804	6173	7915	8901	8901	11332	12471	12515	697	1497	1497	4530	3184	498	5563	<b>5048</b>	82,59	9743	2000

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	Τορ Hit Descriptor	Homo sepiens ubiquitin specific protesse 13 (tsopoptidase T-3) (USP13) mRNA	001300938F1 NIH_MGC_21 Homo sepiens cDNA clone IMAGE:3835480 5	RC1-HT0217-131199-021-h07 HT0217 Homo sepiens cDNA	RC1+HT0217-131189-021-h07 HT0217 Homo sepiens aDNA	60213649SF1 NIH_MGC_83 Horno septems cDNA clone IMAGE:4272888 5	Homo sapiens human endogenous retrovirus W proC8-19 protesse (pro) gene, partial cds	DKFZp434G022_r1 434 (synanym: https3) Hamo sapiens cDNA clane DKFZp434G022 6	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA	wb37c12.x1 NCI_CGAP_GC8 Homo septens cDNA clone IMAGE:2307862 3' shrifer to contains Atu repetitive element,	19036010.r1 Soeres Infert brain 1NIB Homo septens aDNA clone IMAGE:34529 5' strutter to SP-CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN;	yg38g10.rf Soeres infert brain 1NIB Homo septens cDNA clone IMAGE:34629 6' similar to SP-CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN;	DKFZp761A229_r1 761 (synonym: hamy2) Homo sapiens cDNA chone DKFZp761A229 5	2051s12_r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5	zo51a12.r1 Strategone endotheital cell 837223 Homo sapiens cDNA clone IMAGE:590398 6"	Inc60e08.r1 NCI_CGAP_Pr1 Hamo septens cDNA clane IMAGE:745670	Inc80e08.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745670	AU141688 THYRO1 Hama septems aDNA clane THYRO1001033 5	AU141688 THYRO1 Hamo septens cDNA clane THYRO1001033 5	xe82b07.xf NCL_CGAP_Brr35 Home sapiens cDNA clone IMAGE:2614357 3'	QV3-NN1023-010600-189-h01 NN1023 Homo septems cDNA	RC3-CT0278-040500-017-e10 CT0279 Homo sepiens cDNA	RCS-CT0279-040500-017-410 CT0279 Homo sepiens cDNA	CM3-NN0061-140400-147-h12 NN0061 Homo septems cDNA	UHHF-BNO-die-C-03-0-Uirf Nilf _MGC_50 Home septens cDNA clone IMAGE:3078277 6'	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA	Hamo sepiens chramosome 21 segment HS210013	Homo septens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds	we80b07.x1 NCI_CGAP_Cc3 Homo sepiens cDNA clone IMAGE:2504245 3'	we80b07.x1 NCI_CGAP_Co3 Homo espiens dDNA clone IMAGE:2504245 3'	Homo septems chimerin (chimeerin) 2 (CHN2) mRNA	CMO-UT0003-050800-503-409 UT0003 Homo sepiens cDNA
Section Lines	Top H版 Detrabese Source	M	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	NT	EST_HUMAN	NT	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	EST HUMAN	EST_HUMAN	EST HUMAN	<b>EST HUMAN</b>	<b>EST_HUMAN</b>	NT	N	IN	EST_HUMAN	EST HUMAN	Ę	EST_HUMAN
1 9161110	Top Hit Acession No.	4507848 NT	1.0E-36 BE408310.1	1.0E-36 BE148523.1	1.0E-38 BE148523.1	1.0E-36 BF673781.1	1.0E-36 AF166962.1	1.0E-36 ALD4446.1	4827064 NT	1.0E-36 Al867714.1	1.0E-36 R25012.1	1.0E-36 R25012.1	1.0E-38 AL120542.1	1.0E-36 AA148034.1	1.0E-36 AA148034.1	1.0E-36 AA420467.1	1.0E-38 AA420467.1	1.0E-36 AU141688.1	1.0E-36 AU141688.1	1.0E-36 AW103658.1	1.0E-36 BP364169.1	1.0E-36 AW855868.1	1.0E-36 AW855868.1	1.0E-36 AW897636.1	1.0E-36 AW 504143.1	11418177	1.0E-36 AL163213.2	1.0E-36 AF202723.1	9.0E-37 AW009277.1	9.0E-37 AW009277.1	4757979 NT	8.0E-37 BEG98077.1
	Most Similar (Top) Hit BLAST E Vatue	2.0E-36	1.0E-38	1.0E-36	1.0E-38	1.0E-36	1.0€-36	1.0E-36	1.0E-38	1.0E-36	1.0E-36	1.0E-36	1.0E-38	1.0E-36	1.0E-36	1.0E-38	1.0E-38	1.0E-36	1.0E-36	1.0E-38	1.0E-36	1.0E-36	1.0E-36	1.0E-36	1.0E-36	1.0E-36	1.0€-36	1.0E-36	9.0E-37	9.0E-37	8.0E-37	8.0E-37
	Expression Signal	0.57	2.74	1.06	1.06	1.35	1,34	0.82	1.3	3.86	134	26.	0.7	2.77	2.77	1.15	1.15	0.48	0.48	2.72	3.85	0.65	99.0	2.84	2.98	5.51	4.97	4.02	2.3	23	1.17	1.6
	ORF SEQ ID NO:	38185	26899	28189	28190	28249	<del> </del>	32092	32286		32862	32853	33187	34671	34672	34764	34765	34902	34003	35781	36892	37107	37108	37771	38251				83929	33830	29342	
	SEQ ID	22728	13941	15171	15171	15227	16406	18908	19088	19378	19592	19592	19892	21282	24282	24357	24357	21488	21488	22349	23395	23613	23613	24244	24874	25138	25414	25579	20568		1	18426
	Probe SEQ ID NO:	2008	888	2156	2166	2212	3356	5818	8003	6307	8529	6238	888	888	8283	8888	8388	8520	8520	8384	19473	10691	10691	11294	11709	L_	12777	13034	7607	7807	3366	6320

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gie exon propes expressed in Doine Mairow	Top Hit Descriptor	ht03g01.x1 NCI_CGAP_Kid13 Homo saplens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;	ht09g01.x1 NCI_CGAP_Ktd13 Homo sapiens cDNA clone IMAGE:3146256 3' stmilar to contains MER29.b3 MER29 repetitive element ;	RC1-CN0008-210100-012-609_1 CN0008 Hamo sapiens cDNA	H. sepiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes	DKFZp434E0422_r1 434 (synonym: https://doi.orgo/ens.cDNA.clone.DKFZp434E0422.57	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene	Homo sepiens jun dimerization protein gene, partial ods; cros gene, complete ods; and unknown gene	EST380899 MAGE resequences, MAGJ Homo sapiens cDNA	wk25b11x1 NC_CGAP_Brn25 Homo sepiens cDNA clone INAGE:2413341 3' similer to contains PTR5.12 PTR5 repetitive element;	m87g03.x1 NCI_CGAP_Bm25 Homo septens cDNA done IMAGE:2165140 3' similar to contains L1.b3 L1	repetitive element;	Homo sepiens protocadherin alpha 10 atternate Isoform (PCJUH-alpha10) mKNA, complete cas	Homo sepiens Sed1 unc-84 domein protein 2 (SUNZ) miXNA, pential cds	EST178035 Colon carcinoma (HCC) cell line Homo saplens cDNA 6 end	EST178035 Colon carcinoma (HCC) cell line Homo saptens cDNA 5 end	AV750211 NPC Hamo sepiens cDNA dane NPCBGH09 51	Hamo sepiens glycine Ceaetythansferase (2-emino-3-tetabutyrate-CoA ligase) (GCAT), mKNA	Homo sepiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	200604.s1 Scares_fetal liver_spleen_fNFLS_S1 Homo explens cUNA clone IMAGE:4480153	Human endogenous retroviral DNA (4-1), complete retroviral segment	EST52g10 WATM Homo saptens cDNA clone 52g10 similar to human S1S G04101	RC8-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA	ak09c02.s1 Soares_paraffryrdd_tumor_NbHPA Homo saplens cDNA clone IMAGE:14054423'	DKFZp434L2418_r1 434 (synonym: htes3) Homo septems cDNA clone DKFZp434L2418	DKFZp434L2418_r1 434 (synonym: htes3) Homo septens cDNA clone DKFZp434L2418	EST373222 MAGE resequences, MAGF Homo septens CUNA	EST37322 MAGE resequences, MAGE Homo septens CLINA	UKF-2554/G067_T 54/ (synonym: mort) Hamo sapiens aliver drate Ukr-2554/G067_T 54/
Xon Propes	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	Ę	EST_HUMAN	M	Ę	EST_HUMAN	EST HUMAN		EST_HUMAN	Ę	Ę	EST HUMAN	EST_HUMAN	<b>EST HUMAN</b>	Ę	Ę	EST HUMAN	Ę	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN
Single	Top Hit Acession No.	8.0E-37 BE350127.1	8.0E-37 BE350127.1	8.0E-37 AW840840.1	8.0E.37 X87344.1	7.0E-37 AL042800.1	7.0E-37 AF111167.2	7.0E-37 AF111167.2	7.0E-37 AW968623.1	7.0E-37 AI817700.1		7.0E-37 AI536702.1	6.0E-37 AF169689.1	6.0E-37 AF202723.1	5.0E-37 AA307123.1	5.0E-37 AA307123.1	5.0E-37 AV750211.1	7657117 NT	6.0E-37 AF149773.1	4.0E-37 AA702794.1	4.0E-37 M10976.1	4.0E-37 N62051.1	4.0E-37 AW 794502.1	4.0E-37 AA843808.1	3.0E-37 AL048956.1	3.0E-37 AL048956.1	3.0E-37 AW961150.1	3.0E-37 AW961150.1	3.0E-37 AL138274.1
	Most Similar (Top) Hit BLAST E Value	8.0E-37	8.05-37	8.0E-37	8.05-37	7.0E-37	7.0E-37	7.05-37	7.0E-37	7.0E-37		7.0E-37	6.0E-37	6.0E-37	5.0E-37	5.0E-37	5.0E-37	5.0E-37	5.0E-37	4.0E-37	4.0E-37	4.0E-37	4.0E-37	4.0E-37	3.0E-37	3.0E-37	3.0E-37	3.0E-37	3.0E-37
	Expression Signal	3.73	3.73	6.05	889	233	0.92	0.92	1.56	8.45		1.83	0.59	3.58	4.33	4.33	0.88	3.87	6.43	2.41	1.05	26.0	0.69	0.57	3.07	3.07	1.74	3.71	0.73
	ORF SEQ ID NO:	32206	32208	32263	34595		zms	27774	31049	37601		37712	35171		32518	32519	35501				30729		32736		L				32260
	Exan SEQ ID NO:	19013	19013	19062	l _	ł	14788	14788		24069		24194	21749	25487	19286		<u> </u>	24217	25133	15438	17831		19486	22664	15052		15522		19049
	Probe SEQ ID NO:	5927	5827	22	8216	1280	1759	1759	5161	11109		11241	8782	12903	6212	62H2	9189	11285	12333	2431	4814	2008	6419	9711	2033	2033	2519	2976	6964

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					Oll Blo		igia Latin Flores action in Lories mail on
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vætue	Top Hit Acessian Na.	Top Hit Detabase Source	. Top Hit Descriptor
\$	20754	34130	0.75	3.0E-37	3.0E-37 AJ748952.1	EST_HUMAN	et34c05.x1 Baretead colon HPLRB7 Homo sepiens cDNA clone IMAGE-2373898 3' similar to TR-013537 Q13537 SIMILAR TO POGO ELEMENT.;
ङ्क	13494	26426		2.0E-37	2.0E-37 D89790.1	F	Homo sapiens mRNA for AML1, complete cds
ᄧ	13494	26427		2.0E-37		NT	Homo sapiens mRNA for AML1, complete cds
1082	14128		2.49	2.0E-37	2.0E-37 AU131202.1	EST_HUMAN	AU131202 NT2RP3 Hamo saplens cDNA clane NT2RP3002168 5
荔	14128		2.49	2.0E-37		EST_HUMAN	AU131202 NT2RP3 Hamo sepiens aDNA clane NT2RP3002168 5
1981	15002	28005		2.0E-37	2	NT	Homo saplens chromosome 21 segment HS210047
Ş,	48048	30050		2 NE-37	IN 01-CEUSP	5	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xeminomatosis), potvoeotide 1 (CYP27A1b) mRNA
	18564			20E-37	BF03532	EST HUMAN	601458531F1 NIH_MGC_68 Homo septiens cDNA clone IMAGE:3862086 5:
888	19753	33030	0.55	2.0E-37	11890617	Ę	Homo sepiens mouse thiamin pyrophospholdnese hamolog (TPK1), mRNA
6816	19870	33159	3.92	2.0E-37	2.0E-37 AA346720.1	EST_HUMAN	EST52831 Fetal heart II Homo sapiens cDNA 5' end
8328	21288	34713	0.51	2.0E-37		EST_HUMAN	801087534F1 NIH_MGC_10 Homo septens cDNA clone IMAGE:3453657 5
8329	21298	34714	0.51	2.0E-37	2.0E-37 BE537764.1	EST_HUMAN	801087534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5
8372	21341	34752	3.33	2.0E-37	2.0E-37 BF204032.1	EST_HUMAN	601809157F1 NIH_MGC_17 Hamo septens cDNA clone IMAGE:4111408 5
11885	24766	38353	8.89	2.0E-37	2.0E-37 AF176013.1	NT	Homo sepiens J domein containing protein 1 isoform b (JDP1) mRNA, complete cds
12738	25607		1.51	2.0E-37	11417972 NT	NT	Homo sepiens pescedillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
13074	25607		4.68	2.0E-37	11417972 NT	NT	Homo sepiens pescediilo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
68 82	15116	28138	147			NT	Homo sapiens chromosome 21 segment HS21C081
3985	17025	28936	4.58			NT	Homo sepiens ribonuclease III (RN3) mRNA, complete cds
4191	17222	30111	1.09	1.0E-37	1.0E-37 BE872365.1	EST_HUMAN	801448819F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852652 5
4978	17883	30882	221	1.0E-37	1.0E-37 BF371719.1	EST_HUMAN	QVO-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
6119	19197		1.01	1.0E-37	T305360[NT	¥	Mus musculus otogelin (Otog), mRNA
8557	21525	34943	0.7	1.0E-37	1.0E.37 BE546032.1	<b>EST HUMAN</b>	801072419F1 NIH_MGC_12 Hamo sapiens cDNA clane IMAGE:3458308 5
T							zp21b02.r1 Stratagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:610059 5' strritar to
9087	22053	35478	3.45	1.0E-37	1.0E-37 AA171406.1	EST HUMAN	contains L1.t2 L1 repetitive element;
10971	23891	37405	0.44	1.0E-37	1.0E-37 AV730743.1	EST_HUMAN	AV730749 HTF Homo sapiens aDNA clane HTFAHG10 5'
11058	24019	37642		1.0E-37	1.0E-37 M22878.1	NT	Human somatte cytochrome c (HC1) processed pseudogene, complete cds
12646	25329			1.0E-37	1.0E-37 BE771814.1	EST_HUMAN	CN3-FT0096-140700-243-d07 FT0086 Hamo sapiens cDNA
5872	18961	32150		9.0E-38		NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mPNA
2	14264	77224	1.85	8.0E-38	11436955 NT	TN	Homo sepiens Grb2-essociated binder 2 (KJAA0571), mRNA
250	15509	28536	2.18	8.0E-38	8.0E-38 BF346221.1	EST HUMAN	802018401F1 NCI_CGAP_Bm67 Homo sepiens cDNA clone IMAGE:4153992 5
12698	14264	17.7.7.	1.44	8.0E-38	11436955	NT	Homo sepiens Grid2-associated binder 2 (KIAA0571), mRNA
3065	16112	29027	1.88	6.0E-38	6.0E-38 BF033033.1	EST HUMAN	801455722F1 NIH, MGC_66 Hano sepiens aDNA clane IMAGE:3856348 5

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Here we will be seen that the seen of the
2 ID SEQ

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Single Exon Probes Expressed in Bone Marrow	Top Hit Descriptor	Homo sepiens mRNA for enkyrin B (440 kDa)	Homo saptens mRNA for ankyth B (440 kDa)	AV721103 HTB Hamo sapiens cDNA clone HTBARH11 5	MR3-HT0487-150200-113-g01 HT0487 Homo sepiens cDNA	HSC18F031 namalized infant brain aDNA Hamo sapiens aDNA dane c-18f03	Homo sapiens crphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds	hu09g02.x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone INAGE:3168130 3' similer to TR:002710 002710 GAG POLYPROTEIN.;	Homo sapiens mRNA for KDAA0145 protein, partial cds	QV2.HT0698-080800-293-e05 HT0698 Homo sapiens cDNA	Homo sepiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial ods	AV726988 HTC Hamp sepiens dDNA clane HTCAXH07 5	Homo sapiens gene for kinesin-like protein, complete cds	Human topolsomerase I pseudogene 2	CHR220580 Chromosome 22 exan Hamo sapiens cDNA dane C22_788 5	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA	zu62b02.rt Sceres_testis_NFT Hamo sapiens cDNA done IMAGE:742539 6' similar to contains element. MER19 repetitive element ;	Homo sepiens guenine nucleotide binding protein-like 1 (GNL1), mRNA	Homo sepiens KIAA0178 gene product (KIAA0173), mRNA	Hamo sapiens cyclin K (CCNK) gene, exan 7	Homo sepiens mRNA for KIAA1442 protein, partial cds	Homo sepiens chromosome 21 segment HS21C003	Homo sepiens chromosome 21 segment HS21C003	Homo sepiens hypothetical protein FLJ10800 (FLJ10800), mRNA	7844H08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7844H08	Mus musculus obgelin (Obg), mRNA	Mus musculus otogelin (Otog), mRNA	Homo sapiens mRNA for KJAA0612 protein, pertial cds	Homo sepiens hypothetical protein FLJ10600 (FLJ10600), mRNA
xon Probes E	Top Hit Databasse Source	H	H IN	EST_HUMAN A		EST_HUMAN H	H H	EST_HUMAN G	T E	EST_HUMAN Q	H	Ŧ	EST_HUMAN A	NT	H IN	EST_HUMAN C		EST HUMAN IN				NT				T_HUMAN				
Single	Top Hit Acessian No.			.1	.1		.1	2.0E-38 BE222256.1		2.0E-38 BE712790.1 ·	+		2.0E-38 AV726988.1				11418248 NT	1.0E-38 AA401570.1	<b>62288</b>	7681989 NT	.1	1.0E-38 AB037863.1	2	2	8022543 NT	1.0E-38 AA077528.1	7305360 NT	5360	.1	11422250 NT
	Most Similar (Top) Hit BLAST E Value	2.0E-38 Z26634.2	2.0E-38[Z26634.2	2.0E-38 AV721103	2.0E-38 BE165980	2.0E-38 F06450.1	2.0E-38 AF069755	2.0E-38	2.0E-38 D63479.2	2.0E-38	2.0E-38 AF190501	2.0E-38 AF190501	2.0E-38/	2.0E-38 AB012723	2.0E-38 M55630.1	2.0E-38 H55641.1	2.0E-38	1.05-38/	1.0E-38	1.0E-38	1.0E-38 AF270831	1.0E-38/	1.0E-38 AL 163203	1.0E-38 AL 163203	1.0E-38	1.0E-38/	1.0E-38	1.0E-38	1.05.38	1.0E-38
	Expression	0.61	0.61	121	5.59	0.55	1.21	1,04	1.74	4.62	3.66	3.66	3.30	2.13	2.51	8.8	ဇ	238	1.92	1.17	2.01	0.99	10.48	10.48	0.03	0.77	8.58	6.58	3.03	0.55
	ORF SEQ ED NO:	32079	32080	34322		35642	35711		37239	38284	38429	38430	-		_	31810	-		28047	28071	28532	30101	30259	30280	30536	31032	32447	32448	33957	35915
	Escan SEQ ID NO:	18897	18897	72002	21795	22212	<u> </u>	L	23736		24834	24834	25071	25072	25262	25271	25599	14139	15036	15054	15505	17213	17379	17379	17648	18152	19218	19218	$L_{-I}$	22471
	Probe SEQ ID NO:	2807	2807	7988	8828	8248	8816	8298	10815	11819	11965	11955	12240	12242	12538	12548	13065	- <del>2</del>	2015	2035	2602	4182	4352	4352	4627	5143	6143	6143	7634	8098

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Single Exon Probes Expressed in Bone Marrow

_ <del>0</del>		ORF SEQ ID NO: 28817 28859 30349 33916 33916 35041	Signal Signal 11.16 11.1	Most Similar (Top) Hit BLAST E Vafue 3.0E-39   2.0E-39   3.0E-39   t Similar Top Hit Acession AST E No. No. No. 1.00 Hit Acession No.	Top Hit Dafebase Source Source EST_HUMAN EST_HUMAN EST_HUMAN NT EST_HUMAN NT EST_HUMAN NT NT NT NT NT NT NT NT NT NT NT NT NT	Top Hit Descriptor  Top Hit Descriptor  For Hi	
<u> </u>	222911 24689 14548 14566 17710 17710 17751 18534	38271 27520 27520 27530 30603 30604 30643 31442	9.63 3.62 3.62 3.62 6.87 6.87 0.87	2.0E.39 Al689680 2.0E.39 Dege84.1 1.0E.39 AJ006345 1.0E.39 AW95199 1.0E.39 AW95199 1.0E.39 1	2.0E-39 Al686860.1 ES 2.0E-39 D86984.1 NT 1.0E-39 AJ006345.1 NT 1.0E-39 AJ006345.1 NT 1.0E-39 AV0651995.1 ES 1.0E-39 AV0651995.1 ES 1.0E-39 T657020 NT 1.0E-39 T6417342 NT 1.0E-39 T1417342 NT	EST_HUMAN NT NT NT NT EST_HUMAN NT NT NT NT	tu35e03.x1 NCI_CGAP_Pr28*Home sepiens cDNA clone IMAGE:2253052.3*  Human mRNA for KIAA0208 gene, pertiel cds  Home sepiens KVLQT1 gene  Home sepiens KVLQT1 gene  Home sepiens DKFZP434P211 protein (DKFZP434P211), mRNA  EST384085 MAGE resequences, MAGB Home sepiens cDNA  EST384085 MAGE resequences, MAGB Home sepiens cDNA  EST384085 MAGE resequences, MAGB Home sepiens cDNA  EST384085 MAGE resequences, MAGB Home sepiens cDNA  Home sepiens DKFZP434P211 protein (DKFZP434P211), mRNA  Home sepiens seans domain, seven thrombospondin repeats (type 1 and type 1-lites), transmembrane domain  (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA  Home sepiens seans domain, seven thrombospondin repeats (type 1 and type 1-lites), transmembrane domain  (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
6747 16 6747 16 7000 22 7589 22 8910 21	18805 18841 18841 20126 20550 21876	31982 32023 32024 33911	4.7 4.7 1.68 1.08 0.98	1.0E-39 AJZ78170 1.0E-39 AJZ78170 1.0E-39 AJZ78170 1.0E-39 D781321 1.0E-39 O46530	1,1	T_HUMAN	ycogod in Scares feral liver spicen 1NFLS Homo sapkens cDNA clone iMAGE:109402 5' similar to contains.  Alu repetitive element-contains LTR1 repetitive element;  Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (NIX1 gene)  Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (NIX1 gene)  Homo sapiens tubby live protein 3 (TULP3), mRNA  Homo sapiens mRNA for res-related GTP-binding protein, complete cds  RIBONUCLEASE K6 PRECURSOR (RNASE K6)

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Top Hit Descriptor	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA	Homo sepiens AE-binding protein 1 (AEBP1) mRNA	Homo sepiens AE-binding protein 1 (AEBP1) mRNA	Homo sepiens tissue Inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinfiermatory) (TIMP3) mRNA	Umas emissio frantis X mentel referriority 1 (FARE1) mRNA	IN SQUARE INGRED A INCHES INCHES IN THE ANALYSIS AND ANAL	Homo sapiens mixiva for NAA1244 protein, partier cas	Homo sepiens ubiquitin specific protesse 13 (isoperatesse 1-3) (UST 13) mitura	7H15A04 Chromosome 7 HeLa CUNA Library Homo septens CUNA cione 7H 19A04	601288968F1 NIH MGC B Hamo sapients culva gane image con solution o	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds	Hans sapiens chranosane 21 segment HS210046	EST70527 T-cell fymphoma Homo sepiens cDNA 6' end cimilar to similar to zinc finger protein family	EST70527 T-cell lymphoma Homo expiens cDNA 5' end similar to similar to zinc finger protein family	hz40g01.x1 NCI_CQAP_GO8 Homo espiens cDNA cione IMAGE-32710480 3	Homo sepiens KIAA0211 gene product (KIAA0211), mRNA	Homo eaplens faity acid desafurase 1 (FADS1), mRNA	Homo sepiens fatty acid deseturase 1 (FADS1), mRNA	AV653028 GLC Homo saplans cDNA clone GLCDGF04 3"	AV653028 GLC Homo capiens cDNA clone GLCJJGF04 3	Homo sepiens chromosome 21 segment HS21C085	tterborium NCI_CGAP_Pr28 Home septens cDNA clone IMAGE:2248873 3' striker to 115:073505 073505 POL_PROTEIN: ;	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repest	regions	Homo sepiens KIAA0433 protein (KIAA0433), mRNA	AU127831 NT 2422 Hamo septens cuna came in Landaus (2.5)	INCIGENT INCIGENCY AND LED BINGET LIVING CONTRACT OF THE PRINCIPLE OF THE	ALENUIO/-U/USW-WZ-11/2 DIVU 10/ FAIlls Septents was a
Top Hit Database Source									П	EST HUMAN 60	¥	TN.	Ĭ	EST_HUMAN E	EST_HUMAN E	EST HUMAN h				HUMAN	T_HUMAN	T T	EST HUMAN P	Г	N F		٦	T	EST HUMAN IN
Top Hit Acession No.	5803210 NT	4755146	4755145 NT	AEOZEA O MET	2000	878	9.0E-40 AB033070.1	4507848 NT		8.0E-40 BE396541.1	7.0E-40 U60325.1	7.0E-40 U60325.1	7.0E-40 AL163246.2	6.0E-40 AA381275.1	8.0E-40 AA391275.1	6.0E-40 BE504788.1	7681999 NT	11439783 NT	11439783 NT	8.0E-40 AV663028.1	6.0E-40 AV653028.1	5.0E-40 AL163285.2	4.0E-40 A1686005.1		4.0E-40 AF003528.1	7682117 NT	4.0E-40 AU127831.1	4.0E-40 AA742809.1	BE009416.1
Most Similar (Top) Hit BLAST E Vetue	0.0E.40	9.0E-40	9.0E-40	100	9.UE	9.0E-40	9.0E-40	9.0E-40	8.0E-40	8.0E-40	7.0E-40	7.0E-40	7.0E-40	6.0E-40	8.0E-40	6.0E-40	6.0E-40	6.0E-40	8.0E-40	8.0E-40	6.0E-40	5.0E-40	4.0E.40		4.0E-40	4.0E-40	4.0E-40	4.0E-40	4.0E-40
Expression Signal	18:	14.84	14.84		88.0	0.88	4.05	0.78	16.0	2.39	222	22	1.76	7.5	7.5	2.06	1.32	3.38	3.38	9.47	9.47	1.12	3.24		222	8.57	0.44	4.81	5.53
ORF SEQ ID NO:	28646	L	L			29746	28943				34317	34318	37715	28746	28747			33359								30333	34597		35812
Econ SEQ ID NO:	13827	14275	14275		14476	16839	18315	17401	16111	16985	20924	20824	1_		15731	1_	19343	<u> </u>	L	L			<u> </u>	1	15134	İ_			22375
Probe SEQ ID NO:	2527	1230	28		1443	3799	3897	4527	3054	3945	7885	7985	11243	2737	2737	8049	6270	7121	742	10338	10336	2612	780		2117	4415	8278	8324	9410

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Top Hit Descriptor	zh79f11.s1 Soares jetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:4183173'	h78/11.s1 Scenes fetal liver spleen 1NFLS S1 Homo septens CONA cicre IMAGE-41831 / 3	ri42704.s1 NCI_CGAP_AA1 Hamo sepiens aDNA alone IMAGE:886167 3'	ny42704.s1 NCL_CGAP_AA1 Homo sepiens dDNA clone IMAGE:896167 3'	POL POLYPROTEIN (CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H J	AU148345 NT2RW4 Homo sepiens CDNA clone NT2RW4002122 3'	MR2-CT0222-211089-002-610 CT0222 Homo sapiens cDNA	H.saptens V(k) gene low repetitive L-family member (cos 20)	Homo sapiens chromosome 21 segment HS210003	wp04h04.x1 NCI_CGAP_Kd11 Hamo sepiens dDNA clane IMAGE:2483895 3	wp04h04.x1 NCI_CGAP_Kid11 Hamo septems cDNA clane IMAGE:2463895 3	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA	Homo sepiens a disintegrin end metalloprotainase domain 22 (ADAM22), mKNA	Homo septens IQ modif containing GTPase activating protein 1 (IQGAP1), mRNA	Human platelat activating factor acetylhydrolase, brain isoform, 45 kDa subunti (LIS1) gene, exons 3 and 4	Homo sepiens guenine rucleotide binding protein 10 (GNG10) mPNA	Homo sepiens pescedillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo expiens DSCR5b mRNA, complete cds	Homo sapiens Down syndrome candidate region 1 (DSCR1), mraNA	UI-H-BW1-emp-b-03-0-UI,s1 NCI, CGAP, Sub7 Homo explens cUNA come IMAGE:3070421 3	yc03e10.s1 Stratagene lung (#837210) Homo saplens cDNA cione IMAGE: / 8020 3	Homo sepiens target of myb1 (chicken) homolog (TOM1), mKNA	PM4-BT0341-251199-002-F11 BT0341 Homo saplens CUNA	QV0-HT0367-150200-114-g09 HT0367 Homo sabients CLVVA	AU118344 HEWBA1 Homo sapiens cDNA clone HEMBA1005583 5	ow45e08.s1 Scenes_paraffryoid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' striitar to TR:000597 000597 CYTOCHROME CLIKE POLYPEPTIDE, pontains LTR5.b1 LTR5 repetitive element;	ow45e06.s1 Soares_paraffyroid_tumor_NbHPA Homo septens cDNA clone MAGE-1649794 3' similar to TR-000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE, ;contains LTR5.b1 LTR5 repetitive element;	Homo sepiens gane for activin receptor type IIB, complete cds
Top Hit Databese Source	EST_HUMAN		EST_HUMAN I	П	SWISSPROT	П	EST HUMAN	Į.	E E		EST_HUMAN							F		HUMAN	I HUMAN		7	$\Box$	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT
Top Hit Acession No.			1.0E-40 AA573201.1			45.1	1.0E-40 BF334112.1		8.0E-41 AL163203.2	7.0E-41 A1834364.1	7.0E-41 AI034364.1	11545770 NT	11419208 NT	11433010 NT		4758445 NT	11417972 NT	6.0E-41 AB037163.1	7857042 NT	6.0E-41 BF513783.1	5.0E-41 T62628.1	4885636 NT	5.0E-41 BE067042.1	4.0E-41 BE156318.1	4.0E-41 AU118344.1	4.0E-41 AI027117.1	4.0E-41 Al027117.1	4.0E-41 AB008681.1
Most Similar (Top) Hit BLAST E Vatue	1.0E-40 W92708.1	1.0E-40 W92708.1	1.0E-40	1.0E-40	1.0E-40 P26808	1.0E-40	1.0E-40	1.0E-40 Z00015.1	8.0E-41	7.0E-41	7.0E-41	7.0E-41	7.0E-41	7.0E-41	7.0E-41 U72336.1	7.0E-41	7.0E-41	6.0E-41	6.0E-41	6.0E-41	5.0E-41	5.0E-41	5.0E-41	4.0E-41	4.05-41	4.05-41	4.0E-41	4.0E-41
Expression Signal	6.73	67.0	1.92	1.92	0.84	2.42	14.2	1.64	1.59	1.81	1.81	96'0	2.97	1.08	980	28	10.83	0.65	1.67	1.59	1.75	1.03	2.06	1.73	1.16	9.16	9.16	2.75
ORF SEQ ID NO:	32696	32696		l					34633						31218	38272		26304	28167		27838				27094	27411	27412	Ш
SEQ ID	19462	19452	20285	20285	20409	24214	26847	25822	21223	15852	15852	18442	19202	19563	18417	24604	25844	13375	16137	21273	14846	17168	19755	13466	14144	i	ł	
Probe SEQ ID NO:	288	288	7203	7283	7443	11282	12850	12813	8254	83	8	5337	6124	888	7488	44.783	13072	88	2120	8304	1819	4134	888	ફ્ક	118	1408	1408	1420

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Top Hit Descriptor	EST31723 Embryo, 12 week I Homo saplens cDNA 6' end	ZIND ENICED DEOTEIN 49R	CINCENTROLEM 150	Homo saptens KIAA0433 protein (KIAA0433), mikha	Homo septens KIAA0433 protein (KIAA0433), mRNA	EST84555 Coton adenocarcinoma IV Homo sapiens cDNA 5 end	801445847F1 NIH_MGC_65 Hamo sepiens dDNA dane IMAGE:3849803 5	601445647F1 NIH_MGC_65 Hamo sapiens aDNA dane IMAGE:3849803 5	Mus musculus tubulin alpha 6 (Tuba6), mRNA	yx18b03.s1 Soares metanocyte 2Ntb+IM Homo sapiens cDNA clone IMAGE:262061 3'	qf75010,x1 Soares_testis_NHT Hamo sapians cDNA clone IMAGE:1755858 3'	IL3-CT0213-190200-040-F09 CT0213 Homo sapiens cDNA	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA	RC0-HT0613-210300-032-g01 HT0613 Homo saplens cDNA	Homo sapians hypothetical CZH2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo sapiens hypothetical CZH2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo explens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions	Hamo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	Mus musculus neural precursor cell expressed, developmentally down-regulated gene 1 (Nedd1), mRNA	inf07602.st NCL_CGAP_Thy1 Homo seplens cDNA clone IMAGE:943588 similar to TR:0434304 G434304 3678P EXPRESSED SEQUENCE TAG MRNA ;	xx87e04.x1 NCI_CGAP_Bm36 Homo sepiens cDNA clone IMAGE:2592174 3' similar to contains OFR.12	OFR repetitive element;	Hamo saplens chromosame 21 segment HS210085	y/38g04.rf Soares fetal fiver spieen 1NFLS Homo sepiens cDNA clone IMAGE:129174 5	qf58g12.x1 Soares_testis_NHT Homo septens aDNA clane IMAGE:1764278 3'	Inf23g07.s1 NCL_CGAP_Pr1 Hamo septens aDNA clane IMAGE:314652	Inf23g07.s1 NCI_CGAP_Pr1 Hamo septens cDNA clone IMAGE:914652	Homo sapiens phosphatidyfinosital 4 Hinase 230 (pi4K230) mRNA, complete cds	Homo sapiens phosphatidy/finosital 4-ktrase 230 (pi4K230) mRNA, complete cds	xp28f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741789 3" similar to contains L1.f1 L1	repetitive element;
Top Hit Database Source	EST HUMAN	1000000	SWISSTADI	¥		EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST HUMAN	EST_HUMAN	EST_HUMAN	N <sub>T</sub>	EST_HUMAN	K	NT	ĮN.		Ā	¥	EST HUMAN	900	<b>EST_HUMAN</b>	IN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Į.	N	)   	EST HUMAN
Top Hit Acession No.	2 0F.41 AA328285 1	T		11417118 NT	11417118 NT	AA372637.1	6 F	1.0E-41 BE809735.1	6678468 NT	1.0E-41 H99079.1	1.0E-41 AI217868.1	1.0E-41 AW8478121	11626291 NT	9.0E-42 BE179191.1	11560151 NT	11580151 NT	8.0E-42 AF003530.1		8.0E-42 AB026898.1	TN 1509190	B 0F-42 AA4B3898 1		8.0E-42 AW088062.1	7.0E-42 AL163285.2	7.0E-42 R10963.1	7.0E-42 AI204358.1	7.0E-42 AA569592.1		  -	Ļ		6.0E-42 AW 238656.1
Most Similar (Top) Hit BLAST E Value	2 OF 41		2.0E-41 P52742	2.0E-41	2.0E-41	2.0E-41	1.0E-41	1.0E-41	1.0E-41	1.05-41	1.0E-41	1.0E-41	1.06.41	9.0E-42	9.0E-42	9.0E-42	8.0E-42		8.0E-42	8.0E-42	8.05.42		8.0E-42	7.0E-42	7.0E-42	7.0E-42	7.0E-42	7.0E-42	6.0E-42	6.0E-42		6.0E-42
Expression Signal	1 47		1,61	0.72	0.72	221	1.33	1.33	7.8	0.49	1.73	1.56	272	1.08	3.08	3.08	6.85		1.18	1.08	8		1.55	1.48	9.0	1.67	3.47	3.47	335	3.35		5.40
ORF SEQ ID NO:	24845		35721	L.	36168	38281					36169				35939				28155	Í						36052				27896		
Exan SEQ ID NO:	24,402	21.40	22291	22713	22713	24700	16274	16274	17619	18358	22714	24437	25132	21832	22492	22492	13536		15135	18206	25850		25728	13985	21781	22603	24450	24450	14898	14898		15309
Probe SEQ ID NO:	8422	3	8238	8772	8772	11815	3219	3279	4598	2028	8778	1494	12332	888	8238	8528	\$		2118	5197	4.99.78	2	12394	288	8814	888	11508	11508	1873	1873		72877

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Probe SEQ ID NO:	Essan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Veltue	Top Hit Acession No.	Top Hit Defebase Source	Top Hit Descriptor
5030	18052		1.48		6.0E-42 A1284770.1	EST HUMAN	qu24h09.x1 NCI_CGAP_Br12 Homo sepiens dDNA done IMAGE:1865761 similar to contains Atu repetitive element.
5543	L	31580			6.0E-42 AB028990.1	Z	Homo sepiens mRNA for KIAA1087 protein, pertial cds
5865	L				6.0E-42 AB028990.1	Ę	Homo sapiens mRNA for KIAA1087 protein, partial cds
138	1_		5.88		5.0E-42 A.1271735.1	¥	Homo sepiens Xq pseudosutosomal region; segment 1/2
438	L	28443	1.7		5.0E-42 BE217913.1	EST_HUMAN	M31e11.x1 NCI_CGAP_Lu24 Homo septems cDNA chone IMAGE:3175052.3'
487	L		4.65	5.0E-42	5730038 NT	٦N	Homo sepiens SET domein and marinar transposase fusion gene (SETMAR) mRNA
488	13561		1.37	5.0E-42	5730038 NT	NT	Homo sepiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6844	l	33184	1 07	505-42	11433063 NT	Ę	Homo capiens ubiquifin protein ligase E3A (tuman papilioma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
							Homo septens ublquifin protein ligase E3A (human papilloma virus E8-associated protein, Angelman
884	19897	33192	1.07	5.0E-42	11433063 NT	¥	syndrome) (UBE3A), mRNA
6971	L	L		L	11417957 NT	Ę	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
	L						Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delhaz taoform mRNA, complete
7409	20378	33727	1.6		5.0E-42 AF071569.1	NT	Spo
8110	21047	34447	0.51		4826977 NT	N	Homo sepiens reelin (RELN) mRNA
9131	22097	35524	2.98		5.0E-42 AB037715.1	NT	Homo sepiems mRNA for KIAA1294 protein, partial ods
10970	23890	37403	0.48	5.0E-42	11431168 NT	L.	Homo sepiens 3-hydroxyenthranlate 3,4-dioxygenese (HAAO), mRNA
10970	L.	37404	0.48	5.0E-42	11431168 NT	N	Homo sapiens 3-hydrocyanthranilate 3,4-dioxygenase (HAAO), mRNA
12087	L	38655	3.28		5.0E-42 X98411.1	NT	H.sapiens mRNA for myosh-IE
12087	L		3.28		5.0E-42 X98411.1	NT	H. sapiens mRNA for myosh-IE
E S	13815	26758	23.04		4.0E-42 AP055068.1	NT	Hamo expiens MHC class 1 region
致	<u>L</u>		23.04		4.0E-42 AF055068.1	NT	Hamo septens MHC class 1 region
1067	14112	27062	2.03		4.0E-42 AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4223	L	30139	1.24		4.0E-42 X59417.1	TN	H.sapiens PROS-27 mRNA
4255	17284	30168	1.12		4.0E-42 AF246219.1	NT	Hamo septens SNARE protein kinase SNAK mRNA, complete cds
4277	L	30185	4.28	4.0E-42	4508496 NT	LN	Homo sepiens regulatory factor X, 4 (influences HLA class il expression) (RFX4) mRNA
4613	L					NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
2290	L	31155		4.0E-42	4.0E-42 AL163203.2	NT	Homo sepiens chromosome 21 segment HS21C003
9230	18295		-	4.0E-42	4.0E-42 AL163203.2	NT	Hano sapiens chromosame 21 segment HS210003
10850	23770	37269	0.54		4.0E-42 AW371201.1	<b>EST_HUMAN</b>	CMO-BT0282-171289-127-b03 BT0282 Homo septems cDNA
11010	١.	37499	1.88		4.0E-42 AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiems cDNA
11010	l _	37500	1.88		4.0E-42 AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Hamp sepiens cDNA
11741	Ш				4.0E-42 BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_88 Homo septens cDNA clone IMAGE:3862086 5

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Top Hit Descriptor	RC0-TN0079-110900-024-g07 TN0079 Homo sepiens dDNA	AV690218 GKC Hamo septens cDNA dane GKCX26608 b	RC3-NN0070-270400-011-h10 NN0070 Homo septens cDNA	2819293.3prtme NIH_MGC_7 Homo septems cDNA clone IMAGE::2819293 3	EST367438 MAGE resequences, MAGC Homo sepierts cDNA	EST367438 MAGE resequences, MAGC Homo septems obnA	Human hapatocyte growth factor (hHGF) mKNv4, compress cds	ow83405 x1 Scares fetal liver spieen 1NH.S. ST Hamb sepilers authorate involved to	601061284F1 NIH MGC 10 Home seprens curve dame image. 3447020 3	RIBONUCLEASE K3 (KNASE K3)	RIBONUCLEASE K3 (RNASE K3)	RCO-LT0001-150200-032-411 LT0001 Homo sapiens CUNA	Homo saplens chromosome 21 segment HS21 C246	Human endogenous retrovirus pHE:1 (ERV9)	UI-H-BI1-effi-6040-UI.S1 NCI CGAP Sub3 Homo septens cuna dans image: 2/2/6/1 3	Homo sapiens partial C9 gene for complement component C4, edun 1	Hanto sapiens partial C9 gene for complement comparent C9, expn 1	Homo sapiens NADH-ubiquinone ordoreductase AGGG subunit precursor homolog micurA, nucear gene encoding mitochandrial protein, complete cds	Homo sapiens NADH-ubiquinone addareductase AGGG subunit precursor homolog mRNA, nuclear gane	encoding mitochandrial protein, complete cds	Homo septens rec (LOCS1201), mNNA	Homo sepiens PDNP1 gene, exch 17	Home sapiens major histocompatibility complex, cases II, Livi apria (n. Archary) illuvan	Hamo sepiens angin recognition complex, subunit 5 (yeest hamalog)-line (Ortost.) mixtviz, em uai saucu products	Homo saplens KIAA0255 gene product (KIAA0255), mRNA	Homo septens chromosoma 21 segment HS210067	Home sapiens chronosome 21 segment HS21C080	RC3-ST0197-161069-012-403 ST0197 Homo septems cDNA	Homo sapiens proteascme Inhibitor (PI31), mRNA	Homo saplens protessome Inhibitor (PI31), mRNA	Homo sepiens ryanodine receptor 3 (RYR3) mRNA	HSCOFF071 normalized infant brain culva Homo sapiens curva clone cultur
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	M	EST HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	N.	NT	EST_HUMAN	TN	N	· IN		M	NT	NT	N	NT	Z	Z	5	EST HUMAN	1.	Z	NT	EST HUMAN
Top Hit Acessian No.	2.0E-42 BF376834.1	2.0E-42 AV690218.1	-	1	Į.	-		2.0E-42 Al052588.1	2.0E-42 BE538919.1	81649	81649	2.0E-42 AW834834.1	2.0E-42 AL163246.2	67147.1	1.0E-42 AW285809.1	1.0E-42 AJ261818.1	1.0E-42 AJ251818.1	1.0E-42 AF067168.1		1.0E-42 AF067168.1	11423219 NT	1F110296.1	1.0E-42 5174458 NT	4505524 NT	7882027 NT	1 0F-42 AL 183267.2	4 NE 42 A 189280 2	4 OF 42 AW843817 1	5803122 NT	5803122 NT	4506758 NT	1.0E-42 Z46120.1
Most Similar (Top) Hit BLASTE Velue	2.0E-42B	2.0E-42	20E-42	2.0E-42	20E-42	20E-42	20E-42 M29146.1	20E-42	2.0E-42 E	2.0E-42 P81649	2.0E-42 P81649	2.0E-42	20E-42/	1.0E-42 X57147.1	1.0E-42	1.0E-42	1.0E-42/	1.05-42/		1.0E-42	1.0E-42	1.05-42	1.0E-42	1.0E-42	1.0E-42	4 OF 42		1				Ш
Expression Signal	4.08	0.83	3.65	327	11.89	11.89	67.0	0.77	1.17	0.61	19.0	0.82	1.48	2.47	0.78	127	127	42.60		12.69	2.08	1.05	1.88	10.83	Ĺ							0.79
ORF SEQ ID NO:	27488			28456							36823		38515							27240			L			1						
SEQ ID	14512	l	L	1_	L	18940	19894	19968	23128	L.	<u> </u>	<u> </u>	L	L	14089	1	L	<u> </u>	1	15862	L	<u>L</u>			L	L	1	$\perp$	200	L		Ш
Padbe SEQ ID NO:	1479	2483	2655	1 2	0586	988	8838	89	16291	10415	10415	10074	12045	285	<u>§</u>	1103	1103	40.47	3	1247	174	2046	<u>1982</u>	2075	27.5	3/21		42/4	1	2//4	4843	4997

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Probe		CBS Jac	Fyrmocia	Most Similar	Too Hit Aoession	Top Hit	
8 8 8 9 9 9	S S S S S		Signal	BLASTE	<b>₫</b>	Source	i op rin Descriptor
10446	3 23368	36859	4.15	9.0E-43	4757969 NT		Homo sapiens chromodomath protein, Y chromosome-like (CDYL) mRNA
88	13719	26841	41	8.0E-43	8.0E-43 AV736824.1		AV736824 CB Hamo septens cDNA clane CBLAKH08 5
88	<u>l</u>		14	8.0E-43	8.0E-43 AV736824.1	T HUMAN	AV736824 CB Hamo sapiens cDNA clone CBLAKH08 5
ĕ	<u>l_</u>		4.8	8.0E-43			Homo sepiens hypothetical protein FLJ20297 (FLJ20297), mRNA
Ŕ	<u> </u>		4.8	8.0E-43	TN 9728298		Homo sepiens hypothetical protein FLL20297 (FLJ20297), mRNA
ě	1_		4.8	8.0E-43	8923276		Homo sepiens hypothetical protein FL/20297 (FL/20297), mHNA
6783			0.78		8.0E-43 H13952.1		1008-11.11 Sceres placenta Nb241P Homo explens cLNA clans IMAGE:148172 6
3855	1	29613	7.28		7.0E-43 AW246442.1	EST_HUMAN	2822251.5prime NIH_MGC_7 Hamo septems dDNA clane IMAGE:2822251 5
8	<u> </u>		3.41	7.0E-43	7.0E-43 A1836748.1		wp69b01.x1 NCI_CGAP_Bm25 Homo expiens cDNA clone IMAGE:2469955 3' shnifar to TR:015475 015475 UNNAMED HERV-H PROTTEIN ;contains LTR7.b1 LTR7 repetitive element ;
1347	<u> </u>		14.15		6.0E-43 AA491890.1	EST HUMAN	ne72d08.s1 NCI_CGAP_Ew1 Hamo saplens cDNA clone IMAGE:909803 similar to gb1.05085 60S RIBOSOMAL PROTEIN L30 (HUMAN);
2508	L		284		6.0E-43 AV708201.1	Г	AV708201 ADC Homo seplens cDNA clone ADCACC10 67
	1					Г	Homo sepiens ATP-binding cassette, sub-family C (CFTRN/RP), member 3 (ABCC3), transcript variant
	19509	32759	2.16	6.0E-43	9965973 NT	Z	WRP3B, mRNA
	1						hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910901 3' similar to contains
7068	3 20027	33331	1.91	8.0E-43	8.0E-43 AW 468897.1	EST HUMAN	MER'I IS MER'I MER'I Meruwe daman
	<u> </u>				77273077	MAAN III FOO	235606.1 Scares NhHMPu_S1 Homo sapiens con A done iMAGE:003410 5 similar to 1 K. 0320410.0000000000000000000000000000000000
10210	_1	30022			0.0E-43 AA180134.1	EST CHILLIAN	DKEZ-7881 4742 - 1781 (supermr. home) Home sections CDNA close DKFZ-761 1712 5
11437			2.08		6.0E-43 AL119138.1	ESI HUMAN	UNITATION IN THE STATE OF THE S
144	13247		1.8		5.0E-43 AL163213.2	Į.	Homo squeris criminasme 21 segment 122100 13
206	3 13675	28496	386		6.0E-43 AA382780.1	EST_HUMAN	ESTBB033 Tests I Homo saptens CUNA 5 end
2859	15919	28840	1.63		5.0E-43 AV732578.1	EST_HUMAN	AV732578 HTF Hamo sapiens CDNA clane HTFANOX6 5
6438	20021	L	1.15		5.0E-43 AI813509.1	EST_HUMAN	(WZ2e07.x1 NC)_CGAP_Bm52 Homo septems cDNA ctome IMAGE_ZZ60462.3
188			99'0		5.0E-43 AJB13509.1	EST_HUMAN	tw22e07 x1 NCI_CGAP_Bm52 Homo septens cDNA cione IMAGE:2280432 3
882	8 21496		1.0	5.0E-43	5.0E-43 AA442271.1	EST_HUMAN	zy64et03.r1 Sceres_testis_NHT Hamo explens cDNA clone IMAGE:1757420 5
288			7.0		5.0E-43 AA442271.1	EST_HUMAN	2x64et08.r1 Scares bestis_NHT Home septems cDNA clone WAGE:78/420 o
28	<u> </u>		0.59		6.0E-43 H74277.1	EST_HUMAN	yu48g12r1 Scenes fetal liver spicen 1NPLS Hamo sapiens cONA clone IMAGE:228610 5
97.19	9 22747	36198	4.22		5.0E-43 AA465288.1	EST HUMAN	as33008.11 NC_CGAP_GCB1 Homo septems cUNA done IMAGE:813055 5
	1_						0052c10.05 NCI_CGAP_Lu5 Hamo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P90691 P90691
10763		37180	2.36		5.0E-43 AI733244.1	EST_HUMAN	PV14 GENE;
10802	<u> </u>		1.45		5.0E-43 AL049110.1	EST_HUMAN	DKFZp434D0119_r1 434 (synonym: htes3) Homo septens culva cione UNr zp434UU119
11115	_		4.88		5.0E-43 AW863007.1	EST_HUMAN	MR2-SN0007-290400-004-c02 SN0007 Homo septens cDNA
11786	6 23941	П	3.46		5.0E-43 X15804.1	L	Human mRNA for alpha-actinin

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Top Hit Descriptor	Homo sepiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), excn 2 and flanking repeat regions	oy47h03.x1 NCI_CGAP_Bm23 Hamo saplens cDNA clone IMAGE:1669013 3'	Homo sepiens glycyf-tRNA synthetase (GARS), mRNA	Homo sapiens protocadherin beta 6 (PCDHB6), mRNA	qT8a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA done IMAGE:1865354 3' striller to contetins MER10.t3 MER10 repetitive element ;	qj78a02.xf NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3 MER10 recetiive element :	Homo sepiens zinc finger protein 161 (ZNF161), mRNA	ygO6b05.r1 Soares infent brain 1NIB Homo sepiens cDNA done IMAGE:31363 5' similar to contains MER10	repeative etement;	Homo sapens carcium channet alpha I E subunit (CACAA I E) gene, exons 7-45, and perual cols, alternauvery spliced	H.sapiens gene encoding La autoantigen	AMI.1-EVI-1=AMI.1-EVI-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA	Mutant, 5938 ntj	nk55d08,s1 NCI_CGAP_Pr7 Homo septens cDNA clone IMAGE:1017419	Homo saplens mRNA for KIAA1435 protein, partial cds	Human carcinoembryonic antigen (CEA) gene, exon 6	Humen carcinoembryonic antigen (CEA) gene, exan 6	Human TBXAS1 gene for thromboxane synthase, promoter region and exon 1	Mus muscufus otogelin (Otog), mRNA	Mus musculus otogetin (Otog), mRNA	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds	aa88f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' stmilar to contains THR.£2 THR repetitive element ;	Homo sepiens hypothetical protein (HSA011916), mRNA	Homo septens similar to amithine carbamo/fransferase (H. septens) (LOC83648), mRNA	qd61c09.x1 Scares_bestis_NHT Homo capiens cDNA clone IMAGE:1733968 3' shrifar to contains PTR7.t3 PTR7 PTR7 repetitive element;	hu53s08x1 NCI_CGAP_Bm41 Homo seplens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element ;
Top Hit Database Source	± 2	T HUMAN			EST_HUMAN M	EST HUMAN M			EST_HUMAN re					T_HUMAN		H	H				H	EST HUMAN T			T HUMAN	EST_HUMAN N
Top Hit Acession No.	4 0F-43 AF003528.1		60086 8	11416793 NT	4.0E-43 A1244341.1		105967			3.0E-43 AF223391.1				_	3.1		3.0E-43 M59259.1	3.0E-43 D34613.1	7305360 NT	7305360 NT	3.0E-43 U65487.1	3 0F-43   AA458824.1	31721	11420217 NT	2.0E-43 AI190784.1	_
Most Similar (Top) Hit BLAST E Vatue	4.05-43	4.0E-43	4.0E-43	4.0E-43	4.0E-43	4 05-43 /	4.0E-43	1	4.0E-43 R20950.1	3.0E-43	3.0E-43 X97869.1		3.0E-43	3.0E-43	3.0E-43	3.0E-43	3.0E-43	3.0E-43	3.0E-43	3.0E-43	3.0E-43	305-43	3.0E-43	3.0E-43	20E-43	2.0E-43
Expression Signal	3.95	1.18	0.78	1.94	5.73	χ.	1.39		6.35	3.85	1.63		1.32	1.02	86.0	0.51	0.51	6.0	1.86	1.86	4.38	å	1.82	90	828	0.95
ORF SEQ ID NO:	28070		32821		34900						27716				30904	31405	31406	32277		32808			35584		<u> </u>	32955
Exam SEQ ED NO:	15846	18437	L	<u> </u>	<u> </u>	<u> </u>			25115	1425ë	L	L.,		17348				19080	19557	19557	19942			L		
Probe SEQ ID NO:	074	5834	8505	7837	8518	8548	10678		12306	1218	\$		3586	4319	5003	5424	5424	2006	6492	6492	06890	REAR	8472	10223	185	6620

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Table 4
Single Exon Probes Expressed in Bone Marrow

						AUI 1 1955 1	יפוס בייטור רוטיפט בקאיסטטטע ווו סטווס ואמווטיש
Probe SEG ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Velue	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
0Z39	19678	32956	96'0	20E-43	2.0E-43 BE222778.1	EST HUMAN	hu53e08x1 NC_CGAP_Brn41 Homo sepiens cDNA done INAGE:3173750 3' similar to contains element. MER40 repetitive element;
748	20456	33814		20E-48	2.0E-43 AW207390.1	EST_HUMAN	UHHBI1-afra-09-0-U.s1 NCI_CGAP_Sub3 Hamo sapiens cDNA clone IMAGE:2721712 3'
8851	21619		9.34	2.0E-43	2.0E-43 U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
11532	24473		2.98	2.0E-43	2.0E-43 T03007.1	EST_HUMAN	FB1G5 Fetal brain, Strategene Homo septens cDNA clone FB1G5 3'end similar to LINE-1
1657	14689	27684	4.13	1.0E-43	1.0E-43 AF154836.1	NT	Homo sapiens Res-like GTP-binding protein (RABZ7A) gene, exans 1b and 2
1857	14689	27685	4.13	1.0E-43	1.0E-43 AF154838.1	NT	Homo septens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1717	14747	27733	2.13	1.0E-43		¥	Homo sapiens chromosome 21 segment HS210084
2734	15728	28742	5.67	1.0E-43	1.0E-43 BF348289.1	EST_HUMAN	602022313F1 NCL CGAP_Brn67 Homo septems cDNA clone IMAGE:4157686 5
5484	18584	31498	0.77	1.0E-43	4885544	¥	Homo sepiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
6764	19818	33008	6.3	1.0E-43	4607168 NT	N	Homo saplens Sp4 transcription factor (SP4) mRNA
6764	19818	33089	6.3	1.0E-43	4507168 NT	Z	Homo saplens Sp4 transcription factor (SP4) mRNA
7.50	18391	31235	1.67	1.0E-43	1.0E-43 R19751.1	EST HUMAN	yg40e01.11 Soares infant brain 1NIB Home sapiens cDNA done IMAGE:34732 5' stmiler to SP:BD38 MOUSE P28666 BRAIN PROTEIN DM38;
88	21233	34844	76.0	1.0E-43	1.0E-43 AF175265.1	NT	Homo sepiens vecuder sorting protein 35 (VPS35) mRNA, complete cds
8401	21370		3.15	1.0E-43	1.0E-43 AF188490.1	N.	Homo septems 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
9189	22/155	35584	30.83	1.0E-43	1.0E-43 AW963676.1	EST_HUMAN	EST375749 MAGE resequences, MAGH Homo septems cDNA
10654	23576	37073	0.62	1.0E-43	1.0E-43 AW963229.1	EST HUMAN	EST365299 MAGE resequences, MAGB Homo septems cDNA
11311	24261	37787	5.9	1.0E-43	1.0E-43 AI984961.1	EST_HUMAN	wr87h01.x1 NCI_CGAP_Kid11 Hamo sapiens cDNA clane IMAGE:2494705 3'
11683	24658	38238	3.35	1.0E-43	11424378 NT	N	Homo septens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
1224	25074		2.8	1.0E-43	1.0E-43 AL137984.1	EST_HUMAN	DKFZp781D1015_r1 781 (synonym: hamy2) Homo sapiens cDNA done DKFZp781D1015 5
12542	25265	31808	224	1.0E-43	1.0E-43 A1675416.1	EST_HUMAN	wb88b04.x1 NCI_CGAP_Pr28 Homo saplens cDNA clone IMAGE:2313775 9"
12745	25394	31757	2.8	9.0E-44	11418322 NT		Homo septens cacherin EGF LAG seven-pass C-type receptor 1 (CELSR1), mRNA
<b>894</b>	13946	26904	7.09	8.0E-44	8.0E-44 A1222885.1	EST_HUMAN	qh23gO1.x1 Soares_NFL_T_GBC_S1 Homo sapiens aDNA done IMAGE:18456623'
168	13946	26905	7.09	8.0E-44	8.0E-44 A1222985.1	EST_HUMAN	qh23g01.x1 Soares_NPL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1845552.3'
8884	21850	35271	2.88	8.0E-44	8.0E-44 X94354.1		H.sapiens DNA for Cone cGMP-PDE gene
10702	23824	37120	74.0	8.0E-44	11423497	TN	Homo explens small proline-rich protein 2C (SPRR2C), mRNA
10702	23824	37121	0.47	8.0E-44	1423497	NT	Homo septens small proline-rich protein 2C (SPRR2C), mRNA
11489	24442	37983	3.83	8.0E-44	8.0E-44 Y10498.2	IN	Homo sapiens mRNA for thymidine kinase, partial
11995	24872	38469	224	8.0E-44	8.0E-44 (29/39.1	M	Homo sapiens myosin mRNA, partial cds
12495	25237	31801	2.95	8.0E-44	11527389 NT	NT	Homo sepiens polymenase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
12536	25577	31698	1.53	8.0E-44	11418086 NT	NT	Homo sepiens putative nuclear protein (HRIHFB2122), mRNA
12870	25755	31516	268	8.0E-44	11418089 NT	NT	Homo sepiens protein kinase C, alpha binding protein (PRKCABP), mRNA
13029	25677	31698	1.58	8.0E-44	11418086 NT	NT	Homo sepiens putative nuclear protein (HRIHFB2122), mRNA

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	Top Hit Descriptor	ye89e01.71 Soares fetal liver spieen 1NRLS Homo sepiens cDNA clone IMAGE:124920 5'	Homo sepiens LIM domein-containing preferred translocation pertret in liporna (Lrrr) mixwy	Homo sapiens minisatellite ms32 repetit region	Homo sapiens minisatellite ms32 repeat region	Homo sapiens chromosome 21 segment HSZI CUS4	Homo sepiens chromosome 21 unknown miCNA	Homo sapiens chromosome 21 unknown mktwa	Home sapiens serine palmitty/ transferase, suburit II gene, compass cus, and uninowin genes	AU159839 Y78AA1 Hand sapiens duny dians 1784A100450 3	HSAAADEYU P, Human toetal Brain Whore tosture from sapirens curva	EST366120 MAGE resequences, MAGC Hamo septens curva	Homo saplens KIAA0861 gene (partial), X13 gene and LZ1 PL1 gene	Homo sepiens KIAA0651 gene (partial), XT3 gene and LZ1FL1 gene	th40d02.x1 NCI_CGAP_Bm25 Hamo sapiens cDNA clone (MACETT10005 5 Similies to contains Official OFR OFR repetitive element;	ALI124571 NT2RM4 Homo septems cDNA clone NT2RM4000218 6	Done emisses dynamics of comment HSM CMB	TIGHTO Express of Light Services of The Character (20147 3)	U110/2X1 N-1 Cont. 2 Mil Tallo appears Cont.	MASSESSITA NIH MGC /7 HOHD SEPTEMBER GLICA GOIN INVOLUTION OF A CONTRIBUTION OF A CO	Human fibrillin (FBN1) locus paymaransm	RC3-H10585-0104-U-U-Z	Hams septens cerbacy terminal LIM domain protein (CLIM ) minute, carpoor case	Homo sepiens karyophenn aipha 6 (mporun aipha 7) (infrako), ilinak	601491523F1 NIH MGC G8 HOTTO SEDENS COMA CICIO INVICE - 20350209 V	zp18b05,r1 Stratagene tetal retina 837,202 Homo exprets quark dune inimos	EST42209 Endometrial tumor Homo sapiens cONA 5 end similar to similar to alpha-1-antiproteinase F	601510547F1 NIH MGC_71 Hano seplens aDNA dane IMA(3E:3912010.5	Sus scrofa domestica submadilary apomuch miRNA, complete cos	Homo sepiens DEADM (Asp-Giu-Ala-Asp/His) box polypeptide 1 (DDX1) mitNA	Homo sepiens DEADIH (Asp-Giu-Ala-AspiHis) box polypeptide 1 (DUAL) menuk	Homo sepiens transmembrane trafficking protein ( I MPZ), mixiva	Homo sepiens transmembrane trafficking protein ( I MPZI), mirova	Homo septems KAB36 (KAB36) mrkva, comprese cus
-	Top Hit Detabase Source	T_HUMAN								П	7	EST HUMAN	¥	NT	FST HUMAN	Т	Т	Т	Т	LHUMAN	7	LECMAN			7	EST HUMAN	EST_HUMAN	EST_HUMAN	M	NT	N	M	Z	NT
	Top Hit Acession No.	R06035.1	31886							7.0E-44 AU159839.1	20946.1	6.0E-44 AW954050.1	5.0E-44 AJ289880.1	5.0E-44 AJ289880.1	R OF 44 A 1508573 4	7.00 A A 14.04574 A	10124971.1	4.0E-44 AL 163303.2	4.0E-44 Al435225.1	4.0E-44 BE883178.1	21948.1	4.0E-44 BE170618.1	4.0E-44 U80878.1	6912477 NT	3.0E-44 BE880626.1	3.0E-44 AA169851.1	3.0E-44 AA337234.1	3.0E-44 BE884820.1	3.0E-44 AF005273.1	4826685 NT	4826685	5803200 NT	2.0E-44 5803200	AF133588.1
-     	Most Similar (Top) Hit BLAST E Value	7.0E-44	7.0E-44	7.0E-44	7.0E-44	7.0E-44	7.0E-44	7.0E-44	7.0E-44	7.0E-44	6.0E-44 Z20946.1	6.0E-44	5.0E-44	5.0E-44	R OF 44 /	1000	5.UE-44	4.0E-44	4.0E-44	4.0E-44	4.0E-44 L21948.1	4.0E-44	4.0E-44	- 3.0E-44	3.0E-44	3.0E-44	3.0E-44	3.0€ 44	3.0E-44	20E-44	20E-44	20E-44	2.0E-44	2.0E-44
	Expression Signal	0.87	96.0	2.68	2.68	2.55	1.07	1.07	1.04	5.87	0.65	1.83	3.9	2.88	,	8.0	2.63	32	1.02	0.08	0.64	0.49	8.23	96.0	98'0	6.12	1.71	0.55	0.68	1.04	1.04	262	2.52	5.49
	ORF SEQ ID NO:		28283	28957	28958	29824	30177	30178	31055	34908	32531	38536			98376	ORDA		28392		34035	34998		38065			20081						L	27209	Ш
	Esan SEO ID NO:	13726	15257	16035	16035	16915	17200	17299	L	21404	L	24943	13397	13421		1			18062	20668	L	L	L_	L	15539	16171	16045	L	L	1.		L	L	Ш
	Probe SEQ ID NO:	88	2243	2877	2877	3878	4270	4270	5168	8238	828	12070	88	332		3	9739	3425	8050	7711	8614	8230	11669	1801	2537	3114	300	8074	728	105	105	1212	1212	1315

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Table 4
Single Exon Probes Expressed in Bone Marrow

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gie Caul Flobes LApressed in Done manon	Top Hit Descriptor	EST379147 MAGE resequences, MAGJ Homo septens cDNA	EST378147 MAGE resequences, MAGJ Homo sapiens cDNA	Homo saplens chromosome 21 segment HS21C009	pp88g07.x1 NCI_CGAP_GC8 Hamo sapiens cDNA clone IMAGE-2009628 31	AV714608 DCB Hamo saplens cDNA clane DCBBYE03 6	Homo sapiens Sushi domath (SCR repeat) containing (BK65A6.2), mRNA	RC1-CT0198-160809-011-C08 CT0198 Homo sapiens cDNA	RC1-CT0198-150899-011-C08 CT0198 Homo sapiens cDNA	Homo sepiens hypothetical protein FLJ10379 (FLJ10379), mRNA	Homo sepiens hypothetical protein FLJ10379 (FLJ10379), mRNA	Homo saptens mRNA for KJAA0995 protein, partial ods	Homo septens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA	EST80883 Synovial sercoma Homo sepiens dDNA 6" end	Novel human gane mapping to chomosome 22	wbs9c06.x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:2313802.3' stmiller to contains L1.t1 L1	repetitive element;	auß3h07x1 Schreider fetal brain 00004 Homo sapiens cDNA clore IMAGE-2782909 3' similar to SW-1813A HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;	Homo sepiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP4), mRNA	Homo espiens chromosome 21 segment HS21 0003	CM4-CN0044-180200-515-f01 CN0044 Homo saplens cDNA	tg94f07.x1 NCI_CGAP_CLL1 Home septens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1.;	2772403.s1 Soares testis NHT Homo sepiens CDNA clone IMAGE:727877 3' shrifer to contains element	TAR1 repetitive element;	Homo sapiens MCP-1 gane and enhancer region	Homo sepiens MCP-1 gene and enhancer region	Homo sapiens mRNA for inducible nitric adde synthase, complete cds	Homo septens mRNA for inductible nitric adde synthase, complete cds	Homo sapiens zinc finger protein 277 (ZNF277), mRNA	Homo sepiens zinc finger protein 277 (ZNF277), mRNA	Homo sapians bone morphogenetic protein 5 (BMP5), mPOVA	Homo sapiens programmed cell death 5 (PUCD'5), miKNA
ALAI FIODOS LA	Top Hit Database Source		T HUMAN		EST HUMAN $\phi$	EST_HUMAN A		HUMAN	T HUMAN						LHUMAN		<u>≯</u>	EST HUMAN IN	EST HIMAN S	ì		EST HUMAN C			T_HUMAN	H	H	E E	H				
Jeigino.	Top Hit Accession No.	1.0E-44 AW967073.1		1.0E-44 AL 163209.2		1.0E-44 AV714608.1	10092994 NT	1		TN 1022208	TN 10222399	9.0E-45 AB023212.1	5174718 NT	5174718 NT	8.0E-45 AA377885.1			6.0E-45 AI675425.1	A DE 45 AW157570 1	18213					1.1			5.0E-45 AB022318.1	_	11496268 NT	11498268 NT	11418704 NT	4759223 NT
İ	Most Similar (Top) Hit BLAST E Value	1.0E-44	1.0E-44	1.0E-44	1.0E-44	1.0E-44	1.05-44	1.0E-44	1.0E-44	9.0E-45	9.0E-45	9.0E-45	8.0E-45	8.0E-45	8.0E-45	7.0E-45		6.0E-45	A NE AR	8.0E-45	5.0E-45	6.0E-45	5.0E-45		5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45		5.0E-45
	Expression Signal	1.17	1.17	1.23	0.59	12.74	323	2.7	2.7	1.16	1.18	1.52	1.57	8.68	0.85	960		Ŧ	9,6	188	1.56	88,7	1.40		8.41	1.48	1.48	0.84	0.84	1.07	1.07	. 0.66	1.29
	ORF SEQ ID NO:	34894	34902	35385			38325	38388	38389	30622	30523	33147	28663	31005	34827							28050			31654	32439		Ĺ		L	32626		35792
	Exem SEQ (D NO:	21578	21576	21959	22346	24304	24740	24798	24798	17630	17830	19860	16632	18129	21413	16027		14588	4	25048	13048	45039	16278		18886	1_		L	1_	1_		21587	
	Probe SEQ ID NO:	8098	8098	8883	<b>88</b>	1354	11858	11917	11917	4609	4609	9089	2629	5119	8444	2880		1556	-	12836	8	2018	3228		6590	6135	6136	9183	6183	6313	8313	8819	9626

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	Top Hit Descriptor	Hamo sapiens golgin-ilke protein (GLP), mRNA	H.saplens ART4 gene	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5	Homo sepiens TRAF family member-associeted NFKB activator (TANK) mRNA	nc28e07.s1 NCL_CGAP_Pr1 Homo septems cDNA clone IMAGE:1009284 similar to conteins element L1 meditive element:	Hamo sepiens chromosome 12 open reading frame 3 (C12ORF3), mRNA	x136f07.r1 Soares fetal liver spleen 1NFLS Home septens cDNA clone IMAGE:110245 5	Mus musculus dynein, exxn., heavy chain 11 (Dhahci 1), mRNA	Mus musculus dynein, excn, heavy chain 11 (Dhahc11), mRNA	AV723976 HTB Homo sepiens cDNA clone HTBAAG01 5	Homo sapiens golgi autoentigen, golgin subfantily a, 2 (GOLGA2) mRNA	Hamo sapiens chramosame 24 segment HS21C027	Homo sepiens chronosome 21 segment HS210027	H.sapiens DNA for endogenous retroviral like element	Hamo sapiens chramosame 21 segment HS21C018	Homo sepiens partial 54T4 receptor gene, exons 2 to 5	Human eosinophil Charcot-Leyden crystal (CLC) protein (tysophospholipase) gene, promoter and exan 1	601467793F1 NIH_MGC_67 Hamo sepiens aDNA clane IMAGE:3870838 5	RC0-L70001-150200-032-d11 LT0001 Hamp septems cDNA	MR0-HT0923-180800-201-e02 HT0923 Homo sepiens cDNA	8887712.rf Stratagene fetal refina 837202 Homo sepiens cDNA clone IMAGE:838319 5' strutter to	xx72a03 x1 NCI CGAP Owto Hamp sepiens cDNA clone IMAGE:2745868 3'	xp72a03.x1 NCI CGAP Owto Homo septems aDNA clame IMAGE:2746868 3	Homo sapiens calclum channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA	601284360F1 NIH_MGC_44 Homo sepiens cDNA done IMAGE:3606183 5	601284360F1 NIH_MGC_44 Hamo sepiens aDNA clane IMAGE:3606183 5	Homo sepiens RAP1A, member of RAS oncogene family (RAP1A), mRNA	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA	Human pro-a2 chain of collagen type XI (COL11A2) gens, complete cols	Homo sapiens dyromosome 21 open reading frame 1 (C21 orf4), mRNA	601289116F1 NIH_MGC_8 Homo septens cuina cione IMAGETSC198US 5
-	Top Hit Database Source		H	THUMAN		T LIBRAN		T HUMAN			T HUMAN		FX	TA T		- LN	H.	±N.	T HUMAN	EST_HUMAN F	EST HUMAN N	8 18450111 702	Τ	HIMAN		T HUMAN						EST_HUMAN
	Top Hit Acession No.	8923698 NT		2.4	4759249 NT	4 OF 45 AA 228220 4	12		6763651	TN 1539551 NT	3.0E-45 AV723976.1	58451	3.0E-45 AL 163227.2	3.0E-45 AL163227.2		2.0E-45 AL183218.2	2.0E-45 AJ243213.1		1.	20E-45 AW834834.1	2.0E-45 BE834350.1		2.0E-45  AW27020 10.1	Ţ	18157	1,0E-45 BE389855.1		4508412 NT	7857290 NT	1.0E-45 U32169.1	59558	1.0E-45 BE396833.1
	Most Similar (Top) Hit BLAST E Value	5.0E-45	4.0E-45 X95828.1	4.0E-45	4.0E-45	4 OF 45	4 OF 45	3.0E-45 T71480.1	3.0E-46	3.0E-45	3.0E-45	3.0E-46	3.0E-45	3.0E-45	3.0E-45 X89211.1	2.0E-45	2.0E-45	2.0E-45[L01665.1	20E-45	20E-45	2.0E-45		2.0E-45	2 OF 45	20E 45	1.0E-45	1.0E-45	1.0E-45	1.0E-46	1.0E-45	1.0E-45	1.0E-45
	Expression Signal	2.3	10.78	1.91	0.72	8	4	680	1.13	1.13	1.53	3.82	10.88	10.98	4.13	1.88	1.8	5.17	135	1.08	25.96		4.67	187	978	184	209	1,00	49.	7.12	980	4.08
	ORF SEQ ID NO:	38476			30448		24748		32876			L	37087				29016	33004					20002					28474		29088		30413
	SEQ ID NO:	24880	14188	15311	17558	1	25002	1800	19433	19433	21781	22109	23592	23592	25888	15514	16102	19728	20812	21726	25704		24402	24745	255 EK	13482	13482	13545	14219	16177	16550	17528
	Probe SEQ (D NO:	12003	1146	2289	4635	1	3 6	1210/	4884	<b>88</b>	200	9143	10670	10870	12854	2511	3045	6677	8882	8768	11154		11011	1 2 2	1000	124	408	473	1178	3120	3503	4503

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Single Exon Probes Expressed in Bone Marrow

Source Source	H down and that I time	yrūšijū2,r.1 Sogres fetal Iiver spiecn 1NPLS Homo sapiens cižūna cione iima ci£. 204363 5	Homo sepiens percetsomal biogenesis factor 14 (PEX14), mKNA	Homo sapians perodeomal blogenests factor 14 (PEX14), mRNA	Homo sepiens DNA for amyloid precursor protein, complete cds	601511228F1 NIH_MGC_71 Homo sepiens cDNA clone IMAGE:3912535 5	Human mRNA for KIAA0289 gene, partial cds	Homo septens protein kinase C, alpha binding protein (PRKCABP), mRNA	Homo sepiens hypothetical protein FLJ20464 (FLJ20464), mRNA	Homo sepiens Ran GTP as a scrivating protein 1 (RANGAP1), mRNA	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mINNA	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA	Homo saplens chromosome 21 segment HS21C009	2822449,5prime NIH_MGC_7 Hamo septens aDNA dane IMAGE:2822449 6	632708.x1 NC1_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb;,100314_ma2	TUBULIN BETA-1 CHAIN (HUMAN);	832R6s_x1 NCI_CGAP_Gas4 Homo saplens cDNA clone IMAGE:2132169.3' similar to gb:J00314_ma2 primarina perta 4 Autain Animaan	ODOLIN DE 1A-1 CTAIN (TOWNS),	KCSH 10508-28020-012-012 H 10500 FMIID September COVA	Rattus norvegicus espin mRVA, complete cas	601277292F1 NIH _MGC_20 Homo sapiens cDNA done IMAGE:3616118 5	RC4-BT0310-110300-015-f10 BT0310 Hamo septens cDNA	Homo sepiens hypothetical protein FLJ10847 (FLJ10847), mitNA	601822835F1 NIH_MGC_77 Homo septens cDNA clone IMAGE:4042736 5	wm31f08.x1 NCI_CGAP_Ut4 Homo sepiens cDNA clone IMAGE:2437575 3' struitar to contains MER19.t2	MEN 15 topoure existent,	MER (9 reputitive element :	1558H10_x1 NCI_CGAP_Kld8 Homo sepiens dDNA dane IMAGE:2232835 3' similar to TR:060363 060363	SA GENE;	xx42e04x1 NCI_CGAP_U11 Hamo septens cDNA clone INAGE:2706654 3' similiar to gb:1.08069 DNAJ	PROTEIN HOMOLOG 2 (HUMAN);	ULH-BIA epg-5-06-0-UI:s1 NCI_CGAP_Subs Hamo sapiens GUNA Game IMAGE: 3007.280 3	Hamo septens chromosome 21 segment HSZ1C010	7481g01.x1 Lupsid dorsal_root_ganglion Homo sapiens d.Jiva done IMACVE.32784vo s
Top 片供 Detabase Source	$\neg$	T HUMAN				EST_HUMAN							I E	EST_HUMAN		EST_HUMAN		T	HOMAN	П		T HUMAN		EST_HUMAN		ED TOWNS	EST HIMAN	Т	EST_HUMAN		HUMAN	EST HUMAN		EST_HUMAN
Top Hit Acession No.			11422236 NT	11422236 NT		1.0E-45 BE887843.1		11418099 NT	11526291 NT	11418177 NT	11418157 NT	DD/10283 NT		9.0E-46 AW246964.1		8.0E-46 A1433281.1		8.0E-46 AI433261.1	-		7.0E-46 BE386165.1	7.0E-46 BE064386.1	8922708 NT	7.0E-46 BF105845.1		6.0E-46 AIBS4561.1	R OE 48 A 1884 381 4		6.0E-46 A1635448.1		-		5.0E-46 AL163210.2	BE677194.1
<u> </u>	Value	1.0E-45 H57443.1	1.0E-45	1.0E-45	1.0E-45 D87675.1	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	9.0E-48	9.0E-46	9.0E-46		8.0E-46		8.0E-46	8.0E-46	7.0E-46 U46007.1	7.0E-46	7.0E-46	7.0E-46	7.0E-46		6.05-46	A DC AR		8.0E-48		8.0E-48	6.0E-46	5.0E-46	5.0E-46
Expression Signal		1.01	0.57	0.57	0.85	4.82	1.03	9.31	931	6.48	3.98	1.88	7.02	80.8		11.23		1123	6.79	1.17	3.58	1.14	3.92	1.95		5.63	8	3	10.15		0.78	0.51	6.47	1.01
ORF SEQ ID NO:			34746	34746		35880	36287		L.		31715	34859		37284		28474		28475		68282			32488			28778	į,		32556			33933		28608
SEO ID	<u>.</u>	111111	21334	L	L	1		25155	26274	25277	25532	21638	21947		L	15453	1		21358	15262	17832	<u> </u>	L	<u> </u>	<u> </u>	15757		/6/61	19325	<u>.</u>	20393		13306	Ш
Probe SEO ID		4757	8365	8365	8954	92,73	88	12369	12551	12556	12962	8570	8984	10845		2448		2448	6888	2248	4611	4845	9160	8842		2765		8/7	6252		7428	7609	205	3539

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	Top Hit Descriptor	227e11.s1 Scares_fetal_liver_splean_1NFLS_S1 Hamo seplens cDNA clane IMAGE:431896 3'	Homo sepiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds	ZESSE02_CI Scarces_bestis_NHT Homo sepiens cDNA clone IMAGE:728850 6' straitar to SW:RSP1_MOUSE	Mus musculus soam tell associated protein (Stap), mRNA	601445137F1 NIH_MGC_66 Homo septens CDNA clone IMAGE:3846297 5	Homo sepiens small acidic protein (IMAGE145052), mRNA	xq78h03.x1 NCI_CGAP_LLIS4 Homo septens cDNA clone INACE:2750789 3'	Homo sepiens cell division cycle 10 (hamologous to CDC10 of S. cerevisiae) (CDC10) mRNA	EST390625 MAGE resequences, MAGP Homo sapiens cDNA	EST48b095 WATM1 Homo saplens cDNA clone 48b095	np78b02.s1 NCI_CGAP_Pr2 Homo sepiens cDNA clone IMAGE:1132395 similar to gbX76717 H.sepiens MT-11 m8Na. (HUMAN):	Hamo sapiens mRNA for KIAA0980 protein, pertial ads	762501 x1 NCI_CGAP_OV18 Homo sepiens cDNA clone IMAGE:3843705 3'	Homo sepiens centeurin-elpha 2 protein (HSA272185), mRNA	Homo sapiens centaurth-eipha 2 protein (HSA272195), mRNA	7h48e07x1 NCI_CGAP_Li24 Homo sapiens cDNA clone IMAGE:3567852 3' similar to contains element.	7692b01 x1 NCI CGAP Ov18 Hamo sapiens cDNA clane IMAGE:3843705 3'	602072254F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5	602072284F1 NCI_CGAP_Bm67 Homo septens cDNA clone IMAGE:4215398 5	AV716377 DCB Hamo septems cDNA dane DCBAIE03 6	Homo sepiens Xq pseudoeutosomal region; segment 1/2	higased.x7 NG_CCAP_LLZ4 Home sepiens cDNA done IMAGE:3009634 3' similar to TR:075703 075703 HAPOTHETICAL 12 4 KD PROTEIN :	Homo serviews zinc finger protein ZNF286 (ZNF286), mRNA	CITY OF THE PROPERTY OF THE PR	Hamb septents SECT 4 (5, Gerenstage Liber 14.2), mittage	Homo saplens HLA-C gene, exon 5, individual 18323	Homo sepiens HLA-C gene, excn 5, Individual 19323	Homo septens protein phosphetase 2, regulatory subunit B (B56), epsilon isoform (PPPZRGE) mRNA	Homo sapiens 859 kb contig between AMI.1 and CBR1 on chromosome 21q22, segment 3/3
	Top Hit Detabase Source	EST_HUMAN 2	<u> </u>	NAM IN TOU	Name of the last	T HUMAN		HUMAN		TUMAN	Г		Т	HUMAN	1		TUMAN	Т	Т		EST_HUMAN	NT		NAMOL -	L	Ę	F	NT.		NT.
2.6.	Top Hit Acessian No.	2.0E-46 AA678246.1			105.00	3	57233	2.0E-46 AW277214.1	4502094 NT	1.0E-46 AW978516.1		4 70 70 70 70 70 70 70 70 70 70 70 70 70			23762	B923762 NT	254000474	1.0E-40 DF 180247.1	1 OF 46 BF531102.1	1.0E-46 BF531102.1	1.0E-46 AV715377.1	9.0E-47 AJZ71735.1		9.0E-47 AW / (1828.1	11423408	11417968 NT	8.0E-47 Y18538.1	8.0E-47 Y18536.1	5453955 NT	8.0E-47 AJ229043.1
	Most Similar (Top) Hit BLAST E Vatue	2.0E-46	2.0E-46 U78027.1	9 100	2.05-40	2 OF 46	2.0E-48	2.0E-46	1.0E-46	1.0E-46	1.0E-46 H97330.1	4 OF 40	1 05-48	1 OF 46	100	1.0E-46	97	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 0F 46	1.0E-46	1.0E-46	9.0E-47	1	9.05-47	4.0°	9.0E-47	8.0E-47	8.0E-47	8.0E-47	8.0E-47
	Expression Signal	2.13	443	8,	9.5	87.1	182	322	9.08	3.26	28		28	208	5.57	6.67		6.83	1 60	1.52	4.54	324		3.94	1.00	2.25	47.72	47.72	1.77	
	ORF SEQ ID NO:		27862		0100			31619					00700	32058				32102		1						31432				28012
	SEQ ID	14597			⊥	20082			14273	<u> </u>		1	16316		┸	1		19820		1.	L	L.				25843			15722	LJ
	Probe SEQ ID	1564	1647		6010	87.7	41578	12857	1237	2289	2400		3262	7387¥		6080		6766	47277	12322	13068	787		4068	6513	12816	1825	1825	2728	3036

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Table 4
Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor	Homo sapiens mRNA for GCK family kinese MINK-2, complete cds	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds	Homo sapiens KIAA0971 protein (KIAA0971), mRNA	Homo septens chromosome 21 segment HS210048	HSU77054 Human Homo sapiens cDNA clone N7	E28h02x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:22968593'	Homo saplens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds	Homo sepiens RECOLS beta mRNA for DNA helicase recQ5 beta, complete cds	Homo sepiens CDC37 (cell division cycle 37, S. cerevisies, homolog) (CDC37), mRNA	EST00738 Fetal brain, Stratagene (cat#836206) Homo sapians cDNA clone HFBCF07	Homo seplens E1A binding protein p300 (EP300) mRNA	MR4-TN0108-280800-201-d04 TN0108 Hamo sepiens dDNA	601280486F1 NIH_MGC_39 Hamo septens aDNA done IMAGE:3622437 5	601280489F1 NIH_MGC_39 Hamo sepiens cDNA dane IMAGE:3622437 5	RC3-BN0034-220300-015-f05 BN0034 Homo sepiens cDNA	xx8867 x1 NCL_CQAP_Lym12 Homo sepiens cDNA clone INAGE-2848597 3' similer to SW:INTB_MOUSE. Osaxx2 VIRAL INTEGRATION SITE PROTEIN INT-6. [1] :	601497639F1 NIH MGC_70 Homo sepiens cDNA clone IMAGE:3899721 5	801497839F1 NIH_MGC_70 Homo septiens cDNA clone IMAGE:3899721 6	1y54b04.s1 Scares_multiple_sclerosis_2NbHINSP Homo saplens cDNA clone IMACE:277327 3'	Homo sapiens chromosome 21 segment HS210084	Homo sepiens glutamate receptor, tonotropio, terinate 1 (GRIK1) mRNA	Horno septens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds	Human T-cell receptor active alpha-chain mRNA from JM cell time, complete cds	UHHF-BM0-edx-4-07-0-ULT NIH MGC 38 Homo explens cDNA clone IMAGE:3083205 5	UHHF-BM0-edx-4-07-0-ULT NIH_MGC_38 Hamo sepiens cDNA dane IMAGE:3083205 5	ah04e07.x1 Sogres_NFL_T_GBC_S1 Hamo sapiens cDNA clane IMAGE:1843716 3'	W/11h08.x1 NCI_CGAP_Kdd12 Hamo sapiens cDNA dane IMAGE:2402559 3'	w/11h08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA dans IMAGE:2402559 3'	EST375869 MAGE resequences, MAGH Homo septens cDNA	EST375869 MAGE resequences, MAGH Homo septems cDNA	Homo sepiens myosin phosphatase, target subunit 2 (MYPT2), mRNA	Homo septens chromosome 21 segment HS210009	Homo sapiens chromosome 21 segment HS21C009
Top Hit Detabase Source	MT	NT	NT.	M	EST_HUMAN	EST HUMAN	K	N	F	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	FCT HIMAN	EST HUMAN	EST HUMAN	EST_HUMAN	NT	M	NT	¥	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	NT	¥
Top Hit Acesston No.	8.0E-47 AB041926.1	8.0E-47 AB041928.1	7662421 NT	.2	6.0E-47 U77054.1	.1	1	6.0E-47 AB042824.1	11423972 NT	5.0E-47 M78590.1	4557556 NT	4.0E-47 BE938896.1	4.0E-47 BE616483.1	4.0E-47 BE616483.1	4.0E-47 AW993777.1	4 PC 47 AWE46500 4	3.0E-47 BE907634.1	3.0E-47 BE907634.1	3.0E-47 N57483.1	3.0E-47 AL163284.2	4504116 NT		3.0E-47 M12959.1	3.0E-47 AW408800.1	3.0E-47 AW408800.1	3.0E-47 A1222413.1	3.0E-47 AI819755.1	3.0E-47 AI819755.1	3.0E-47 AW963796.1	3.0E-47 AW963786.1	505318	2	2.0E-47 AL163209.2
Most Similar (Top) Hit BLAST E Vatue	8.0E-47	8.05-47	8.0E-47	6.0E-47	6.0E-47	6.0E-47	6.0E-47	6.0E-47	5.0E-47	5.0E-47	4.0E-47	4.0E-47	4.0E-47	4.0E-47	4.0E-47	4 05 47	3.0E.47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	2.0E-47	2.0E-47	2.0E-47
Expression	0.78	0.78	99:0	22	0.49	6.5	0.86	0.88	6.56	4.6	4.48	96'0	2.45	2.45	0.81	7 1	1.73	1.73	8.7	7.86	0.7	621	0.98	4.78	4.78	1.72	0.59	0.59	0.59	0.59	1.57	2.24	2.24
ORF SEQ ID NO:	29698	29599	31131	28575	35427	36025	36465	38468	33064		27403	33447	-35214	35215	35356		28538	28539	26826	26949	29288		30301	32429	32430		33831	33882	36679	35580	28181	26973	26974
SEQ ID NO:	16883	16683	18262	15557	22008	22576	22897	22897	19785	24107	14433	20132	21782	24782	21881	2	13617	13617	13877	13897	16368	17030	17417	19208	19208	19772			22161	22151	13252	14021	14021
Probe SEQ ID NO:	3840	3640	5254	2555	9040	9631	10070	10070	67.29	11147	1400	7008	8825	8825	8965	13011	1 92	92	818	4	3315	3880	4389	6128	6128	8716	7608	7608	9185	9185	149	696	696

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	Top Hit Descriptor	wq98b02.x1 NCi_CGAP_GC8 Homo saplens cDNA clane IMAGE:2479851 3'	Homo sapiens KIAA0428 gene product (KIAA0426), mRNA	ng43h12.s1 NCL_CGAP_Co3 Homo septens cDNA clone IMAGE:837607 3'	Homo saplens ring finger protein (C3HC4 type) 8 (RNF8), mRNA	mf23g07.s1 NCI_CGAP_Pr1 Homo saplens cDNA clone IMAGE;914652	mf23g07.s1 NCI_CGAP_Pr1 Hamo sapiens cDNA clane IMAGE:914662	Homo saplens Rev/Rex activation domain binding protein-related (RAB-R) mRNA	EST377239 MAGE resequences, MAGI Homo septems cDNA	ov61h03.x1 Soares_testis_NHT Hamo sepiens cDNA clane IMAGE:16418453'	Homo sapiens regulator of G-protein signaling 6 variant form (RGS6) mRNA, complete cds	601463832F1 NIH_MGC_67 Harno saplens cDNA clane IMAGE:3887487 5	601463932F1 NIH_MGC_67 Homo saplens cDNA done IMAGE:3887487 6	Homo sapiens 5-hydroxydyptamine 1D receptor pseudogene with an Alu repeat insertion	Homo saplens DNA for amyloid precursor protein, complete cds	Homo sapiens DNA for amykold precursor protein, complete cds	Homo septens SPH-binding factor mRNA, partial cds	Homo sapiens BTG family, member 3 (BTG3), mRNA	Human tyrosine kinase receptor (ad) mRNA, complete cds	y/82/e08.s1 Soares infant brain 1NIB Homo sepiens cDNA clone IMAGE-29866 3' similar to contains OFR	Idealive contrait,	gpsgrt/3.xf Scares_feta_jung_NbHL19W Homo sapiens cDNA clone IMAGE:1831189 3'	601155321F1 NIH_MGC_21 Hamo sapiens cDNA dane IMAGE:3138863 5	601155321F1 NIH_MGC_21 Hamo sapiens cDNA clane IMAGE:3138893 6	RC3-ST0197-130400-017-h02 ST0197 Homo septens cDNA	at19e06.x1 Barstead aon'a HPLRB6 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:MZ2895 RAS-RELATED PROTEIN RAP-1A (HUMAN);	hi84a11.x1 Soares_NFL_T_GBC_S1 Homo septems cDNA clone IMAGE:2878972.3" struiter to gb.M28326	KEKATIN, 17PE ICT I CSKELE I AL 18 (HUMAN);	Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5 region	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively	peolitos	CM2-MT0100-310700-280-f05 MT0100 Hamo saplens cDNA	601511714F1 NIH_MGC_71 Hamo sepiens cDNA dane IWAGE:3913106 5	601511714F1 NIH_MGC_71 Homo saplens cDNA clone IMAGE:3913106 5
	Top Hit Database Source	EST_HUMAN	١. ١	EST_HUMAN		T_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	¥	EST_HUMAN	EST_HUMAN	N	N.	FA.	N.	¥	NT	Manual World	1	Т		EST_HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	NT			EST_HUMAN	EST_HUMAN	EST_HUMAN
	Top Hit Acession No.	2.0E-47 Al969279.1	7862109 NT	2.0E-47 AA524514.1	4504886 NT	2.0E-47 AA569592.1	2.0E-47 AA569592.1	5174648 NT	2.0E-47 AW985168.1	2.0E-47 Al041128.1	2.0E-47 AP073921.1	2.0E-47 BE778475.1	2.0E-47 BE778475.1	09731.1			2.0E-47 AF071771.1	11526136 NT		7 00707	(42423.1	1333429.1	.1	1	1.0E-47 AW813908.1	1.0E-47 Al880898.1		1.0E-47 AW 684648.1	30115.1		_	9.0E-48 BF359947.1	9.0E-48 BE888196.1	9.0E-48 BE888196.1
	Most Similar (Top) Hit BLAST E Vatue	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47 L09731.1	2.0E-47 D87675.1	2.0E-47 D87675.1	2.0E-47	2.0E-47	2.0E-47 M76125.1	- 100	Z.UE-4/ K42423.1	1.0E-47 AISS3429.	1.0E-47	1.0E-47	1.0E-47	1.05-47		1.0E-47	1.0E-47 L30115.1		9.0E-48/	9.0E-48	9.0E-48	9.0€-48
	Epression Signai	1.08	22	3.87	28.1	1.48	1.48	1.68	122	0.7	122	1.28	1.29	1.43	1.76	1.76	1.75	0.78	2.31		212	6.91	1.18	1.18	2.55	99		0.77	2.41		3.85	2.0	0.84	0.84
-	ORF SEQ ID NO:		27604	27698	30282	30327	30328	30445	30760		32160	32380	32381		34877	34678	35457	36235	87478	473.70	31413	27405			26608	33278			37138				32035	
	Exer SEQ ID NO:	14603	14620	14718	17402		17439	17557	17887	18196	18969	19168	19168	25692	21268	21266	22034	22781	23955			1437		16875	18122	18979	L_	22186	23643				18855	
	Probe SEQ ID NO:	1570	1697	1687	4374	441	4411	4534	4850	5187	2880	8809	888	7984	78287	76238	8908	9845	11800	7	2000	464	3835	3835	5112	7244		8220	10721		1616	3569	5763	5763

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Top Hit Descriptor	MR4-BT0857-060400-201-e10 BT0657 Homo sepiens cDNA	Human endogenous retrovinus HERV-P-147D	m03f05.s1 NCI_CGAP_Pr22 Homo capiens cDNA clone IMAGE:1219137 3' similar to contains PTR6.b1	PTR5 repetitive element;	UI-H-BW1-ent-e-10-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens d/INA cicne IMA/GE:308/2073	2x80c03.r1 Scenes overy furnor NbHOT Homo sepiens cDNA clone IMAGE:8100b2 5	finite? Regional genomic DNA specific cDNA library Homo septents cDNA clone CK17-26	yn55e10.r1 Soares infant brain 1NIB Homo saplans cDNA clone IMAGE:52182 5' simiter to SP:M68_MOUSE P35903 MEMBRANE GLYCOPROTEIN ;	TCBAP+ID3842 Pediatric pre-B cell acute lymphoblastic leukemia Baykar-HGSC project≕ i CBA Homo contace chala chore TCBAP3842	September CONTROL OF THE PROPERTY OF THE PROPE	1018g0; st NCI CAAP Thei natio separas concentrations of	notegot, st NCL CGAP Phet Hamb septems dunk dans implace. Holova's	Homo saptens mRNA for KIAA1501 protein, perner cos	Homo sepiens mRNA for KJAA1501 protein, partial cds	Homo sepiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear tacon or kappa ugni. polywentide cene enhancer in B-cetts 3 (p65)) (RELA), mRNA	AV749464 CB Home embre clink done CRC253(10 5	AV (4545) LO Italia equals Color Gala Color Color (MACSF-840052 5)	2(3) COURT NOTICE OVER WITH THE CONTRACTOR THE CONT	Homo sapiens displatin resistance essociated overapressed protein (LOCO) 747, him who	Homo capiens amyloid beta (A4) precursor protein (protease neath-II, Abthelmer disease) (APP), mRNA	Homo sapiens EBNA-2 co-ectivator (100kD) (p100), mRNA	Homo septens EBNA-2 co-excitvator (100kD) (p100), mRNA	Homo sepiens RNA binding motif protein 6 (RBMB) mRNA	Hamo sepiens chromosome 21 segment HS21C102	Homo septens chromosome 21 segment HS21C046	12/7001 X1 NC1 CGAP Co16 Hamo septems cDNA clame IMAGE: 20/35904 3' SImiliar to 1 K: 014308 014308	SIMILARITY TO U73941;	td17c01x1 NCI_CGAP_Co16 Homo sepiens cDNA clone IMAGE:2075904 3' stmiler to 1 K:014568 014668 SIMII ARITY TO U73941:	Homo sertiens NF2 gene	Homo septens mRNA for KIAA1071 protein, partial cds	Homo seniens mRNA for KIAA1071 protein, pertial cds	
Top Hit Databese Source	EST_HUMAN I	E			EST_HUMAN	EST_HUMAN :	EST_HUMAN	EST_HUMAN		Т	1	HOMAN	M	ᅜ			Т	HOMAN		¥			N.	NT	K		EST_HUMAN	ECT UIMAN	121	LN	Ę	
Top Hit Acession No.		3.0E-48 AF087913.1		3.0E-48 AA659830.1					Ι,			-			44400000	00770		$\cdot$	7706534 NT	4502166 NT	7657430	7857430 NT	5032032 NT				1.0E-48 AI889077.1	4 05 40 4 10000 27 4	7100001 7.1	1.0E-48 AB028994.1	4 05 40 4000004 4	4D020007.1
Most Similar (Top) Hit BLAST E Vedue	3.0E-48 BE084571.1	3.0E-48 A		3.0E-48 A	3.0E-48 B	2.0E-48 A	2.0E-48 A	2.0E-48 H24Z78.1		2.0E-48 BE246065.	2.0E-48 A	2.0E-48	2.0E-48	2.0E-48 A	2,00	Z.UE-48	2.0E-48	2.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48/	1.0E-48/		1.05-48/	9 10				
Expression Signal	2.41	188		4.11	6.80	24	123	0.65		0.92	0.63	. 0.63	3.9			3.52	_	3.8	3.37	1.61			5.06				1.17			3.0		0.7
ORF SEQ ID NO:	32278				37700						32188		<u> </u>					20025		26888				١.	L		32736		32/3/	22082	١	33063
Exan SEQ ID NO:	19081	1.		24702	L	_	L		1	17585	18998		١		<u></u>		21668	13128		13030	1_		┸			L	19487	1_	- 1.			19802
Probe SEQ ID NO:	5007	7245	2	8734	41221	145	12	173		4562	5912	5912	7762	7762	,	1111	8688	12318	89	874	1077	1077	28	1033	3500		6420		828	848	\$	6748

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	Top Hit Descriptor	Homo sapiens huntingtin (Huntington disease) (HD) mRNA	Homo sepiens mitogen-ectivated protein kinase kinase kinase 13 (MALSK13), micha	Homo sapiana mitogen-activated protein kinase kinase kinase 13 (MAL-3K13), mixna	Homo sepiens Chediak-Higashi syndrome 1 (CHS1) mKNA	Homo sepiens mRNA for KIAA1245 protein, partial cots	QV3-HT0613-060400-147-401 H10513 Homo sapiens CLIVA	601888096F1 NIH MGC_17 Hamp septems aDNA done IMAGE:4122119 o	Homo saptens B cell mindr protein (SLPOS), mixing	Homo sepiens B cell linker protein (SLP66), mithA	15d5 Human refina cDNA randomly primed sublibrary Homo sapicars curva	Mus muscalus (-box 20 (1 bx20), mkWA	Mus muscalus T-box 20 (Tbx20), mRNA	inst8h08.rt NCI_CGAP_GCB1 Homo septens cDNA clone IMAGE:1184021 5	Human inositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds	Homo sepiens gene for ectivin receptor type IIB, complete cds	ts38d12.x1 NCI_CGAP_UM Hamo sapiens dDNA clone IMAGE:22308/1 3' similar to contains Alu repetuive element.contains element PTR5 repetitive element;	Homo saptens professome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA	Homo sapiens proteesoms (prosome, macropain) 26S subunit, ATPasse, 4 (PSMC4) mRNA	Homo saplens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPass, 4 (PSMC4) mitNA	Homo sapiens professome (prosome, macropain) 26S subunit, A I Pass, 4 (PSMC4) mixiva	Homo sepiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mKNA	Homo sapiens chromosome 21 segment HS21 C084	wrzsho4xt scares_NFL_T_GBC_S1 Hamo sepiens cDNA clane IMAGE_2356663 3' smilla' to I n:Uovez3 054623 RSEC15. ;	DKFZp782C033_s1 782 (synonym: hmel2) Homo sapiens cDNA clane DKFZp782C033 3'	wf25h04.x1 Soares_NFL_T_GBC_S1 Homo capiens cDNA clone IMAGE:2356863 3' strriter to TR:054823 054823 RSEC15.;	ba55g05x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900504 3' struiter to gb:X17208 40S	RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein miKNA mom a repeauve esament, complete (MOUSE);	DKFZp761A138_s1 761 (synonym: harny2) Homo saplens cDNA clone DKFZp761A138 3'	U140742 PLACE4 Homo sapiens cDNA done PLACE4000148 5	
	Top Hit Database Source						EST_HUMAN C	T HUMAN			T_HUMAN			T_HUMAN		TN TN	EST HUMAN 8	ľ						TN TN	EST HUMAN	Т			EST HUMAN		EST HUMAN	1
280	Top Hit Acession No.	4755137 NT	4758695 NT	N 28695 N	502838	1.0E-48 AB033071.1	1		11429808 NT	429808	1.0E-48 W28785.1	10048417 NT	10048417 NT	5.1	8.0E-49 U23850.1	1.1	8 OF 40 A1823722.1	TN 0686275	5729990 NT	5729900 NT	5728990 NT	5728990	5729990 NT	7.0E-49 AL163284.2	7 0F-49 A1807194.1	7.0E-49 AL120837.1	7 0F-40 A907191 1		6 0F 40 AW 731740.1	6.0E-49 AL162091.1	6 0E-49 AU140742.1	
	Most Similar (Top) Hit BLAST E Vetue	1.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48	8.0E-49	8.0E-49	8.0E-49	8.0E-49	8.0E-49	8.05-40	7.0E-49	7.0E-49	7.0E-49	7.0E-49	7.0E-49	7.0E-49	7.0E-49	7.0F-40	7.0E-49	7 0F 40		6.0F.40	6.0E-49	8.0E-49	
	Expression Signal	3.16	0.49	0.49	1.19	7.13	0.69	4.48	3.85	3.85	1.63	9	3	0.57	3.32	21	230	224	224	1.63	1.53	2.06	2.06	2.85	1 57	1 33	78.0		88 88	1.14	0 65	
-	ORF SEQ ED NO:	28794	35578	36577	35980	36017	36260	36330	37151	37152		32478	32479	33460	35029						26399	26398		02212	l _	1			Luca		32000	
	Exam SEQ ID NO:	20437	22149	22140	22530	79522	22808	22868	23658	23658	25830	19248	19246	20143	21606	23272			13468	L	L	13468	1_	14263	1	1		1_	79300	1	L	ł
	Probe SEO ID NO:	7471	9483	988	8998	2298	9824	9941	10738	10738	12280	6171	6171	7017	8838	10348	1,35	140	4	388	888	ğ	88	1225	2632	EGAR.		388		4142	aron a	3

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Top Hit Descriptor	UHHBI3-do-e-05-0-UI.s1 NCI_CGAP_Sub5 Home septens CDNA clone IMAGE:3068048 31	EST77525 Pancreas tumor III Homo sapiens CLIVI 9 end	EST77525 Pencress tumor III Homo saptens CLIVA 3 et al. Company Apple 144025-4546043	2/20c08.s1 Sogres, fetal liver sheen Tintilo Sofreria Ward with a liver sheet the sheet sh	Homo sapiens chromosome 21 sagment m3210010	Homo sapiens chromosome 21 sagment NOZIOU10	zp.20-07.r1 Strategene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:010900 5' similar to TR:0233226 G233226 RTVL-H PROTEIN:;conteins LTR7.f3 LTR7 LTR7 repetitive element;	Homo sapiens pulsaive lumar suppressor of 10 (01.10) illinois, controls con	Homo sapiens similar to rifosomal protein S27 (metallopenstimulin 1) (H. sapiens) (LOC83362), mRNA	x08601.x1 NCI_CGAP_UM Hamo septens cDNA clone IMAGE:28/8865 3' Similar to vrr: buscu.zo CE06703 ;	Homo sepiens mRNA for entyrtn B (440 tDa)	Homo sapiens mRNA for enkyrin B (440 kDa)	Homo saniens UDP-N-ecrety-einha-D-calactosamine:polypeptide N-acety/galactosaminy/transferase 8	(GelNac-T8) (GALNT8), mRNA	Homo septens UDF-N ecosy apha-L-gerazosanin's poypepude in ecosyngae community and a community of the commun	Hamp sepiens KIAA0623 gene product (KIAA0523), mixtva	Homo sapiens copine III (GPNE3), mithA	Homo sepiens capine III (G*NE3), mtVA	ZISOROS, FINCIL CGAP GCB1 Hamo sapiens curry came invasce, vacent of	Homo septens glutaritions of desirance as of media A (SS 1 - A) and glutalistic of desirance and a septens, complete ods	H. sapiens mRNA for excely-CoA carbodyesse	2831-005.1 Scares retina N.2041iK rigino separa Curto, Cauta Innoca_occor o sellina di repositive elementi ;	Human type IV collegen (CUL4AP) game, axon 40	ESTZBerz WAIMT Home septems curve come zoerz	EST425/2 Endometria unito nuno sapara Corro o ara	MICS-H 10407-150200-115-got 1110-901 miles expense CDNA clone IMAGE:282571 5	
Top Hit Database Source	$\Box$	EST_HUMAN E	П	T HUMAN		Ę	r HUMAN	¥		T HUMAN	П	5							EST_HUMAN	M	Į.	EST_HUMAN	¥	EST HUMAN	EST HUMAN	EST HUMAN	ESI HOMAN
Top Hit Acession No.	6.0E-49 AW452218.1	6.0E-49 AA366556.1				5.0E-49 AL163210.2	5.0E-49 AA172121.1		11436355 NT	4 DE 49 AW189533.1	4.0E-49   226634.2	100 10 738894 3	74007	11625737 NT	11525737 NT	7882209 NT	11425374	11425374 NT	4.0E-49 AA210798.1	4.0E-49 AF240788.1	3.0E-49 XB8968.1	3.0E-49 AA016131.1 ·	3.0E-49 U46999.1	3.0E-49 H39479.1	3.0E-49 AA337561.1	2.0E-49 BE165980.1	20E-49 N28446.1
Most Similar (Top) Hit BLAST E Value	8.0E-49 A	6.0E-49	8.0E-49	6.0E-49	6.0E-49	5.0E-49 /	5.0E-49	5.0E-49 U17714.1	5.0E-49	4.05-49	405-40	9, 20,	10:4 10:4	4.0E-49	4.0E-49	4.0E-49	4.0E-49	4.0E-49	4.0E-49	4.0E-49	3.0E-49	3.0E-40	3.0E-49	3.0E-49			
Expression Signal	74	8.4	4.09	1.1	8.21	8.21	3.44	9.75	6.07	ų k	18	3	8.	0.66	990	0.71	0.53	0.53	8.71	3.19	1.27	1.83	211	10.82	1.54	В	1.6
ORF SEQ ID NO:	38107	38446	38447		26708		27828					2	ļ	33811			l				28640	<u> </u>	30919				1 28213
Exan SEQ ID NO:	24547	24850	1_	١.	İ.	13775	14837	L		l	13087	3	20423	20452				1		<u> </u>		ı	١.	L	<u> </u>		3 1629H
Probe SEQ ID NO:	11600	44072	41972	12645	713	713	88	2760	8286		2767	?	7457	7487	7487	8100	87.8	978	12508	12504	585	88	5019	288	11633	883	3236

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Single Exon Probes Expressed in Bone Marrow

Most Similar   Top Hit Acession   Top Hit Signal   BLAST E   No.   Source   Source   No.   Source	0.78 2.0E-49 AF026564.1 NT	3.1 EST HUMAN	T HUMAN	2.0E-49 AF163864.1 NT	T HUMAN	57887 NT	1.0E-49 BE255216.1 EST_HUMAN	6.72 1.0E-49 BF131007.1   EST_HUMAN	1.0E-49 H18291.1 EST_HUMAN	1 1.0E-49 AW984840.1 EST_HUMAN	0.58 1.0E-49 AV703000.1 EST_HUMAN	0.58 1.0E-49 AV703000.1 EST_HUMAN	3.3 1.0E-49 BE398110.1 EST_HUMAN	33754 3.3 1.0E-49 BE398110.1 EST_HUMAN 601290330F1 NIH_MGC_8 Homo septens GNNA done IMAGE:3620863 6	33848 22 1.0E-49 N25884.1 EST HUMAN similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);	22	0.69 1.0E-49 11321580 NT	0.69 1.0E-49 11321580 NT	0.78 1.0E-49 8994184 NT	BE409340.1 EST_HUMAN	1.22 1.0E-40 ALO43129.2 EST_HUMAN	1.99 1.0E-49 AB020335.1 NT	1.7 1.0E-49 BE159343.1 EST_HUMAN	2.78 1.0E-49 11418322 NT Homo sapiens cacherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA	EST_HUMAN	2 NT	FZ.	2.14 8.0E-50 X95097.2 NT	4 8.0E-50 · 4501890 NT	23720 2.18 8.0E-50 4826658 NT Homo sapients capping protein (actin filament) muscle 2-line, beta (CAPZB), miNNA
			1.6	2.5	9.3					0														27	10,1					
D ORF SEQ		18952 3324	21405	25821	13955	14589 Z756	14845 2783		19270 3250						20485 3384			Ĺ						25241	25997	13273 2618	13782 2671			15704 2877
Probe Exam SEQ ID SEQ ID NO:	3583 164		8436 21		900 130		1818 14	L.				<u> </u>	L				L			١.		L	1_	上		171 13	720 13	ll	li	l

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Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	QV0-BT0703-280400-211-e08 BT0703 Homo saplens cDNA	RC6-TN0073-150800-011-A12 TN0073 Homo sapiens d.NVA	ROB-TN0073-150800-011-A12 TN0073 Homo sepiens cONA	nq59e12.s1 NCL_CCAP_Co9 Home sepiens cDNA clone IMAGE:4148206 3' similar to gb-X69391 60S RIBOSOMAL PROTEIN L6 (HUMAN);	wm55g11.x1 NCI_CGAP_U2 Homo saplans cDNA clone IMAGE:2438908 3'	ho38h04.x1 NCI_CGAP_Ut1 Homo sepiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3	MER29 repetitive element;	EST182775 Jurkat T-cells VI Homo sepiens cDNA 5 end	EST182775 Jurkat T-cells VI Hamo sapiens cDNA 5 end	CMO-BT0792-300500-398-b05 BT0792 Homo saptens cUNA	CMD-BT0782-300500-398-b05 BT0782 Hamo septens cDNA	n45h10.s1 NCI_CGAP_Pr4 Home sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.t3 PTR5.	repounte esement	no54e09.s1 NCLCCAP_SS1 Homo septens CJNA cione IMAGE:1104520 3 similiar to go. 23741_finat FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);	Homo septens cycleinyl-IRNA synthetasa (CARS), mRNA	QV1-BT0681-280300-127-f12 BT0681 Homo sapiens cDNA	Human endogenaus retrovirus RTVL-H2	601109717F1 NIH_MGC_16 Hamp sapiens cDNA dane IMAGE:3350309 5	obosto6.s1 NCI_CGAP_Kid3 Hamo sapiens cDNA clane IMAGE:1322827 3	Homo sepiens protein tyrosine phosphalase, non-receptor type 12 (PTPN12), mixtha	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (P. I.PN12), mrvvA	Homo sepiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, socreted, (semaphorin) 3A (H. sepiens) (LOC63232), mRNA	Homo septems FYVE dometh-containing dual specificity protein phosphalase FYVE-DSP1 a mRNA, complete	cds	Homo sepiens FYVE domain-containing duel specificity protein prospitatase FTVE-USF 14 illinuw, cutiphase cds	Homo sepiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA	Homo sepiens mRNA for KIAA1598 protein, partial cds	Homo sepiens t-complex 10 (a murine top homolog) (TCP10), mRNA	Human mRNA for KIAA0289 gene, partial cds	Homo sepiens Grizz-essociated brinder 2 (NIAAU3/1), minna
######################################		EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN		Г	7	╗	┑	EST HUMAN	EST_HUMAN		EST HUMAN	EST_HUMAN	7	EST_HUMAN	7	EST_HUMAN	EST HUMAN	M	Νī	¥		Ž	5	Z	Ę	Z	Ŋ	Ę
	Top Hit Acession No.	7.0E-50 BE089591.1										5.0E-50 BF332838.1		5.0E-50 AA557883.1	4.0E-60   AA601143.1	<b>4</b> 683	4.0E-50 BE087536.1		=	1	11418317 NT	11418317 NT	11421514 NT		3.0E-50 AF233436.2	2 OF EN A C 222438 2	01589		418514	3.0E-50 AB002297.1	11436955 NT
1	(Top) Hit BLAST E Vatue	7.0E-50 B	7.0E-50 B	7.0E-50 B	7.0F-60 A	7.0E-50 AI872137.1		6.0E-50 B	8.0E-50 A	6.0E-50 A	5.0E-50	5.0E-50 B		5.0E-50 A	4.0E-60	4.0E-50	4.0E-50 E	3.0E-50 M18048.1	3.0E-50 E	3.0E-50	3.0E-50	3.0E-50	3.0E-50		3.0E-50/	2000	30F-50	3.0E-50/	3.0E-60	3.0E-50	3.0E-50
	Expression Signal	88.0	12	12	80	38.08		6.69	96'2	28.7	1.18	1.18		5.65	1.45	45.0	0.83	286	1.11	0.88	9.0	9.0	1.56		4.3	67					1.89
	ORF SEQ ID NO:	1	33500		<u> </u>				37652			L			٠	32813	L	L	28549				33472		34234		34230				37920
	SE CE SO CE CE CE SO CE C	13686	20178	20178	35,400	24088		21524	24124	<u>l</u> _	L	L	<u> </u>	22412	i		١.	L		L	L		l		20849		218043	┸	┸	<u>L</u> _	
	SEQ ID NO:	624	606	6965	75.00	300		8556	41168	11188	1808	1808		8448	88	6497	7445	1955	2525	3310	88	6834	8089		2067		908	40477	40188	10885	11438

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Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor		Homo saplens CTL2 gane	Homo sapiens MHC class 1 region	Homo septens midline 1 (Opitz/BBB syndrome) (MID1) mRNA	Horno sapiens decorin D mRNA, complete cds, afternatively spilced	Homo sapiens serine palmitbyl transferase, subunit II gene, complete cds; and unknown genes	Mus musculus mRNA for high-sulfur keralin protein, partial ods	AU124065 NT2RM2 Homo sepiens cDNA clone NT2RM2001609 5	Homo sapiens TFF gene cluster for trefoil factor, complete cds	Homo sapiens TFF gene cluster for trefoil factor, complete cds	Human HALPHA44 gene for alpha-tubulin, exans 1-3	Human HALPHA44 gene for alpha-tubulin, exons 1-3	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA	Macace mulatha cyclophilin A mRNA, complete cds	Homo saplens chromosome 21 segment HS210009	Homo sapiens Xq pseudoautosomal region; segment 1/2	Homo sapiens Xq pseudoautosomal region; segment 1/2	Homo sapiens RGH2 gene, retrovirus-like element	hd44602.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2912378 3' similar to TR:085336   095638 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II.;	m,677x03.s1 NCI_CGAP_GCB1 Homo expiens cDNA done IMAGE:1283381 3'	abz3g04.x5 Stratagene lung (#837210) Homo sepiens cDNA clone IMAGE:841686 3' similer to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN;	2651c09.r1 Scares_pregnant_uterus_NbHPU Homo sepiens cDNA clone IMAGE:486352 5	ab23g04.x5 Strategene tung (#837210) Homo septens cDNA clone IMAGE:841696 3' stmiter to SW-PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN;	ab23g04.35 Strategene lung (#837210) Homo sepiens cDNA clone IMAGE:841688 3' stmiter to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN;	yw24g08.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5"	yw24g08.r1 Morton Fetal Cochlea Homo saplens cDNA clone IMAGE:253210 57	np88609.s1 NCI_CGAP_Lu1 Homo septens cDNA done IMAGE:1142440 3' similar to gb:X12671_ms1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA	AU138590 PLACE1 Homo sapiens cDNA clone PLACE1008887 5
Top Hit Database	Source	TM	NT	TN	NT	NT	TN	EST_HUMAN	M	M	TN	M	FN	NT	¥	M	N.	F	Ę	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	439587 NT	EST HUMAN
Top Hit Acession	Ž	AJ245621.1	2.0E-50 AF055068.1	557752	1	2.0E-50 AF111168.2		2.0E-50 AU124065.1	1	2.0E-50 AB038162.1	2.0E-50 X06956.1	2.0E-50 X06956.1	9910283 NT	D910283 NT	2.0E-60 AF023861.1	1.0E-50 AL163209.2	1.0E-50 AJZ71735.1	F		9.0E-61 AW 611226.1	9.0E-51 AA744837.1	9.0E-51 AJ794154.1	9.0E-61 AA043738.1	9.0E-51 AI791154.1	9.0E-51 AI791154.1	H89078.1	9.0E-61 H89078.1		11439587	8.0E-51 AU138590.1
Most Similar (Top) Hit	Vatue	3.0E-50	2.0E-50	2.0E-50	2.0E-50	2.0E-50	2.0E-50	2.0E-50	2.0E-50	2.0E-50	2.0E-50	2.0E-50	2.0E-50	2.0E-50	2.0E-50	1.0E-50	1.0E-50	1.0E-50	1.0E-50	9.0E-61	9.0E-51	9.0E-51	9.0E-51	9.0E-51	9.0E-51	9.0E-51	9.0E-61	8.0E-51		8.0E-51
Expression	E	8.4	8.8	6.73	96.0	0.83	0.75	0.51	1.09	1.09	87.8	87.8	1.43	1.43	1.52	2.26	120	0.55	78.0	1.01	0.71	0.65	12	0.52	0.62	1.5	1.5	6.51	2.04	0.98
ORF SEQ		37468		27078			30197	33380		35048	35189	35180	2998	36658		26461			36970						<u> </u>				L	
Esan SEQ ID	Ö	23947	13837	14125		16853	L	20073			L	L.,	23169			13535	L	50802		19174	L		<u> </u>	L			L	L		Ш
Probe SEQ ID	Ö	11792	2	1081	1437	3300	4289	7051	8659	8859	8786	8788	10244	10244	11971	462	2373	2870	10553	888	6350	9020	8/96	8988	8988	11804	11804	4599	7914	9819

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ighe Exon Probes Expressed in Done Wandw	Top Hit Descriptor	QV4-NT0028-200400-180-405 NT0028 Hamo sapiens cDNA	xr34e03.x1 NCI_CGAP_Ktd11 Homo septens cDNA clone IMAGE:2696564 3' similar to TR:C92340 Q92340 ATYPICAL PKC SPECIFIC BINDING PROTEIN.;	DKFZp434B2229_r1 434 (synanym: htes3) Hamo sepiens aDNA dane DKFZp434B2229 6"	DKFZp434B2229_r1 434 (synonym: htess) Hamo sapiens cDNA clone DKFZp434B2229 5	UI-H-BW0-eip-b-05-0-UI.s1 NCI_CGAP_Sub8 Homo septens cDNA done IMAGE:2729817 3'	Homo sepiens HSPC331 mRNA, pertial cds	Homo sepiens publitive DNA binding protein (M88), mRNA	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA	Homo sepiens KIAA0929 protein Mss2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA	Homo sapiens solute cerrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA	Human haptoglobin related (Hpr) gene exon 3	Homo sapiens mitogen-ectivated protein kinase kinase 1 (MKK4) gene, excn 4	Homo sepiens mitogen-activated protein kinase kinase 1 (MKK4) gene, excn 4	Homo sapiens ribosomal protein S8 kinasa, 70kD, polypeptide 1 (RPS6KB1) mRNA	Homo sapians non-kinasa Cdc42 effector protein SPEC2 (LOC56860), mRNA	Homo sepiens cerebral cell adhesion molecule (LOC51148), mRNA	Homo sapiens hypothetical proteth FLJ11042 (FLJ11042), mRNA	Homo sepiens hypothetical protein FLH1042 (FLJ11042), mRNA	Homo saplens B9 protein (B9), mrRNA	Human ankyrin (ANK1) gene, arcn 2	Homo sapiens interfeukin 17 receptor (IL17R), mRNA	Homo sepiens chromosome 21 segment HS21C003	Homo septens T-cell fyrightoms treasion and metastasis 1 (TIAM1) mRNA	Novel human gene mapping to chamosome X	Homo sepiens 26S protessome-associated pad1 homolog (POH1) mRNA	Homo sapiens mRNA for nucleoporin 155	Human Ku (p70/p80) subunit mRNA, complete cds	Human Ku (p70/p80) subunit mRNA, complete cds	Homo sapiens KNA binding moir protein 3 (KbM3), mKNA
Xon Probes Ex	Top Hit Database Source	EST_HUMAN Q	EST_HUMAN O	EST_HUMAN D	EST_HUMAN D	EST_HUMAN L				•				F F	TA T											N		H.			
	Top Hit Acession No.	7.0E-51 AW889219.1	Ţ	7.0E-61 AL078628.1	7.0E-51 AL079628.1	7.0E-61 AW 295603.1	7.0E-51 AF161449.1	B678763 NT	7857288 NT	T657288 NT	9910553	9810553 NT	6.0E-61 X01788.1	. 1.	6.0E-51 AF070083.1	4506736 NT	11416751 NT	11429665 NT	11428525 NT	11428525 NT	7861535 NT	6.0E-51 U50093.1	11628289 NT	5.0E-51 AL163203.2	4507500 NT	6.0E-61 AL133204.1	31980	AJ007558.1	M30938.1		5803136 NT
	Most Similar (Top) Hit BLAST E Value	7.0E-51	7.0E-61	7.0E-51	7.0E-51	7.0E-51	7.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-61	6.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-61	5.0E-51	5.0E-51	6.0E-61	5.0E-51	5.0E-51	5.0E-51	5.0E-51	5.0E-51
	Expression	1.08	0.72	4.1	1.4	1.54	213	0.91	5.54	17.23	0.69	0.69	28	8.29	8.29	1.13	1.03	228	0.62	0.62	204	1.14	1.65	8.57	1.9	1.23	1.02	7.72	1.85	1.85	4.07
	ORF SEQ ID NO:	29268	28349	30116	30117	30288	38466	27534	28024	29458	30247	30248	32403	32417	32418	33469	33408	31233			36436	36525	82088	26798		26998	27620	28619	29919		38108
	Exam SEQ ID NO:	16348	16424	17227	17227	17408	24870	14563	15017	16533	17365	17365	19184	19194	19194	20149	20088	18389	22458		_	23046	24523	13851		15868	14644	15600			24548
	Probe SEQ ID NO:	3285	3374	4198	4188	4378	11883	1530	1896	3487	4338	4338	9105	6116	B118	6926	7076	7457	9492	9492	10042	10120	11585	782	쳟	88	1612	2599	3965	3985	11610

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	Top Hit Descriptor	Homo sapiems mRNA for KIAA0457 protein, partial cds	AV682474 GKB Hamo sepiens dDNA clane GKBAGF05 5"	EST91296 Synowial sarcoma Homo sapiens cDNA 5' end	ob34109.25 NCI_CGAP_KI45 Homo espiens cDNA clone IMAGE:1325609 3' similer to SWNME1_MQUSE P35439 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;	obsantions NCI_CGAP_Kids Home sapiens cONA done IMAGE:1325609 3' similar to SW. NIME1_MOUSE P35436 GLUTAMATE [NIMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;	203a01.r1 Soares_fetal_liver_spleen_1NFLS_S1 Hamo sapiens cDNA clane IMAGE:423672 5	Homo sapiens myeloid/lymphoid or mbed-lineage leukemia (triffiorax (Drosophiia) homolog); translocated to, 4 (MILT4), mRNA	Homo sapiens eukaryotic translation Initiation factor 44, Isoform 1 (EJF4A1) mRNA	AV742248 CB Homo sepiens cDNA clone CBFBCC125"	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA	Homo sapiens small inducible cytoldine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA	b12058t Testis 1 Homo sepiens cDNA done b12058	ts39g02.x1 Sogres_NhHMPu_S1 Hamo septens cDNA clone IMAGE:2089108 3"	7088602.x1 NCI_CGAP_Ov18 Homo sepiens cDNA clone IMAGE:3644091 3' similar to TR:P87892 P87892 PROTEASE :	AV760550 MDS Homo seplens cDNA clone MDSC3802 5	zi85a07.s1 Soares fetal_liver_spleen_1NRLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.tS THR repetitive element;	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' shrilar to contains THR.t3	THR repetitive element;	H.sepiens mRNA for teminin-5, alpha3b chain	Homo espiens hypothetical protein FLJ13558 similar to N-myc downstream regulated 3 (FLJ13558), mRNA	Homo sepiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA	Homo sepiene hypothetical protein FLJ13556 similar to N-myo downstream regulated 3 (FLJ13556), mRNA	Homo sepiens hypothetical proteth FL/13556 similar to N-myc downstream regulated 3 (FL/13556), mRNA	Homo sepiens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA
W 80001 1110V	Top Hit Database Source		EST_HUMAN A	est_human er	EST_HUMAN PR	EST HUMAN P	EST_HUMAN Z	•		THUMAN			T_HUMAN	EST HUMAN to	FST HEIMAN P	Т	$T^{T}$	Г	EST_HUMAN T	H						
J Sign	Top Hit Acesslon No.			2.0E-51 AA378559.1	2.0E-61 A/732851.1		_	11419169 NT	4503528 NT	AV742248.1	4759074 NT	4759071 NT	1.0E-51 T18862.1	1.0E-61 AI672532.1					8.0E-52 AA720574.1	8.0E-52 X84900.1	11968028 NT	11968028 NT	11968028 NT	11968028 NT	11416585 NT	11416585 NT
•	Most Similar (Top) Hit BLAST E Vatue	2.0E-51	2.0E-51	2.0E-51	20E-51	2.0E-51	2.0E-51	2.0E-61	1.0E-51	1.0E-51	1.0E-51	1.0E-51	1.0E-51	1.0E-61	1.05.61	4 OF 54	9.05-82		8.0E-52	8.0E-52	8.0E-62	8.0E-52	8.0E-52	8.0E-52	8.0E-52	8.0E-52
	Expression Signal	0.53	1.54	1.14	7.03	7.03	2.3		8.48	33.7	0.89	0.99	3.94	860	, c	180	200		803	1.77	2.98	2.98	6.44	6.44	0.69	0.69
	ORF SEQ ID NO:	36368			31545			31740	28140		30362	30353	l						26184	27500	27969	27670	27669	27870		34083
	SEQ ID NO:	22804	23720	23758	18613	18613	24991	25430	13225	14524	17463	17463	18585	20854	200	2000	25.303		13256	14528	14694		14694	14694		Ш
	Probe SEQ ID NO:	7268	10799	10838	11655	11655	12122	12803	114	149	4437	4437	5463	7941	8725	2007	4260		133	1495	1662	1662	4019	4019	7760	7760

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Single Exon Probes Expressed in Bone Marrow

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Top Hit Descriptor	os45d12.y5 NCL_CGAP_Br2 Hamo septems cDNA clans IMAGE:1808311 5	Hamo septens transducin (beta)-like 1 (TBL1) mRNA	Homo expiens transducin (bets)-the 1 (TBL1) mRNA	Macaca mulatha beta-tubutin mRNA, complete ods	2/45g05.s1 Soares_fetal_liver_spleen_1NPLS_S1 Homo septens cDNA clone IMAGE:453272 3'	Homo sapiens NADH dahydrogenase (ubiquinane) Fe-S pratein 5 (1540) (NADH-coenzyme Q reductase) (NDUFS5) mRNA	Homo sepiens SET domain and martner transposase fusion gene (SETMAR) mRNA	Horno expiens SET domain and martner transposase fusion gene (SETMAR) mRNA	wi48c04.x1 NCI_CGAP_LL19 Homo sepiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element :	w/49c04.x1 NCI_CGAP_Lu19 Homo saplens cDNA clone IMAGE:2406150 3' stmitar to contains THR.b2	THR repetitive element;	AV715377 DCB Hamo sepiens cDNA clane DCBAIEO3 5	zd40g12.rt Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:344038 5	Homo septens LIM dometin kinase 2 (LIMK2), mRNA	xn72e07.x1 NCI_CGAP_CML1 Home sapiens cDNA clone IMAGE:2700036 3' stmiler to contains Atu	Independent Control of the Control o	WF67405.X1 Somes_NFL_1_GBC_S1 Hamo septens CUNA date IMAGE-2300046.3 Similar to INCATOOSS [Q16859 CARBOXYLESTERASE]	Zu 75h12.s1 Scares testis NHT Homo saplens cDNA clone IMAGE 743879 3	Homo sepiens gutamette-emmonia ligase (glutamine synthese) (GLUL) mRNA	Homo sepiens anysulfatese D (ARSD), transcript variant 1, mRNA	pol-reverse transcriptase homotog (retroviral element) [human, endogenous retroviral element RTVL-Hp1,	Genomic, 680 m]	Human P-glycoprotain (MDR1) gane, exon 4	Hurman PMS2 related (hPMSR2) gene, complete cds	Human eldolase C gene for fluctose-1,6-bisphosphata aldolase	Homo sapiens basic transcription factor 2 p44 (btt2p44) gene, partial cds, neuronal apoptosis inhibitory	protein (naip) and survival motor neuron protein (smn) genes, complete cds	Homo saplens chromosome 21 segment HS21C027	Rattus norvegicus putative four repeat ion charmel mRNA, complete cots	dr08g05.y1 Morton Fetal Cochlea Homo septens cDNA clone IMAGE:2483145 5	Homo sepiens chromosome 21 segment HS21 0002
Acessian Top Hit Database Source	EST HUMAN	NT	NT	NT	EST HUMAN	ĮŅ.	F	TN.	FST HUMAN	ľ	EST HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	IN.	MANUEL TOTAL	ESI JUMAN	EST_HUMAN	EST_HUMAN	IN	¥		뒫	ᅜ	¥	Ę		M	NT	M	EST_HUMAN	5
Top Hit Acesstan	AJ792146.1	5032158	5032158 NT	2.0E-62 AF147880.1.	2.0E-62 AA778795.1	TN 6878974	5730038	5730038 NT	2 OF 52 AIR31462 1		2.0E-52 AI831462.1	2.0E-52 AV715377.1	V70260.1	11417990 NT		2.0E-52 AW 236297.1	2.0E-52 Al808985.1	1.0E-52 AA634445.1	4504028 NT	4502238 NT		361070.1	W29426.1	J38964.1	07292.1		J80017.1	1.0E-52 AL163227.2	1.0E-52 AF078779.1	1.0E-52 AW020370.1	1.0E-52 AL163202.2
Most Similar (Top) Hit BLAST E Vedue	2.0E-52 A	2.0E-52	2.0E-52	2.0E-62	2.0E-52 A	2 OF-52	20E-52	2.0E-52	2.05.50		2.0E-52	2.0E-52	2.0E-62 W70260.1	2.0E-62		2.05-52/	2.0E-62	1.0E-52	1.0E-62	1.0E-52		1.0E-62 S61070.1	1.0E-52 M29428.1	1.0E-52 U38964.1	1.0E-62 X07292.1		1.0E-52 U80017.1	1.0E-52	1.0E-52	1.0E-52	1.0E-52
Expression	0.73	0.62	0.52	11.69	78.0	4	6.19	6.19	8	2	3.09	2.73	12.63	2.73		18.5	7.5	1.45	9.6	217		1.88	4.22	24	235		0.55	1.13	0.7	1.21	1.14
ORF SEQ ID NO:	33416				35684		36893			2000	38030	38048				31300		26524				28041					34486		35855		
SEQ ID	20105	21058	21058	21966	22254	23683	23308	23396	2,75	24418	24479	24492	24646	24819		25982	25319	13605				16129	L	L		1_	21087	_	L	<u> </u>	23871
Probe SEQ ID NO:	7120	8121	8121	8	8878	7600	10474	10474	97,	986	11538	11551	11688	11839		12231	12633	88	1373	25.42		3072	5406	6533	7884		8150	888	9543	10941	10951

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Top Hit Descriptor	Homo sepiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds	Homo sepiens gene for AF-6, complete cds	Homo sepiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3		#44f07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2089077 3' similar to contains THR.t1   THR repositive element:	1	Π			Homo saplens chromosome 21 segment HS21C085	Homo sapiens chromosome 21 segment HS21C085	Homo saplens hook1 protein (HOOK1), mRNA	tydeho4.x1 NCI_CGAP_Ut3 Hamo sapiens cDNA clane IMAGE:2278327 3'				Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	Ť	Г	Homo sepiens MIL1 protein (MIL1), mRNA	QV1-HT0412-280300-123-c04 HT0412 Hamo septens cDNA	H.saplans graf gene	H.sapiens graf gene	GIF≒growth inhibitory factor [human, brain, Genomic, 2015 nt]	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA	Hamo sapiens FGFR1 ancogene partner (FOP), mRNA		Homo sepiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds	Homo sepiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA
Top Hit Database Source	¥	M	F	NT	EST_HUMAN	EST HIMAN	EST HUMAN	١	EST_HUMAN	EST_HUMAN	F	Þ	¥	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	5	EST HUMAN	K	Z	<b>EST_HUMAN</b>	¥	¥	¥	Ę	Ę	EST_HUMAN	¥	F
Top Hit Acessian No.	1.0E-52 U48296.1	1.0E-52 AB011399.1	4508064 NT		7.0E-53 BF238465.1	7 OF 53 A1424782 4		58543	5.0E-63 BE729270.1	5.0E-53 AW813563.1	4.0E-53 AL163285.2	2	7705414 NT	4.0E-53 AI613037.1	4.0E-63 F13080.1	4.0E-53 BF128701.1	4.0E-53 BF128701.1	3 NE 43 AB028808 4			11526297 NT	3.0E-53 BE160025.1	3.0E-63 Y10388.3			3835090	5901963 NT	AA36655		4502316 NT
Most Similar (Top) Hit BLAST E Value	1.0E-52	1.0E-52	9.0E-53	9.0E-53	7.0E-53	7.05-89	6.0E-53	5.0E-53	5.0E-63	5.0E-53	4.0E-53	4.0E-63	4.0E-53	4.0E-53	4.0E-63	4.0E-53	4.0E-53	9 05 59	3.0E-53	3.0E-63	3.0E-53	3.0E-53	3.0E-63	3.0E-53	3.0E-53	3.0E-53	3.0E-53	2.0E-53	2.0E-53	. 2.0E-53
Expression Signal	1.84	1.3	6.0	0.91	2.56	8	0.89	8	1.54	1.67	2.37	2.37	1.11	0.62	0.71	2.83	2.83	790	101	0.92	1.09	96'0	96.0	96:0	12.56	0.60	9.53	253	6.08	11.44
ORF SEQ ID NO:	37601	31608	29762	30336			31098		38580		26079	26080	30764			38044		30000			31979	32629	33613	33614		L	L		28367	
SEQ ID	24077			17445		OKORO			L	25253	13171	13171	17876	22712			1_	4,5000	16788	L	<u> </u>	18389	20276		١.	22177		13531	15346	<u> j</u>
Probe SEQ ID NO:	11117	13114	3805	4418	12477	42004	5275	4128	12110	12522	51	51	4859	9771	10114	11548	11548	8	3744	6483	2029	6318	7305	7305	8647	9211	9412	458	2335	2543

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	Top Hit Descriptor	Homo saptens core-binding factor, runt domain, alcha subunit 2, transfocated to, 1; cyclin D-related (CBFA2T1) mRNA	Homo sepiens core-bhiding factor, runt domain, alpha subunit 2; transfocated to, 1; cyclin D-related (CBFAZT1) mRNA	Homo sapiens leucine aminopeptidase (LOC51056), mRNA	Homo sepiens dihydropyridine receptor alpha 2 subunit (CACNAZD1) gene, exon 6	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds	Homo sepiens SKAP65 homologue (SKAP-HOM) mRNA	Homo saplahs chromosome 21 segment HS21 C081	Homo sepiens chromosome 21 segment HS21 C081	PM1-CT0398-170800-001-g03 CT0396 Home septens CJNA	PM1-CT0398-170800-001-g03 CT0398 Homo sepiens cDNA	EST387707 MAGE resequences, MAGN Homo sapiens cDNA	15429, seq. F Human fetal heart, Lambda ZAP Express Homo septems cDNA 6	2822885.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822865 5	Homo saplens Xq pseudoeutosomal region; segment 2/2	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	601176725F1 NIH MGC 17 Homp septers CANA Gone IMAGE:3031919 b	CMA-NN1029-150800-543-e02 NN1029 Homo septems cDNA	RC5-BN1058-270400-031-D01 BN1058 Homo sapiens dDNA	IBS71.seq.F Human fetal heart, Lambda ZAP Express Homo sapients ounk o	H. saplens mRNA for hmRNPcore protein A1	H.saplens mRNA for myosimHE	H.saplans mRNA for myosin-IE	Homo sepiens IQ modif containing GTP asse activating protein 1 (IQCAPT) mixina	601272863F1 NIH_MGC_20 Homo septens CUNA cione IMAGE:3014U31 b	Homo sepiens insulin-like growfth factor 2 receptor (IGFZR) mRNA	Homo sepiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCAB), miNNA	HF44405.X1 Sogres_NRT_GBC_S1 Hamp sapiens cDNA clane IMAGE-2834742.3"	f44e05.x1 Soares_NRT_GBC_S1 Homo sepiens cDNA clone IMAGE:2834752.31	eT8c12.s1 Sceres_testis_NHT Homo sepiens cDNA clone 1377046 3' similar to contains MER30.t3 MER30 repetitive element;	Homo sapiens mRNA for monocyte chemotectic protein-2	
	Top Hit Database Source					TN.				EST_HUMAN F		EST_HUMAN E	EST_HUMAN	EST_HUMAN	± LN			EST HUMAN		EST_HUMAN	EST_HUMAN I		ᅜ	NT.		T_HUMAN			THUMAN	EST_HUMAN	EST_HUMAN	T	
285	Top Hit Acesston No.	4757915 NT	4757915 NT	TN05087 NT	2.0E-63 AP083822.1	2.0E-53 M61873.1	4506982 NT	2.0E-53 AL163281.2	2.0E-53 AL163281.2	2.0E-63 BF334740.1	2.0E-53 BF334740.1	2.0E-83 AW975598.1	2.0E-53 AA095852.1	2.0E-53 AW245678.1	1.0E-83 AJ271736.1		1.0E-63 AB026898.1	1.0E-63 BE296388.1	1.0E-63 BF364201.1	1.0E-83 BE012071.1	1.0E-53 AA248072.1	1.0E-63 X79636.1	1.0E-63 X98411.1	1.0E-53 X98411.1	4506786 NT	3E38678	4504610 NT	F005700 NT	8.0E-54 AW 592568.1	8.0E-54 AW 592568.1	7.0E-54 AA812537.1	7 0E 84 V18845 4	1 182.1
	Most Similar (Top) Hit BLAST E Value	2.0E-53	2.0E-63	2.0E-53	2.0E-53	2.0E-53	2.0E-53	2.0E-53	2.0E-53	2.05-63	2.0E-53	2.0E-53	2.0E-53	2.0E-53	1.0E-83		1.0E-63	1.0E-53	1.0E-53	1.0E-63	1.0E-53	1.0E-53	1.0E-63	1.0E-53	9.0E-54	8.0E-64	8.0E-54	8.0E-54	8.0E-54	8.0E-54			7.0E-57
	Expression Signal	1.17	1.17	1.46	8.0	2.78	123	96'0	98'0	3.33	3,33	1.13	0.61	15.48	7		1.29	1.32	1.43	0.84	0.55	13.12	3.08	3.08	5.13	1.73	2.4	23.25	1.67	1.67			20.0
	ORF SEQ ID NO:	28744			29234	30016		31074	31075	L					27450		28389	30902	33198	L	34647		38574	38575	31353					L		1	2/808
	Exam SEQ ID NO:	16730	<u> </u>	L	L	1_		18202	_		L	١.		L	1		16469	18015		L	21236		24978	_	1	L			1_1	1_			14873
	Probe SEQ ID NO:	2738	2736	3232	3259	4088	4520	5183	5183	5500	6500	8203	8340	9763	1440		3421	5001	6850	7459	8267	24	12105	12105	5375	R	1852	6045	11982	11987	386		1847

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					,   		
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Defebese Source	Top Hit Descriptor
2215	15229	28252	4.54		7.0E-54 NZ7177.1	EST_HUMAN	yw69d12.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sepiens cDNA clone IMAGE:257399 3' similar to contains LTR7.b3 LTR7 repetitive element;
10487	23409	90696	1.81	7.0E-54	11417222 NT	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC83182), mRNA
11623	24561		3.26		7.0E-64 AI160189.1	EST_HUMAN	qb97g03.x1 Scares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR:t1 OFR repetifive element;
53	13145	26045	2.05		6.0E-54 AB003818.1	NT	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
385	13498		29'0	6.0E-54	8922148 NT	NT	Homo sapiens hypothetical protein DKFZp434Mt035 (DKFZp434Mt035), mRNA
385	13498	28431	0.67	6.0E-54	8922148 NT	NT	Homo septens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3296	16349		66'0	6.0E-64	8922148 NT	TN	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3546	16592	29517	96'0	6.0E-54	AL16324	NT	Homo sapiens chromosome 21 segment HS210047
4030	17068	69662	1.48	6.0E-54	4502872 NT	NT	Homo sepiens chioride channel 6 (CLCN6) mRNA
4489	17514	30402	87.0		6.0E-64 AV754748.1	EST_HUMAN	AV754748 TP Hamo sapiens cDNA clane TPGAAC10 5
4819	17836	30734	0.94		6.0E-54 AV724885.1	EST_HUMAN	AV724885 HTB Hamo sepiens cDNA clane HTBACE02 6
4880	17897	30786	1.85	6.0E-54	TN 905806 NT	ΝŢ	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4909	17828		1.23			NT	H.sapiens she pseudogene, p68 Isaform
5035			1.27	6.0E-54	6.0E-54 Y09846.1	NT	H.sapiens shc pseudogene, p68 Isoform
11771	23926	37446	1.6	6.0E-54	11433623 NT	NT	Homo sapiens KIAA0071 protein (KIAA0071), mRNA
11771	23926	37447	1.6		11433623 NT	¥	Homo saplens KIAA0071 protein (KIAA0071), mRNA
2160	15176	28197	3.75	5.0E-54 P51528		SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
184	13284		319.6		4.0E-54 AF110103.1	¥	Tupela belangeri beta-actin mRNA, partial cds
					,		EST177696 Jurkat T-cells VI Homo sapiens cDNA 5 and similar to giyceraldehyde-3-phosphate
957			22.88		<u>-</u>	EST HUMAN	denydrogenese
1822	14849		291	4.0E-54	4.0E-54 D38521.1	M	Human mRNA for KIAA0077 gene, partial cds
1822	14849	27843	167	4.0E-54		NT	Human mRNA for KIAA0077 gene, partial cds
							wd28d11x1 Sogres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329289 3' similar to TR:002711
3217	16272		1.03			EST HUMAN	002711 PRO-POL-BUTPASE POLYPROTEIN;
7524	20488		89.0		4.0E-54 BE544889.1	EST_HUMAN	601075004F1 NIH_MGC_12 Hamo septems aDNA dane IMAGE:3461017 5
88	13209	26133	13.65		3.0E-64 AA313487.1	EST_HUMAN	EST185371 Colon carchroma (HCC) cell line Homo sepiens cDNA 5' end
2832	16631		1.1	3.0E-54	Al908757.1	EST_HUMAN	IL-BT189-190399-007 BT189 Hamo sepiens oDNA
6007	19090	32290	1.52		4502434 NT	¥	Homo sepiens BMX non-receptor fyrosine kinase (BMX) mRNA
7619		33942	1.49		-	EST_HUMAN	ai92c08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3*
7619	20579	33943	1.49		3.0E-54 AA844081.1	EST_HUMAN	ei92c08.s1 Soeres_perethyroid_turnor_NbHPA Homo espiens cDNA clone IMAGE:1388270 3'
8081	ı	34418	0.51	3.0E-54	3.0E-54 AI742822.1	EST_HUMAN	wg44b11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE-2367833 3"

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Top Hit Descriptor	Homo sapiens golgi autoantigen, golgin subfamily a, 5 (GOLGA5), mRNA	602019408F1 NCI_CGAP_Bm67 Hamo sapiens cDNA clane IMAGE:4155121 5	270712.1 Scense_testis_NHT Homo septens cDNA done IMAGE:727727 5 stmiter to TR:G191316 G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN.;	EST366829 MAGE resequences, MAGC Hamo septens cDNA	RC1-BT0313-131189-011-b09 BT0313 Homo sepiens cDNA	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA	Homo sapiens nuclear antigen Sp100 (SP100) mRNA	nt78s09.s1 NCI_CGAP_Pr3 Homo sapiens cDNA cione IMAGE:1204600 similar to contains element L1 repetitive element;	eu.62g.03.y1 Schmelder fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' stmilar to SW:CUL1_HUMAN Q13616 CULLIN HOMOLOG 1;	Homo eaplens chromosome 21 segment HS210010	wy60b/12x1 Soares_NSF_FB_9W_OT_PA_P_31 Homo sepiens cDNA clone IMAGE:2552827 3° shrifer to TR:062084 Q62084 PHCSPHOLIPASE C NEIGHBORING ;	n45909.s1 NCI_CGAP_Pre Homo sapiens cDNA clone IMAGE:995488 similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN);	Homo sepiens chaperonin containing T-complex subunit 6 (CCT6) mRNA	Hamo sapiens syncytin precursor, mRNA, complete cds	Homo sapiens peptidykarginine delminase type III (LOC51702), mRNA	Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA	Homo sepiens small inducible cytoldne subfamily A (Cys-Cys), member 14 (SCYA14) mRNA	1243c11.y1 NCI_CGAP_Brn52 Homo sapiens cDNA done IMACE-2231348 5	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA	Homo sepiens mRNA for KIAA 1591 protein, partial cds	Homo sapiens mRNA for KIAA1501 protein, partial cds	Homo saplens EVI5 homolog mRNA, complete cds	Homo sapiens mRNA for KIAA0995 protein, partial cds	Homo sapiens mRNA for KIAA0995 protein, partial cds	Homo sapiens neurofibromin 1 (neurofibrometosis, von Recklingheusen disease, Watson disease) (NF1), mRNA	Homo sersiens mRNA for brain rvanodine receptor, complete cds	Homo serciens Janus Idnase 2 (a protein tyrosine kinase) (JAK2), mRNA	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
Top Hit Database Source		EST_HUMAN			LHOMAN			EST HUMAN		1	EST HUMAN							EST_HUMAN	Ä	NT.	NT	¥		¥				
Top Hit Acession No.	11434806 NT	3.0E-64 BF345600.1	3.0E-54 AA383362.1		3.0E-64 AW748965.1	1900	4507164 NT	2.0E-54 AA655008.1	-		2.0E-64 AW057524.1		502642	2.0E-54 AF208161.1	7706446 NT	4506962 NT	4759069 NT	BE047884.1	11428657	1	2.0E-54 AB046811.1	ļ	1	2.0E-64 AB023212.1	TWANDSALL	2 0F-64 ARMH025 4	2477	11416782 NT
Most Similar (Top) Hit BLAST E Value	3.0E-54	3.0E-64	3.0E-54	3.0E-54/	3.0E-54/	2.0E-54	2.0E-54	2.0E-54/	2.0E-54	2.0E-54/	2.0E-54/	2.05-54 /	2.0E-54	2.0E-54 /	20E-54	2.0E-54	2.0E-54	2.0E-54	2.0E-54	2.0E-54	2.0E-54/	2.0E-64/	2.0E-54	2.0E-64	20 20 20	205-54	2 OF 54	2.0E-54
Expression Signal	4.82	3.55	211	4.08	1.67	6.22	1.48	132	20.1	1.45	4.	543	1.73	1.18	0.89	1.07	1.8	1.26	88	10.03	10.03	0.77	67.0	67.0	1	8.7	2 5	0.88
ORF SEQ ID NO:		37902	38239	31850			27371	27564	28570	28631	28887				30822		31591	31952	32131		32246					2000		
Exam SEQ ID NO:	24312	24367	24661	25134	26942	13709	14401	14583	15547	15607	15964	10005	17281	17496	17831	18284	18648	18779	18946	18046	19046	19868	20206	20208	7000	22014	22.202	23402
Probe SEQ ID NO:	11363	11423	11696	12334	12380	<b>₹</b>	1367	1550	2546	2808	2005	3550	4232	472	4914	6278	<b>666</b> 1	<b>58</b>	9856	598	5964	8814	8883	888		200	4080	10480

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SEQ 1D NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:	Exan SEQ ID NO: 22319 22319 22319 22319 22319 22319 22319 15059 15	ORF SEQ ID NO: 368901 368902 368907 28134 28134 28135 28135 28135 28135 28135 28135 28135 38078 28135 38078 39078 39078 30078 30078 30078 30078 30078 30078 30078 30078 30078	Signal 1.94 1.34 1.34 1.34 1.34 1.34 1.34 1.34 1.3		AB01465 AB01465 AB01465 AB01465 AB01465 AB01465 AB01465 AB01465 AB01711 BE7244 BF7244 BF7244 BF7244 BF7244 BF7244 BF7244 BF7244 BF7244 BF7244 BF7244 BF7244	TOP HIS Detebase Source Source Source THUMAN THUMAN ST HU	Top Hit Descriptor   Top Hit Descriptor   Top Hit Descriptor   Top Hit Descriptor   Database   Da
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	П	Homo septens mannose-6-phosphate receptor (cation dependent) (M8PR) mRNA	Oryctologus cunicutus New Zealand white elongetion factor 1 elpha (Rebefla2) mRNA, complete cds		Homo sapiens mRNA for KIAA0903 protein, pertial cds			Homo sepiens SMA3 (SMA3), mRNA	Homo septens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)	Homo sapiens mRNA for KIAA0406 protein, pertial cds	Homo sapiens mRNA for KIAA0406 protein, pertial cds	Homo sapiens CLP mRNA, pertial cds	Homo septens mRNA for KIAA1219 protein, pertial cds		Homo sapiens chromosome 21 segment HS210067	Homo sepiens chromosome 21 segment HS21C010	Ė	Homo sapiens DSCR56 mRNA, complete cds	Homo sapiens DSCR6b mRNA, complete cds	Homo sapiens hypothetical protein FL/20128 (FL/20126), mRNA	Homo sapiens PRO1851 mRNA, camplete cds	Home saplens hect domain and RLD 2 (HERC2), mRNA	Homo sapiens hect domain and RLD 2 (HERC2), mRNA	Homo septens F-box protein FBL4 (FBL4) mRNA, complete ods	Home saplens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA	Homo sapiens discs, large (Drosophila) homolog 2 (chepsyn-110) (DLG2), mRNA	Homo sapiens SKAP65 homologue (SKAP-HOM), mRNA	Homo sapiens phospholipid scramblase 1 gene, complete cds	Homo sepiens phospholipid scramblase 1 gene, complete cds	Human infant brain unknown product mRNA, complete cds	seq1575 b4-BSMA Cot8-HAP-Ft Homo sapiens cDNA clone b4+B3MA-COT8-HAP-Ft61 5' similar to similar to chinese Hamster DHFR-coamplified protein mRNA
Top Hit Database Source	EST_HUMAN	NT	. <u>F</u>	EST_HUMAN	¥	<b>EST_HUMAN</b>	EST_HUMAN	NT.	NT TN	NT	N.	NT	NT	Į,	EST_HUMAN	IN	TN	EST_HUMAN	INT	NT	NT	NT	INT	INT	NT	LN.	ᅜ	NT	ᅜ	Z	M	EST_HUMAN
Top Hit Acession No.	2.0E-55 BE886059.1	4505060 NT	1.0E-55 008823.1	1.0E-55 AI026718.1	1.0E-66 AB020710.1	1.0E-85 BE277861.1	1.0E-55 BE277861.1	5803174 NT	1.0E-65 AF000990.1	1.0E-65 X13111.1	1.0E-66 AB007868.2	1.0E-55 AB007868.2	1.0E-55 L54057.1	1.0E-65 AB033045.1	1.0E-55 W28189.1	1.0E-55 AL163267.2	1.0E-55 AL163210.2	1.0E-65 N77261.1	1.0E-55 AB037163.1	1.0E-65 AB037163.1	8923125 NT	1.0E-55 AF119856.1	11433046 NT	11433046 NT	1.0E-55 AF199420.1	11432894 NT	11432994 NT	11421649 NT	1.0E-55 AF224492.1	1.0E-66 AF224492.1	1.0E-55 U50950.1	1.0E-55 T10045.1
Most Similar (Top) Hit BLAST E Vatue	2.0E-55	1.0E-55	1.0E-55	1.0E-55	1.0E-66	1.0E-55	1.0E-55	1.0E-66	1.0E-65	1.0E-65	1.0E-66	1.0E-55	1.0E-55	1.0E-65	1.0E-55	1.0E-55	1.0E-55	1.0E-55	1.0E-55	1.0E-65	1.0E-55	1.0E-55	1.0E-55	1.0E-55	1.0E-55	1.0E-55	1.0E-66	1.0E-55	1.0E-55	1.0E-65	1.0E-55	1.0E-55
Expression Signal	1.51	2.4	88.01	0.75	422	1.85	1.65	3.95	131	52.04	4.62	4.62	4.78	86.0	98'0	4.23	1.08	121	1.79	1.73	13	0.56	7	7	99.0	1.25	1.25	0.49			1.65	1.58
ORF SEQ ID NO:		26136	26218			27890	27001		28376		28580	28581		28811	28388		30238		30789	30770	31063	31634	32718	32719		34704					37452	
Eton SEQ ID NO:	24983	13212	13282	13845	14194	14988	14988	15344	15824	L	15562	15562	<u> </u>		16468			17782	L		18188	18671	19470		20015		21290		L	L		l I
Probe SEQ ID NO:	12113	88	26	9/9	1152	1967	1967	2333	2345	2524	2561	2561	2819	289	3420	4015	4323	4762	4885	4866	5177	5275	6402	9402	7282	8321	8321	8410	8418	8418	11776	11795

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ngie Exon Probes Expressed in bone Marrow	Top Hit Descriptor	Hamo sapiens DNA-binding protein (LOC56242), mRNA	601237702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608552 5	yn62g03.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element;	RC1-CT0252-231099-013-b07 CT0252 Hamo septems cDNA	RC1-CT0252-231099-013-b07 CT0252 Hamo septens cDNA	RC3-BN0663-170200-011-h01 BN0063 Homo sapiens cDNA	ULH-Blop-eau-e-05-0-Ul.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2710544 3'	43c5 Human retina cDNA randomly primed sublibrary Homo saplens cDNA	CHR220038 Chramosame 22 evan Hamo sepiens aDNA dane C22_65 5	Homo sapiens beta-tubulin mRNA, complete cds	Homo septens beter-tubutin mRNA, complete ods	Homo sepiens tubulin, beta polypeptide (TUBB) mRNA	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	regions	wbostoa.x1 NCL_CGAP_GC8 Homo sepiens oDNA clone IMAGE:2305191 3' stratler to SW:DCOR_MUSPA P27119 ORNITHINE DECARBOXYLASE ;	WEOSTOB.X1 NCI_CGAP_GC8 Homo sapiens cDNA clome IMAGE:2305191 3' stmlier to SW:DCOR_MIUSPA	P27119 ORNITHINE DECARBOXYLASE;	Homo sapiens uncharacterized bone memow protein BM031 mRNA, complete cds	Homo sapiens uncharacterized bane marrow protein BM031 mRNA, complete cas	Homo sapiens tymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allete, partial cds	tm65g12.x1 NCI_CGAP_Bm26 Hamo saplens cDNA clone IMAGE:2163046 3	tm65g12.x1 NCI_CGAP_Bm25 Hamo sapiens cDNA clone IMAGE:2163046 3'	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA	Homo sepiens 6'-3' excribonuclease 2 (XRN2), mRNA	EST28889 Cerebellum II Homo sapiens cDNA 5' end	EST28889 Cerebellum II Homo sapiens cDNA 5' end	Homo sapiens MHC class 1 region	601310203F1 NIH_MGC_44 Homo sepiens cDNA clone IMAGE:3631848 5	Homo sapiens chromosome 21 segment HS21C068	Homo sepiens superfeiller viralicidic ectivity 2 (S. cerevistee homolog)-like (SKIVZ.), mKNA	801438154F1 NIH_MGC_72 Hamp septens a JNA dane IMAGE.3823100 5
Xon Propes E	Top Hit Database Source	MT	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	NT	NT		М	EST HUMAN		EST_HUMAN	NT	NT	IN	EST HUMAN	EST_HUMAN	NT	NT	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	N.	¥	EST_HUMAN
Single	Top Hit Acession No.	10567821 NT	9.0E-56 BE379074.1	119834.1	7.0E-56 AW361213.1	7.0E-56 AW361213.1	5.0E-56 AW997712.1	5.0E-56 AW015507.1	V28189.1	155099.1	4.0E-56 AF141349.1	4.0E-56 AF141349.1	4507728 NT	4507728 NT		4.0E-56 AF003528.1	4.0E-56 AI632488.1		4.0E-56 AI632488.1	4.0E-66 AF217508.1	4.0E-56 AF217508.1	4.0E-56 AF043349.1	4.0E-56 AI498068.1	4.0E-56 A1498068.1	8924029 NT	6912743 NT	3.0E-56 AA325828.1	3.0E-56 AA325826.1	3.0E-56 AF055068.1	3.0E-66 BE393512.1	3.0E-66 AL163268.2	5902085 NT	3.0E-58 BE893572.1
}	Most Similar (Top) Hit BLAST E Vatue	1.06-55	9.0E-56	7.0E-66 H19834.1	7.0E-56	7.0E-56	€.0E-56	5.0E-36	5.0E-56 W28189.1	5.0E-56 H55099.1	4.0E-56	4.0E-56	4.0E-56	4.0E-56		4.0E-56	4.0E-56		4.0E-56	4.0E-56	4.0E-56	4.0E-56	4.0E-56	4.0E-56	3.0E-58	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-58	3.0E-58
	Expression Signal	1.74	1.89	6.5	2.13	2.13	1.89	19.0	1.7	5.41	12.5	12.5	4.9	6.4		3.69	118		1.16	5.85	5.85	3,94	7.82	7.82	1.74	66'0	1.83	1.83	1.73	1.1	4.84	2.34	1.81
	ORF SEQ ID NO:	38374	33912	28753	34229	34230	27713	35923		31309	28049	26050	28730	28731	<b> </b> -	26516	28844		28645	32700	32701	37293	37743	37744	27349	27794	29109	28410		228833	30368	30517	
	Exan SEQ ID NO:	24783	L	15737			14731	22478	23878	25930	13150	13150		1		13598	15620		15620	19455	19455	23792	24220		14380	14808	16199	16199	16887	16978	17480		17858
	Probe SEQ (D NO:	11902	7590	2743	7902	7802	<u>1</u> 3	9516	10754	12507	8	8	2719	2719		2823	2863		2843	6387	6387	10872	11288	11268	1345	1779	3142	3142	3847	3838	454	4603	4841

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Oligie Lyon Flores Lypicosed III Doile Mallon	Top Hit Descriptor	Homo saplens hypothetical protein FLJ20371 (FLJ20371), mRNA	QV4-ST0234-181199-037-f05 ST0234 Homo septens cDNA	x05d10.x1 NCI_CGAP_Bm53 Homo saplens cDNA clone IMAGE:2759251 3' similar to gb:U05876 INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);	zv51b12.r1 Sceres_testis_NHT Homo sepiens cDNA clone IMAGE:757151 5	Homo sepiens glutamate receptor, ionotrophic, AMPA 4 (GRIA4) mRNA	60094440F1 NIH_MGC_17 Hamo sapiens cDNA clane IMAGE:2890864 67	Homo sapiens aconitase 2, mitochandrial (ACO2), mRNA	Homo sapiens mRNA for KIAA0898 protein, partial cds	Homo septems mRNA for KIAA0880 protein, partial cds	Homo sapiens mRNA for KIAA0960 protein, partial cds	Homo sepiens KIAA0716 gene product (KIAA0716), mRNA	Homo septens mRNA for KIAA0837 protein, partial cds	Homo sepiens mRNA for KIAA0837 protein, partial cds	Homo sepiens paired box gene 5 (B-cell lineage specific activator protatn) (PAX5), mRNA	Hamo septens hypofhetical protein FL/20371 (FL/20371), mRNA	Homo capiers Ras suppressor protein 1 (RSU1), mRNA	Homo sapians SH3-domain binding protein 1 (SH3BP1), mRNA	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA	Homo sapiens NME7 (NME7), mRNA	Homo sapiens NME7 (NME7), mRNA	Homo septens Kruppel-like factor 8 (KLF8), mRNA	Homo sapiens phosphatidylinosital 4-kinese 230 (pi4K230) mRNA, complete cds	Homo septems phosphatidylinosital 4-kinase 230 (pi4K230) mRNA, complete cds	Home sapiens large conductance calclum- and voltage-dependent potassium channel alpha subunit (Madit)		Hano seprens Ad paradosanosantai regirat, segimenti 1/2.	Homo sepiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, commiste cits)	toning was the file markets from EQA formers and flower than EQ asserted and the Asserted	From September Languar Protein ingester Eart (Hadited Paparating to be Educated Protein, Angellited syndrome) (UBE3A) mRNA	Inc1307.s1 NCL_CGAP_Pr1 Homo sapiens cDNA done IMAGE:1008037 shriter to SW:RS10_HUMAN P46783 40S RIBOSOMAL PROTEIN S10.;	EST54770 Hippocampus II Homo saplens cDNA 5 end
8001 L 110Y	Top Hit Detabase Source	IN	EST_HUMAN	EST HUMAN	EST_HUMAN	M	EST_HUMAN	NT	NT	NT	M	NT	NT	NT	NT	IN	M	M	N	NT	NT	NT	M	LN	ķ		Z	5	1	¥	EST HUMAN	EST_HUMAN
Join Miles	Top Hit Acession No.	8923349 NT	8.0E-57 AW816405.1	8.0E-57 AW284689.1	1	4557830 NT	8.0E-57 BE299918.1	11418185 NT	1.1	.1	AB023177.1	7862283 NT		AB020644.1	11428710 NT	8923349 NT	11431260 NT	11545732 NT	11545732 NT	7242158 NT	7242158 NT	6005979 NT	7.0E-67 AF012872.1				5.0E-57 A.Z/1/35.1			4507798 NT	3.0E-67 AA230279.1	3.0E-57 AA348335.1
	Most Similar (Top) Hit BLAST E Vatue	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-67	8.0E-57	8.0E-57	8.0E-57	8.05-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	7.05-57	7.0E-57	7.0E-57	7.0E-67	7.0E-67	L	/20E-0/	5.0C-57	10.4	4.00	3.0E-67	3.0E-67	3.0E-57
	Expression Signal	1.11	3.14	9.74	2.19	1.11	1.32	1.69	0.54	12.65	12.65	0.71	2.69	269	0.44	2.8	1.67	3.29	1.39	1.09	1.09	0.65	263	263	,	33.	3.96	64	7 7	0.83	68.40	0.95
	ORF SEQ ID NO:	28032	26319	28898		30852	<b>5960E</b>	31435	32863	32941	32942	34003	34357	34358	37267	26032	<i>1</i> 9988	31751	31751	78287	29238	85262	20840	14862		Te/ne		814.00		20813		28431
	Exan SEQ ID NO:	13134	13391	13940	14860	17962	18083	25849	19601	19666	19666	20640	20961	20961	23768	13134	24960	25386	25386	16317	16317	16338	16931	16831		33)	25884	489/19	8	13863	14368	15407
	Probe SEQ ID NO:	14	282	885	1883	4946	5073	5312	6239	8099	8089	7682	8024	8024	10848	11807	12088	12733	12749	3283	3263	3284	3891	3894		P P	13075	2778	8/9	805	283	2400

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					2.R		
Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2714	15708	28724	1.19		3.0E-67 BE676622.1	EST_HUMAN	783b10.x1 NCI_CGAP_CL11 Homo septens cDNA done IMAGE:3286443 3° strailer to WP:Y47149C.2 CE20263 ;
27.14		28725	1.19	ļ 	3.0E-67 BE676622.1	EST_HUMAN	733b10.x1 NCI_CGAP_CLL1 Homo sepiens cDNA clone IMAGE:3286443 S' shniter to WP:Y47H9C.2 CE20283;
3711	16754		28.47		3.0E-57 AW853984.1	EST_HUMAN	RC3-CT0254-110300-027-d10 CT0254 Hamo sepiens aDNA
6145	19220	32450	1.37	3.0E-57	11225608 NT	NT	Homo sapiens engiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
6246	Ш	32540			3.0E-67 BE799637.1	EST_HUMAN	601589886F1 NIH_MGC_7 Hamo septems cDNA clane IMAGE:3844302 6
8484	21452	34870	2.61		3.0E-57 W28130.1	EST_HUMAN	42/8 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8510	21478	34891	1.9	3.0E-57	11545798 NT	NT	Homo sepiens hypothetical protein FLJ11636 (FLJ11636), mRNA
8510	21478	34892	1.9		11545788 NT	IN	Homo sapiens hypothetical protein FLJ11656 (FLJ11658), mRNA
8624	24592	35011	0.56		1427757	NT	Homo septens KIAA0849 gene product (KIAA0849), mRNA
8772	21739	35160	99'0		105282.1	NT	Human famesyl pyrophosphate synthetase mRNA, complete cds
8210	22/76	35606	4.95	3.0E-57	AU117859.1	EST_HUMAN	AU117659 HEMBA1 Hamo sapiens cDNA clane HEMBA1001910 5
9605	22609	36060	7.0	3.0E-57	11545798 NT	NT	Homo sepiens hypothetical protein FLJ11858 (FLJ11858), mRNA
9605	80922	36061	7.0	3.0E-57	11545788 NT	NT	Homo sapiens hypothetical protein FLJ11666 (FLJ11699), mRNA
11254	24207	37729	2.96		3.0E-57 AW248374.1	EST_HUMAN	2820473.5prime NIH_MGC_7 Hamo sepiens cDNA clane IMAGE:2820473 5
12384	25951	31314	2.53	3.0E-57	3.0E-57 W23871.1	EST_HUMAN	zb46d11.r1 Soares fetal lung NbH1.19W Homo sapiens cDNA clone IMAGE:308549 5
1500	14533	27504	1.05			NT	Homo septens SNARE protein kinase SNAK mRNA, complete cds
1500	14533	27505	1.05		2.0E-57 AF246219.1	NT	Homo sepiens SNARE protein kinase SNAK mRNA, complete cds
3462	16498	,	2.19		2.0E-57 AL163204.2	NT	Hamo sapiens chramosome 21 segment HS210004
3562	16608	. 29529	0.65		2.0E-57 R07702.1	EST_HUMAN	ye88h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5
3562	16808	29530	39'0		2.0E-57 R07702.1	EST_HUMAN	ye38h01.11 Soares fetal liver spieen 1NRLS Homo sapiens cDNA clone IMAGE:125809 5
3951	16991	29907	98.0		2.0E-57 BE073264.1	EST_HUMAN	MR0-BT0551-080300-103-b03 BT0551 Homo sepiems cDNA
4538	17561	30448	6.69		2.0E-67 AL163283.2	NT	Homo sepiens chromosome 21 segment HS210083
6139	18148	31027	1.74		2.0E-57 AL163206.2	LN	Homo sepiens chromosome 21 segment HS210006
							2591c05.r1 Sceres retina NZb4HR Homo sepiens cDNA clone IMAGE:380584 5 similar to contains L1.13 L1
5751	18845		1.67	2.0E-67	2.0E-57 AA016131.1	EST HUMAN	repetitive element;
							7n80f04.x1 NCI_CGAP_Ov18 Homo sepiens cDNA clone IMAGE:3570866 3' straiter to contains TAR1.t1
9150	19225		32.23		2.0E-57 BF115268.1	EST HUMAN	MEKZ reportive element;
6283		32591	0.7		<u>2</u>	FA.	Homo captens small inducible cytokine subtemity A (Cya-Cys), member 22 (SCYAZ2), mRNA
8978		35368	1.02	2.0E-57		뒫	Homo seplens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
10205	23130		1.63	2.0E-57	2.0E-57 AF057722.1	Z.	Homo sapiens 17-beta-hydroxystercid dehydrogenase IV (HSD17B4) gene, excns 3 and 4
11601			1.88	2.0E-67	11424084 NT	붛	Homo expiens hypothetical protein FL/20041 (FL/20041), mRNA
11601	24539	38038	1.88	2.0E-57	11424084 NT	¥	Homo sepiens hypothetical protein FL/20041 (FL/20041), mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

	indescribing	Homo sepiens partial mRNA for PEX5 related protein	Homo saplens partial mRNA for PEX5 related protein	ULHF-BNO-aid-g-07-0-ULH NIH_MGC_50 Hamp septens aDNA dane IMAGE:3078348 5	hosza68.x1 NCI_CGAP_LL24 Homo sapiens oDNA clone IMAGE:3039062 3' similar to TR:000246 000246 HYPOTHETICAL 9.3 KD PROTEIN ;	ha33d06x1 NCI_CGAP_Kdd12 Homo sepiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3	THR repetitive element;	EST11348 Uterus Homo septens cDNA 5' end	601309465F1 NIH_MGC_44 Homo sapkens dDNA clone IMAGE:3631000 5	21445948F1 NIH MGC 65 Homo saptens cDNA clone IMAGE:3850Z11 5	t34k07.x1 NCI_CGAP_Ov23 Homo septens cDNA clone IMAGE:2220181 3' similar to 1R:013475 013476 UNNAMED HERV-H PROTEIN;	#34b07.xf NCI_CGAP_Ov23 Homo septens cDNA clone IMACE-2220181 3' similar to TR:O15475 O15475	UNNAMED HERV-H PROTEIN;	Homo sapiens putative protein O-mannosytransiarase (POM I 2), mrdvA	Homo sapiens putative protein O-mannosyltransferase (POM 12), mrdvA	omo sapiens DHHC1 protein (LOC51304), mRNA	601346704F1 NIH_MGC_8 Hamo sepiens cDNA clane IMAGE:3687577 5	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 23) (MEF28) mRNA	ULHF-BNO-ait-g-10-0-ULH NIH_MGC_50 Homo saplens cDNA clone IMAGE:3079867 5'	ULHF-BNO-ait-g-10-0-ULT NIH_MGC_50 Hamo sapiens cONA clane IMAGE:3078867 5	AU130889 NT2RP3 Hamo sapiens cDNA clane NT2RP3001263 5	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Beykor-HGSC project=TCAA Homo sapiens cDNA done TCAAP1219	TCAAP1E1219 Pediatric acuts myelogencus leukemia cell (FAB M1) Baykor-HGSC project=TCAA Homo	sapiens cDNA done TCAAP1219	Homo sapiens chemoldne MIP-2 gamma (MIP-2 gamma) mRNA, complete cds	Homo sepiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA	Homo sapiens hypothetical protein FLI20454 (FLI20454), mRNA	Homo sepiens synaptojanih 1 (SYNJ1), mRNA	RC4-NT0057-160600-016-b05 NT0057 Hamo sapiens CJNA	CM3-UM0043-240300-127-607 UM0043 Hamo sapiens cUNA	CMS-UMOOAS-240300-12/-60/ UMOOAS Inding Septems CONA
Top Hit	Source	F	IN IN	EST_HUMAN		Т	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST HUMAN	П	T HUMAN				EST_HUMAN		T HUMAN	Г	Ť	EST HUMAN	Π	EST HUMAN	NT				EST_HUMAN	EST HUMAN	EST_HUMAN
Ton Hit Acression	Š	2.0E-57 AJ245503.1	2.0E-67 AJ245503.1	Ļ			1.0E-57 AW470791.1	9.0E-58 AA297847.1	9.0E-68 BE395061.1	8.0E-58 BE868715.1	8.0E-68 AI798378.1		8.0E-58 AI798378.1	11434921 NT	11434921 NT	7706132 NT	7.0E-58 BE561971.1	TN 5474542	7.0E-48 AW 504109.1	7.0E-58 AW 504109.1	6.0E-58 AU130689.1	8 0E-58 BE242150.1		6.0E-58 BE242150.1	6.0E-58 AF106911.1	11434746 NT	11526291 NT	4507334 NT	5.0E-58 BE783984.1	5.0E-58 AW 797948.1	5.0E-58 AW 797948.1
Most Similar		2.0E-57/	20E-67	1.0E-67	1 05.57		1.0E-57	9.0E-58	9.0E-58	8.0E-58	8.05-68		8.0E-58	8.0E-58	8.05-58	8.0E-58	7.0E-58	7.05.68	7.0F-58	7.0E-58	6.0E-58	8.0F-58		6.0E-58	6.0E-58	8.0E-58	6.0E-58	5.0E-58	5.0E-58	5.0E-58	5.0E-58
	Signal	1.74	1.74	1.40	77.7		3.65	1.9	2.37	2.43	284		2.84	1.98	1.98	2.65	98.0	8	R	273	4.05	1 60		1.62	1.16	1.02	1.41	4.35	7.63	3.77	3.77
O U	0 0 0 0 0 0	38145		28278				32033	31738		26844		26845	7887Z		Ĺ	33769		27769			ļ		28894		37091	L	26321			
Escar	SEQ ID	24579	24570	16264	2000	13037	25261	18853	25424	13658	43724		13721	14899	14899	16045	20415		24137	1	L	1	.1	15970	L		L		<u> </u>		14239
Probe	SEQ ID	11642	44642	2240	1	3	12537	9760	12795	\$	ASS		855	1874	1874	2987	7449		1100	1427E	285	204.2		2912	6294	10872	12629	88	711	1199	1199

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Prob.   Exat   Dr.   Signal   City   H   Top HB   Decades   Drawns   Top HB   Decades   City   H   Top HB   Decades   Drawns								
14239         27196         3.1         5.0E-58 AW707048.1         EST HUMAN           14239         27196         3.1         5.0E-58 AW707048.1         EST HUMAN           17346         3.0         5.0E-58 AM707048.1         EST HUMAN           17346         3.0         5.0E-58 AM268183.1         EST HUMAN           18804         2.2         5.0E-58 AM268183.1         EST HUMAN           18804         2.2         5.0E-58 AM26828.2         NT           18807         3.2860         0.94         5.0E-58 AM182285.2         NT           18673         3.2861         1.16         5.0E-58 AM18238.2         NT           20189         3.3483         0.7         5.0E-58 AM18238.1         NT           2024         3.2863         0.7         5.0E-58 AM26438.1         NT           2024         3.3625         0.7         5.0E-58 AM26438.1         NT           21271         3.4683         7.52         5.0E-58 AM26438.1         NT           22648         3.5104         1.34         5.0E-58 AM26438.1         NT           22649         3.5629         1.34         5.0E-58 AM26837.1         NT           22641         3.6608         0.7         5.0E-58 AM26837.1 <td>Probe SEQ ID NO:</td> <td>SEQ ID</td> <td>ORF SEQ ID NO:</td> <td>Expression Signal</td> <td>Most Similar (Top) Hit BLAST E Vetue</td> <td>Top Hit Acession No.</td> <td>Top Hit Detabase Source</td> <td>Top Hit Descriptor</td>	Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vetue	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
14239         27196         3.1         5.0E-68 AW197948.1         EST_HUMAN           17316         30166         0.86         5.0E-68 AR688183.1         EST_HUMAN           18674         32801         0.26         5.0E-68 AR688183.1         EST_HUMAN           18873         32801         0.24         5.0E-68 AR688745.1         EST_HUMAN           18873         32801         0.24         5.0E-68 AL182385.2         NT           20180         33482         0.7         5.0E-68 AL182385.2         NT           20180         33482         0.7         5.0E-68 AL182385.2         NT           20180         33482         0.7         5.0E-68 AL182384.1         NT           20180         33482         0.7         5.0E-68 AR051334.1         NT           20180         33482         0.7         5.0E-68 AR051334.1         NT           20240         35088         0.7         5.0E-68 AR051334.1         NT           20240         36090         1.34         5.0E-68 AR048334.1         NT           22840         36104         1.34         5.0E-68 AR048334.1         NT           22840         36104         1.34         5.0E-68 AR048337.1         NT	1200		L		5.0E-58	AW 797948.1	EST HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
17316         29306         3.85         5.0E-58         AA988183.1         EST_HUMAN           17316         90186         0.96         5.0E-58         AI930745.1         EST_HUMAN           18804         32812         5.97         5.0E-58         H23072.2         EST_HUMAN           18873         32861         1.16         5.0E-58         H23072.2         EST_HUMAN           18673         32862         0.94         5.0E-58         H23072.2         EST_HUMAN           18673         32862         0.97         5.0E-58         AF05133.4.1         NT           20189         33482         0.7         5.0E-58         AF05133.4.1         NT           20240         33625         0.8         5.0E-58         AF05133.4.1         NT           20240         33620         0.7         5.0E-58         AF05133.4.1         NT           20240         33630         1.34         5.0E-58         AF05133.4.1         NT           22648         36104         1.34         5.0E-58         AF05133.4.1         NT           22649         36104         1.34         5.0E-58         AF05133.4.1         NT           22649         37182         0.51         5.	1200				5.0E-58	AW797948.1	EST HUMAN	CMS-UM0043-240300-127-e07 UM0043 Homo sepiens cDNA
17316         30165         6.0E-58         AIGSST45.1         EST_HAMAN           18804         22         5.0E-58         11466282 NT         EST_HAMAN           18804         22         5.0E-58         11466282 NT         EST_HAMAN           18873         32861         6.0E-68         HZ3072.1         EST_HAMAN           18667         32860         0.94         5.0E-58         HZ3072.1         EST_HAMAN           20168         32861         1.16         5.0E-58         AF051334.1         NT           20169         33462         0.7         5.0E-58         AF051334.1         NT           20284         33625         0.7         5.0E-58         AF051334.1         NT           21271         34688         7.52         5.0E-58         AF051334.1         NT           22648         36089         0.76         5.0E-58         AF046837.1         NT           22649         36090         1.34         5.0E-58         AB046837.1         NT           22650         3610         1.34         5.0E-58         AB014511.1         NT           2266         3610         1.34         5.0E-58         AB014511.1         NT           2266	3334			3.85		AAG88183.1	EST_HUMAN	or88e07.81 NCI_CGAP_LLE Homo sepiens cDNA clone IMAGE:1603908 3'
18804         2.2         5.0E-58         11406282         IV           18804         3.22612         5.97         5.0E-58         H23072.1         EST HJMAN           18873         3.2261         5.97         5.0E-58         AFD51334.1         NT           20169         3.2261         1.16         5.0E-58         AFD51334.1         NT           20169         3.3462         0.7         5.0E-58         AFD51334.1         NT           20169         3.3462         0.7         5.0E-58         AFD51334.1         NT           20284         3.3625         0.8         5.0E-58         AFD51334.1         NT           20284         3.36104         1.34         5.0E-58         ABD46837.1         NT           2244         3.6020         0.78         5.0E-58         ABD4681.1         NT           22404         3.6620         1.0         5.0E-58         ABD4681.1         NT           22687         3.7184         0.51         5.0E-58         ABD4681.1         NT           22687         2.01         5.0E-58         ABD4681.1         NT           25694         3.7183         0.51         5.0E-58         ABD4681.1         NT      <	4287			0.95			EST HIMAN	based7xf NCI_CGAP_GC8 Homo sepiens cDNA clone IMAGE:2238468 3' similar to SW:PROZ_ACACA Preset PROFITIN II:
18873         32812         5.97         5.0E-58 H23072.1         EST HJMAN           19697         32860         0.84         5.0E-58 AL163285.2         NT           19697         32861         1.16         5.0E-58 AF051334.1         NT           20169         33462         0.7         5.0E-58 AF051334.1         NT           2024         33462         0.7         5.0E-58 AF051334.1         NT           2024         33625         0.8         5.0E-58 AF051334.1         NT           21271         34683         7.52 E.0E-58 AF051334.1         NT           22644         35025         0.8         5.0E-58 AF046837.1         NT           22648         36109         1.34 E.0E-58 AF046837.1         NT           22649         36109         1.34 E.0E-58 AF046837.1         NT           22640         37181         0.51 E.0E-58 AF046811.1         NT           22640         37181         0.51 E.0E-58 AF046811.1         NT           22666         2504         1.48 E.0E-58 AF04681.1         NT           25667         2747         1.42 A.0E-58 AF052302 NT         NT           13856         25667         2747         4.0E-58 B196251.1         NT           1	6710			22		11496282	Z.	Homo saplens placenta-specific 1 (PLAC1), mRNA
19697         32860         0.94         6.0E-68         AL163285.2         NT           20169         32861         1.16         8.0E-38         AF051334.1         NT           20169         33462         0.7         6.0E-58         AF051334.1         NT           20284         33625         0.8         5.0E-58         AF051334.1         NT           20284         33625         0.8         5.0E-58         AF051334.1         NT           21271         34683         7.52         5.0E-58         AF051334.1         NT           21684         35026         0.78         5.0E-58         AF051334.1         NT           22648         36103         1.34         5.0E-58         AE046837.1         NT           22648         36104         1.34         5.0E-58         AE231227         NT           22648         36104         1.34         5.0E-58         AE04687         NT           22649         36104         1.34         5.0E-58         AE04687         NT           22604         1.34         5.0E-58         AE04687         NT           22604         1.48         6.0E-58         AE04687         NT           25605<	6302	L	32812	597	5.0E-58		J۳	ym51h07.r1 Soares Infant brain 1NIB Homo septens cDNA clone IMAGE:52071 5
19672         32851         1.16         5.0E-38         11421330         NT           20169         33482         0.7         6.0E-88         AF051334.1         NT           20284         33625         0.8         5.0E-88         AF051334.1         NT           21271         34683         7.52         6.0E-88         AF051334.1         NT           22648         36104         1.34         6.0E-88         AB046837.1         NT           22648         36104         1.34         6.0E-88         AB046837.1         NT           22648         36104         1.34         6.0E-88         AB046837.1         NT           22849         36104         1.34         6.0E-88         AB16312.1         NT           23404         36807         1.01         6.0E-88         AB14511.1         NT           23687         37184         0.51         6.0E-88         AB044511.1         NT           25604         1.34         6.0E-88         AL06-88         1142623         NT           25604         1.34         6.0E-88         AL04634         NT         NT           25604         1.48         6.0E-88         11428423         NT	9634		32860	980		2	N.	Hamo sepiens chramosame 21 segment HS210085
20169         33482         0.7         £.0E-58 AF051334.1         NT           20169         33483         0.7         £.0E-58 AF051334.1         NT           20284         33625         0.8         £.0E-58 AF051334.1         NT           21271         34683         7.52         £.0E-58 AB046837.1         NT           22648         36104         1.34         £.0E-58 AB046837.1         NT           22648         36104         1.34         £.0E-58 AB046837.1         NT           22648         36104         1.34         £.0E-58 AB046837.1         NT           22640         36901         1.34         £.0E-58 AB04451.1         NT           23697         37183         0.51         £.0E-58 AB04451.1         NT           23697         1.48         £.0E-58 AB04451.1         NT           25604         1.48         £.0E-58 AB04451.1         NT           25604         1.48         £.0E-58 AB04451.1         NT           25604         1.48         £.0E-58 AB04453.1         NT           25604         1.48         £.0E-58 AB04453.1         NT           13459         26803         1.42         4.0E-58 AG0548         NT           1638 <td>6815</td> <td></td> <td></td> <td>1.16</td> <td></td> <td></td> <td>M</td> <td>Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA</td>	6815			1.16			M	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA
20169         33463         0.7         5.0E-58         AF051334.1         NT           20284         33625         0.8         5.0E-58         4885400         NT           21271         34683         7.52         5.0E-58         8922663         NT           21684         3508         0.76         6.0E-58         AB046837.1         NT           22648         36104         1.34         6.0E-58         6.231227         NT           22648         36104         1.34         6.0E-58         6.231227         NT           23677         3629         1.01         6.0E-58         AB14541.1         NT           23687         37183         0.51         6.0E-58         AB14511.1         NT           23687         37184         0.51         6.0E-58         AB14511.1         NT           25604         1.48         6.0E-58         AB14511.1         NT           25604         2.08         6.0E-58         11428423         NT           25604         1.48         6.0E-58         4604634         NT           13459         2.838         1.48         4.0E-58         4604634         NT           1638         2.8881	6945		33482	0.7	5.0E-58		FA.	Hamo sapiens nibrin (NBS) mRNA, complete cds
20284         33625         0.8         \$.0E-58         4885400         NT           21271         34683         7.52         \$.0E-58         8922663         NT           21684         35088         0.76         \$.0E-58         8922663         NT           22648         36104         1.34         \$.0E-58         \$.03127         NT           22648         36104         1.34         \$.0E-58         \$.03127         NT           22404         36901         1.01         \$.0E-58         \$.01404         NT           23404         36901         1.06         \$.0E-58         AL163218.2         NT           23404         36901         1.06         \$.0E-58         AL163218.2         NT           23404         36901         1.06         \$.0E-58         AL163218.2         NT           23687         37184         0.51         \$.0E-58         AL1436423         NT           25604         1.48         \$.0E-58         11418177         NT           25605         2.08         \$.0E-58         11426423         NT           13459         2.8388         1.42         4.0E-58         4504634         NT           1678	6945		33483	0.7	5.0E-58	AF051334.1	N	Homo sepiens nibrin (NBS) mRNA, complete cds
21271         34683         7.52         5.0E-58         8922663         NT           21684         35088         0.76         6.0E-58         AB046837.1         NT           22648         36104         1.34         6.0E-58         5231227         NT           22648         36104         1.34         6.0E-58         5231227         NT           22640         36901         1.34         6.0E-58         AL163218.2         NT           23687         37183         0.51         6.0E-58         AL163218.2         NT           23687         37184         0.51         6.0E-58         AB01451.1         NT           25604         1.48         6.0E-58         AB01451.1         NT           25604         1.48         6.0E-58         AB01451.1         NT           25604         1.48         6.0E-58         11418177         NT           13459         2.8388         1.48         6.0E-58         11418177         NT           13469         2.8388         1.42         4.0E-58         4503648         NT           16387         2.8388         1.14         4.0E-58         4503648         NT           16387         2.8453 </td <td>7313</td> <td></td> <td>33825</td> <td>0.8</td> <td>5.0E-58</td> <td></td> <td>N<sub>T</sub></td> <td>Homo sepiens holocytochrome c synthase (cytochrome c heme-tyese) (HCCS) mRNA</td>	7313		33825	0.8	5.0E-58		N <sub>T</sub>	Homo sepiens holocytochrome c synthase (cytochrome c heme-tyese) (HCCS) mRNA
21684         35088         0.76         6.0E-58         AB046837.1         NT           22648         38103         1.34         6.0E-58         6231227         NT           22648         36104         1.34         6.0E-58         6.531227         NT           223404         36901         1.01         6.0E-58         4.1430647         NT           23404         36901         1.66         6.0E-58         AL163218.2         NT           23687         .37183         0.51         6.0E-58         AB01451.1         NT           23687         .37184         0.51         6.0E-58         AB01451.1         NT           25604         .217         6.0E-58         AB01451.1         NT           25604         .1.48         6.0E-58         11418177         NT           13450         .26803         1.34         4.0E-58         450263         NT           14887         .27471         1.14         4.0E-58         4503648         NT           16786         .28603         1.11         4.0E-58         106470.1         NT           16787         .28706         1.02         4.0E-58         6031650         NT           2460	8302		34683	7.52			M	Homo sapiens hypothetical protein FLJ10828 (FLJ10828), mRNA
22648         38103         1.34         £.0E-58         £231227         NT           22648         36104         1.34         £.0E-58         £231227         NT           23141         36629         1.01         £.0E-58         £31227         NT           23404         36901         1.66         £.0E-58         AL163218.2         NT           23687         .37183         0.51         £.0E-58         AB01451.1         NT           23687         .37184         0.51         £.0E-58         AB01451.1         NT           25604         .217         £.0E-58         AB01451.1         NT         NT           25605         .277         £.0E-58         AB01451.1         NT         NT           25606         .278         £.0E-58         11428423         NT         NT           25607         .2666         £.0E-58         11418177         NT         NT           13459         .26803         1.42         4.0E-58         4502603         NT           14887         .2771         1.14         4.0E-58         H504634         NT           16788         .28631         1.11         4.0E-58         H504634         NT <td>9696</td> <td></td> <td>35088</td> <td>0.78</td> <td></td> <td>AB0468</td> <td>TN</td> <td>Homo sepiens mRNA for KIAA1617 protein, pertial cds</td>	9696		35088	0.78		AB0468	TN	Homo sepiens mRNA for KIAA1617 protein, pertial cds
22648         36104         1.34         5.0E-58         5231227         NT           23141         36629         1.01         6.0E-58         11430647         NT           23404         36901         1.66         6.0E-58         11430647         NT           23687         . 37183         0.51         6.0E-58         AB014511.1         NT           23687         . 37184         0.51         6.0E-58         AB014511.1         NT           25604         . 1.48         6.0E-58         11428423         NT           25606         . 2.08         6.0E-58         11418177         NT           13459         . 28388         1.85         4.0E-58         4502302         NT           13485         . 26803         1.42         4.0E-58         4504634         NT           14487         . 27471         1.14         4.0E-58         4504634         NT           16786         . 2881         . 2.02         4.0E-58         106470.1         NT           16786         . 28706         1.01         4.0E-58         6031650         NT           24607         . 34454         0.69         4.0E-58         11424059         NT	9696		36103	1.34			LN.	Homo sapiens ribonuclease 8 precursor (RNASE8PL) mRNA
23141         36629         1.01         6.0E-58         11430647         NT           23404         36901         1.66         6.0E-58         AL163218.2         NT           23687         . 37183         0.51         5.0E-58         AB014511.1         NT           23687         . 37184         0.51         6.0E-58         AB014511.1         NT           25604         . 1.48         6.0E-58         11428423         NT         14486           25605         . 2.08         6.0E-58         11418177         NT           13459         28388         1.85         4.0E-58         4502302         NT           13856         26803         1.42         4.0E-58         4504634         NT           13856         26803         1.42         4.0E-58         4504634         NT           16387         28881         2.02         4.0E-58         106473         NT           16786         28603         1.11         4.0E-58         106470.1         NT           16787         28706         1.02         4.0E-58         6031650         NT           24607         38184         7.62         4.0E-58         11424059         NT      <	9895		36104	1.34	5.0E-58		NT	Homo sapiens ribonuclease 6 precursor (RNASE6PL) mRNA
23404         36901         1.66         5.0E-58 AL163218.2         NT           23687         . 37183         0.51         5.0E-58 AB014511.1         NT           23687         . 37184         0.51         5.0E-58 AB014511.1         NT           25604         . 2.17         6.0E-58 AB014511.1         NT           25605         . 1.48         6.0E-58 AB014511.1         NT           25606         . 1.48         6.0E-58 AB014511.1         NT           13459         . 28388         1.86         4.0E-58 AB014511.1         NT           13856         . 26903         1.42         4.0E-58 AB02302 NT         NT           14487         . 27471         1.14         4.0E-58 AB02648 NT         NT           16387         . 28308         1.11         4.0E-58 BB403631.1         NT           16786         . 28706         1.01         4.0E-58 BB463857.1         EST_HUMAN           24607         . 38184         7.62         4.0E-58 BB478597.1         EST_HUMAN           13424         0.84         3.0E-58 R17819.1         EST_HUMAN	10216		36629	1.01	6.0E-58	11430647	F	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
23687         37183         0.51         5.0E-58 AB01451.1         NT           23687         37184         0.61         6.0E-58 AB01451.1         NT           25604         2.17         6.0E-58 AB01451.1         NT           25604         1.48         6.0E-58 T1428423         NT           25605         2.08         6.0E-58 T1418177         NT           13459         28388         1.85         4.0E-58 T402403         NT           13856         26803         1.42         4.0E-58 T402403         NT           14887         27471         1.14         4.0E-58 T402403         NT           16387         28308         1.11         4.0E-58 T40270.1         NT           16387         28706         1.11         4.0E-58 T6310.1         NT           16786         28706         1.02         4.0E-58 T650 NT         ST HUMAN           24607         38184         7.62         4.0E-58 T1424059 NT         ST HUMAN           24607         38184         7.62         4.0E-58 T1724059 NT         ST HUMAN	10482		36901	1.86	5.0E-58	2	NT	Homo saplens chromosome 21 segment HS21C018
23687         37184         0.61         6.0E-68         AB014511.1         NT           25694         2.17         6.0E-58         11426223         NT           25695         1.48         6.0E-58         11418177         NT           13459         26303         1.85         4.0E-58         4502302         NT           13450         26903         1.42         4.0E-58         4504634         NT           14487         27471         1.14         4.0E-58         4504634         NT           15638         26803         1.42         4.0E-58         4504634         NT           15638         26804         1.14         4.0E-58         4504634         NT           16787         27471         1.14         4.0E-58         D16470.1         NT           16788         28706         1.01         4.0E-58         D16470.1         NT           21057         34454         0.69         4.0E-58         E631650         NT           24607         38184         7.62         4.0E-58         E11424059         NT           24607         38184         7.62         4.0E-58         RE483857.1         EST_HUMAN           24507 <td>10766</td> <td></td> <td>. 37183</td> <td>0.51</td> <td>5.0E-58</td> <td>1</td> <td>NT</td> <td>Homo septens mRNA for KIAA0611 protein, partial cds</td>	10766		. 37183	0.51	5.0E-58	1	NT	Homo septens mRNA for KIAA0611 protein, partial cds
26678         2.17         5.0E-58         11526263         NT           256904         1.48         6.0E-58         11428423         NT           25666         2.08         6.0E-58         11418177         NT           13459         26388         1.86         4.0E-58         4502302         NT           13469         26903         1.42         4.0E-58         4504634         NT           14487         27471         1.14         4.0E-58         4503648         NT           16788         28881         2.02         4.0E-58         D16470.1         NT           16785         29706         1.01         4.0E-58         D16470.1         NT           21057         34454         0.69         4.0E-58         E643857.1         EST_HUMAN           24607         38184         7.52         4.0E-58         E1724059         NT           24607         38184         7.62         4.0E-58         E17424059         NT	10768		37184	0.51	6.0E-58	AB014511.1	NT	Homo saplens mRNA for KIAA0811 protein, pertial cds
25904         1.48         6.0E-58         11428423 INT           25665         2.08         6.0E-58         11418177 INT           13459         26308         1.85         4.0E-58         4502302 INT           13856         26803         1.42         4.0E-58         4504634 INT           14487         27471         1.14         4.0E-58         4503648 INT           15638         28681         2.02         4.0E-58 ID6470.1         INT           16787         25308         1.11         4.0E-58 ID16470.1         INT           16785         29706         1.02         4.0E-58 ID16470.1         INT           21057         34454         0.69         4.0E-58 IB468367.1         EST_HUMAN           24607         38184         7.52         4.0E-58 IR17879.1         EST_HUMAN	12352			2.17	5.0E-58		NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
26665         2.08         6.0E-68         11418177         NT           13459         26388         1.86         4.0E-58         4502302         NT           13456         26903         1.42         4.0E-58         4504634         NT           14487         27471         1.14         4.0E-58         4503648         NT           15638         28681         2.02         4.0E-58         D16470.1         NT           16787         26308         1.11         4.0E-58         D16470.1         NT           16786         29706         1.02         4.0E-58         E643657.1         EST_HUMAN           24607         38184         7.52         4.0E-58         R17879.1         EST_HUMAN	12791	]		1.48	6.0E-58		N	Homo sapiens acety-Coenzyme A carboxylase sipha (ACACA), mRNA
13459         26388         1.85         4.0E-58         4502302         NT           13487         27471         1.14         4.0E-58         4504634         NT           15638         28681         2.02         4.0E-58         4503648         NT           15638         28681         2.02         4.0E-58         D16470.1         NT           16785         29706         1.01         4.0E-58         D16470.1         NT           21057         34454         0.69         4.0E-58         BE463857.1         EST_HUMAN           24607         38184         7.52         4.0E-58         R17879.1         EST_HUMAN	13015			2.08	6.0E-68	114	NT	Horno saplens Ran GTPase activating protein 1 (RANGAP1), mRNA
13856         26803         1.42         4.0E-68         4604634         NT           14487         27471         1.14         4.0E-68         4503648         NT           15638         28681         2.02         4.0E-68         D16470.1         NT           16387         28708         1.11         4.0E-68         D16470.1         NT           16705         28708         1.02         4.0E-68         BE483857.1         EST_HUMAN           24607         38184         7.52         4.0E-68         R17879.1         EST_HUMAN           13424         0.84         3.0E-58         R17879.1         EST_HUMAN	373		26388	1.86	4.0E-58		4	Homo sapiens ATP synthasa, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP50) mRNA
14497         27471         1.14         4.0E-68         4503648 NT           15638         28681         2.02         4.0E-58 US6251.1         NT           16387         28308         1.11         4.0E-58 D16470.1         NT           16785         29708         1.02         4.0E-58 D16470.1         NT           21057         34454         0.69         4.0E-58 BE483857.1         EST_HUMAN           24607         38184         7.52         4.0E-58 R17879.1         EST_HUMAN           13424         0.84         3.0E-58 R17879.1         EST_HUMAN	707		26803	1.42	4.0E-68		N.	Homo sapiens interleukin 10 receptor, beta (IL.10RB), mRNA
15638         28681         2.02         4.0E-58 U36251.1         NT           16387         25308         1.11         4.0E-58 D16470.1         NT           16785         29706         1.02         4.0E-58 E3 E43857.1         EST_HUMAN           24607         38184         7.52         4.0E-58 R17879.1         EST_HUMAN           13424         0.84         3.0E-58 R17879.1         EST_HUMAN	1484	14497	27471	1.14	4.0E-58		Į.	Homo sapiens coagulation factor IX (plasma thrombopiastic component, Christmas disease, hemophilia B) (F9) mRNA
16387         29308         1.11         4.0E-58         D16470.1         NT           16785         28708         1.02         4.0E-58         E631650 NT           21057         34454         0.69         4.0E-58         BE463857.1         EST_HUMAN           24607         38184         7.52         4.0E-58         11424059 NT         EST_HUMAN           13424         0.84         3.0E-58         R17879.1         EST_HUMAN	2839	L	28861	202	4.0E-58		N-	Human beta-prime-adaptin (BAM22) gene, exan 3
16796         28708         1.02         4.0E-58         6031690 INT           21057         34454         0.69         4.0E-58         BE463857.1         EST_HUMAN           24607         38184         7.52         4.0E-58         11424059 INT           13424         0.84         3.0E-58 R17879.1         EST_HUMAN	3336	L	29308	1.11	4.0E-68	D16470.1	4	Human mRNA, Xq terminal portion
21057         34454         0.69         4.0E-58 BE463857.1         EST_HUMAN           24507         38184         7.52         4.0E-58         11424059 NT           13424         0.84         3.0E-58 R17878.1         EST_HUMAN	3753		29706	1.02	4.0E-58		¥T	Homo sapiens EGF-like repeats and discoidin Like donains 3 (EDIL3), mRNA
24807 38184 7.52 4.0E-58 11424059 NT 13424 0.84 3.0E-58 R17878.1 EST_HUMAN	8120		34454	0.69	4.0E-58	BE463857.1		hy/8a02x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3197642.3"
13424 0.84 3.0E-58 R17879.1 EST_HUMAN	11671	24607	38184	7.62	4.0E-58		ΛŢ	Homo saplens E18-664Oa essociated protein 5 (E18-AP5), mRNA
	335	13424		0.84	3.0E-58			1910e02.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone INAGE:31693 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor	Homo saplans peptide YY (PYY) mRNA	602185789F1 NIH_MGC_45 Hamp sepiens cDNA dane IMAGE-4308943 5	602185789F1 NIH_MGC_45 Homo septens cDNA clone IMAGE:4308943 57	QV0-BT0702-170400-194-f09 BT0702 Homo sepiens cDNA	HSC1T0081 normalized Infant brain cDNA Homo sepiens cDNA clone c-1tg08	AV712977 DCA Hamo sapiens dDNA clane DCAAZG04 5"	Homo espiens 5-eminolevulinate synthase 2 (ALAS2) gene, complete cds	be08b07.yf NIH_MGC_7 Homo septens cDNA clone IMAGE:2823733 5' stmilar to gb;X89391 605 RIBOSOMAL PROTEIN L6 (HUMAN); db;X81987 M muscatus mRNA for TAX responsive element binding	protein (MOUSE);	xe08a09.xf Sceres_NPL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2567704 3'	601499961F1 NIH_MGC_70 Homo sepiens cDNA clone IMAGE:3901911 5	601499981F1 NIH MGC_70 Homo sapkans dDNA done IMAGE:3901911 5	UHHBW1-ems-g-11-Q-UI,s1 NCI_CGAP_Sub7 Hamo sepiens aDNA clane IMAGE:3071060 3'	am67e02x1 Johnston frontal cortex Homo septents oDNA clone IMAGE:1639674 3' similar to WP-2X328.1 CE65065 UBIQUITIN CONJUGATING ENZYMEN; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM	BINDING PROTEIN;	yq08h06.r1 Soares fetal fiver spleen 1NFLS Homo sepiens cDNA clone IMAGE:196379 57	qm84c01.x1 NCL_CGAP_Lu5 Hamo sapiens cDNA clone IMAGE:18954243'	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds	Homo sapiens endocytic receptor Endo (ENDO 180) mRNA, complete cds	601890812F1 NIH_MGC_17 Homo septens cDNA clone IMAGE:4131891 6	hm26f08.x4 NCI_CGAP_Thy4 Hamo septens cDNA dane IMAGE:3013671.3"	Human complement component C5 mRNA, 3 and	Homo sapiens NADH dehydrogenase (ubiquinane) 1 beta subcomplex, 9 (22AD, B22) (NDUFB9), mRNA	EST368252 MAGE resequences, WAGD Homo sapiens cDNA	EST369262 MAGE resequences, MAGD Homo septens cDNA	Homo saplens partial AF-4 gene, exons 2 to 7 and Alu repeat elements	hy10f08.x1 NCI_CGAP_GC8 Hamo sapiens cDNA clane IMAGE:3198935 3'	Hamo sapiens sterol regulatory element binding transcription factor 2 (SREBF2) mRNA	Homo sapiens chondroitin suffate proteoglycan 2 (versioan) (CSPG2) mRNA	Homo septens chandrattin suffate proteoglycan 2 (versican) (CSPG2) mRNA	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNP4) mRNA
Top Hit Defebase Source		T HUMAN	EST_HUMAN (8	EST HUMAN	EST_HUMAN !	EST_HUMAN A	Г	<b>.</b>	EST_HUMAN P	EST HUMAN X	EST_HUMAN (8	EST_HUMAN 6	EST_HUMAN L		EST HUMAN B		EST_HUMAN	H.	TN T	EST_HUMAN 6	EST HUMAN h	TA T		T_HUMAN	EST_HUMAN E	F	EST_HUMAN h				
Top Hit Acessian Na.	4758981 NT	3.0E-58 BF569848.1	3.0E-58 BF569848.1	3.0E-68 BE089509.1	3.0E-58 F07056.1	3.0E-58 AV712977.1	2.0E-58 AF068624.1		2.0E-58 BE208632.1	2.0E-58 AW074831.1	2.0E-58 BE907188.1	2.0E-58 BE907188.1	2.0E-58 BF513488.1		2.0E-58 AI124874.1	2.0E-68 R92567.1	2.0E-68 AI291407.1	2.0E-68 AF134838.1	2.0E-58 AF134838.1		2.0E-68 AW872641.1	1.0E-68 M85134.1	6274549 NT	1.0E-58 AW957182.1	1.0E-58 AW957182.1		1.0E-58 BE466132.1	4759169 NT	4758081 NT	4758081 NT	4507628
Most Similar (Top) Hit BLAST E Value	3.0E-58	3.0E-58	3.0E-58	3.0E-68	3.0E-58	3.0E-58	2.0E-58		2.0E-58	2.0E-58	2.0E-58	20E-58	2.0E-58		2.0E-58	2.0E-68	2.0E-58	2.0E-68	2.0E-58	2.0E-58	2.0E-68	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58
Expression Signal	232	257	257	19:0	67.0	3,92	8.85		8.41	0.75	3.25	3.25	1.09		1.85	0.83	0.83	2.68	2.68	18.24	1.48	99.0	5.86	2.03	2.03	96.0	98.0	121	1.19	1.19	7.0
ORF SEQ ID NO:	27303	29165	29168	32703	32916	33136	26944			31380	31413	31441	32483		32547	32584	33348	33683	33684	37576	37788	26719	27084	27333	27334	27400	27681	28825	29520	29521	29687
Exan SEQ ID NO:	14424		16248	19458	19647	19851	13882		14320		25638	82952		·	19317	18350	20046	20334	20334	24053	24362	13785	14114	14365	14365	14431	14704			16594	16775
Probe SEQ ID NO:	1380	3183	3183	6390	6587	6797	88		1294	6400	5431	5431	6175		6244	6278	7112	7364	7384	11093	11312	723	<u>\$</u>	1330	1330	1397	1672	2814	3548	3548	3733

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Table 4
Single Exon Probes Expressed in Bone Marrow

Top Hit Top Hit Descriptor Source	ozk3h01.x1 Sogres_NhHMPu_S1 Hamo espiens cDNA clane IMAGE:1678129 3'	RC1-BT0254-280100-015-e01 BT0254 Homo saplens cDNA	Homo sepiens hypothetical protein (LOC51260), mRNA	EST385637 MAGE resequences, MAGM Homo sapiens cDNA	Hamo sapiens myamesin (M-proteth) 2 (165kD) (MYOM2), mRNA	AV751001 NPC Hamo sepiens aDNA dane NPCACH09 5	z1891705.r1 Soeres_testis_NHT Hamo sepiens aDNA clane IMAGE:730497 6"	z189105.r1 Scares_testis_NHT Hamo sepiens cDNA clane IMAGE:730497 5	Homo sepiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA	H.eapiens Immunoglobulin kappa light chain variable region L14	Hamo septens TATA box binding protein (TBP) mRNA	EST96683 Testis I Homo sepiens cDNA 5' end	EST86683 Testis I Homo saplens cDNA 6' end	wh50d08.x1 NCI_CGAP_Kid11 Homo septems cDNA clone IMAGE:23841713'	601458531F1 NIH_MGC_68 Hamo septens aDNA clane IMAGE:3882086 5	om81a04.s1 NCL_CGAP_Kid3 Homo sapiens cDNA clone INAGE:1553550 3' similar to TR-013732 Q13732 SA CENE PRODUCT PRECURSOR.;	on06h02.yt Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn06h02 random	aus3h05.x1 Schneider fetal brain 00004 Homo septens cDNA done IMAGE:2783886 3' similer to TR:075786 075789 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1. ;	au83h05.x1 Schneider fetel brein 00004 Homo sepiens cDNA clone IMAGE:2783865 3' similar to TR:O75786 075786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1. ;	wf48c11.x1 Soares_NRL_T_GBC_S1 Hamo septens aDNA clane BAAGE:2368838 3"	H. saplens DNA for ZNF80-th/ked ERV9 long terminal repeat	Hamo septems alsorin 2 related protein (A2LP), mRNA	au86c07.x1 Schneider febi brain 00004 Homo sepiens cDNA clone IMAGE:2781228 3' similar to contains	Homo septens polymerase (RNA) III (DNA directed) (39(D) (RPC39), mRNA	AV762869 MDS Hamo sablens aDNA clane MDSEIC12 6	Homo saplens hypothetical protein (LOC57143), mRNA	Human mRNA for KIAA0184 gene, partial cds	Homo sepiens phosphetidylinositol 4-phosphete 5-kinese, type II, beta (PIPSK2B) mRNA, and translated products
Top Hit Detabase Source	EST HUMAN	EST HUMAN R		EST HUMAN E		EST_HUMAN A		EST HUMAN Z				EST_HUMAN E	EST_HUMAN E		EST_HUMAN 6	EST_HUMAN S	EST HUMAN		EST HUMAN T	EST HUMAN W	Г				T HUMAN			
Top Hit Acession	1.0E-58 AH41063.1	1.0E-58 BE061860.1	122031	1.0E-58 AW973537.1	4506314 NT	1.0E-59 AV751001.1			11432004 NT		4507378 NT	8.0E-59 AA382291.1	_		_	_	6.0E-69 Af760870.1		-		5.0E-59 X83497.1	TN 8696909	TO TO	JE.		5.0E-59 11434908INT		4505818 NT
Most Similar (Top) Hit BLAST E Value	1.0E-58	1.0E-58	1.06.68	1.0E-58	1.0E-68	1.0E-58	1.0E-58/	1.0E-58	1.0E-58	1.0E-58 X63392.1	8.0E-59	8.0E-59/	8.0E-59/	8.0E-59/	6.0E-59	8.0E-59/	6.0E-89/	5.05-59	5.0E-39/	\$.0E-59/	5.05-59	6.0E-59	10 10	3.0E-50	5 0F-50	50E-50	4.0E-69 [D80006.1	4.0E-59
Expression	5.17	1.18	9.0	0.5	0.59	9.0	0.55	0.55	0.58	2.61	21.09	0.71	0.71	3.74	3.8	9,	99.0	1.19	1.19	7.83	7.38	0.58	3	18.7	18	3.1	322	0.75
ORF SEQ ID NO:	30908	3222	33374		35619						28276	33468	33459			34489	34972		27788	28112	L			35553				
Ean SEO ID NO:	18020	19027	20068	21420	22187	22238	22400		1	24942	16252	20141	20141	1	1	i	24558	14797	14797	16201	17708	18888		10475	22007	24206	13863	1 1
Probe SEQ ID NO:	9009	ğ	8	245	1228	8883	9438	9436	10548	12068	882	7015	315	8824	178	9151	8898	1788	1788	3144	4687	200		2 2	3 8	11283	ğ	1242

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Single Exon Probes Expressed in Bone Marrow

Single Exon Probes Expressed in Bone Marrow	ORF SEQ Expression (Top) Hit Acession Detablese ID NO: Signed Vatue	Homo septens phosphatidy/inositol-4-phosphate 5-kinase, type II, beta (PIPSK2B) mRNA, and translated (78 27240 0.75 4.0E-59 4505818 NT products	31888 1.04 4.0E-59 11034810 NT	77 38576 1.8 4.0E-59 7657428   MT Hamo sapiens origin recognition complex, subunit 6 (yeast homotog)-like (ORCKI), mRNA	2.98 4.0E-59 AF057720.1 NT	6.8 3.0E-59 AW986524.1 EST_HUMAN	28250 4.47 3.0E-59 7682247 NT	27738 11.42 3.0E-59 4505880 NT	27739 11.42 3.0E-59 4505860 NT	28171 6.05 3.0E-59 AB028035.1 NT	28172 6.05 3.0E-69 AB028035.1  NT	29/16 2.91 3.0E-50 4502014 NT	29117 2.91 3.0E-59 4502014 NT	29781 1.26 3.0E-59 4508044 NT	30628) 1.4 3.0E-59/AL163284.2 (NT	30785 1.66 3.0E-69 7427522 NT	1.05 3.0E-59M85981.1 NT	32656 1.98 3.0E-59 8924074 NT	33906 2.12 3.0E-69 6464137 NT	34642 1.5 3.0E-59 X12556.1  NT	34643 1.5 3.0E-59 X12556.1 NT	36809 0.84 3.0E-69 X70251.1  NT	36810 0.84 3.0E-59 X70251.1  NT	1.37 3.0E-59 11417886 NT	7.97 3.0E-59 11417888 NT	32268 0.82 2.0E-59 BF508383.1 EST_HUMAN	32269 0.82 2.0E-59 BF508383.1  EST_HUMAN	0.61 2.0E-69 AA470073.1 [EST_HUMAN	33307) 0.57 2.0E-59 AF135187.1 NT	0.52 2.0E-59 BF373329.1 (EST_HUMAN	4.9 2.0E-59 AA309774.1 EST HUMAN	138 1.55 2.0E-59/BF385554.1 EST HUMAN (RCD-NT0036-100700-032-807 NT0036 Homo sepiens c.DNA
		14278 2724	18711 3186		25810	13130	13327 2625	14753 2773		15156 2817		16203 2911	16203 2911		17732 3062		101	19415 3265						219	311		19070 3228	20202	20007 3330	21019	22822	23813
	Probe Exon SEQ ID SEQ ID NO: NO:	1242 142	5615 187	12107 24977	12482 258	1	228 133	1723 147	1723 14753	2139 151		١			,	4878 178	5091 18101		7684 20646	8263 21232	8263 21232	10404 23326	10404 23326	12470 252		L		6079 202	7272 200			10893
	E D Z	L			-				Ľ						Ĺ										Ľ			Ĺ				[

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Top Hit Descriptor Source			EST_HUMAN   ffto7h04.x1 NIH_MGC_17 Homo saplens cDNA clone IMAGE-2961854 5		EST HUMAN CROOKE KIVILH PROTEIN, CONTRINS LIKY, REPORTIVE GERMENT;	_	EST_HUMAN 601178757F1 NIH_MGC_17 Homo sepiens cONA clone IMAGE:3531927 5	Os66h11.s1 NCI_CGAP_GCB1 Homo sepiens cDNA clone IMAGE:1309029 3' similar to TR:Q13597	ESI JUMAN CIONI MANDI TONINI COMPLETI CONTROLLO CONTROLL	٦		HUMAN	Homo saplens zho finger protein 275 (ZNF275), mRNA	Homo sepiens 3-hydrasylsobutyny-Coenzyme A hydrolese (HIBCH), mRNA	Homo sepiens 3-hydroxylsobutyny-Coenzyme A hydrotese (HIBCH), mRNA	Homo saplens mRNA for transcription factor	EST_HUMAN   EST389849 MAGE resequences, WAGO Homo sapiens cDNA	Homo saplens smell nuclear ribonucleoprotein D3 polypeptide (184D) (SNRPD3) mRNA	Homo saplens differentiation-related gene 1 (nickel-specific Induction protein) (RTP) mRNA	Homo sepiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA	Homo septens mRNA for KIAA1081 protein, partial cds	Prehamen-binding protein-hepetocyte growth factor ectivator homolog litumen, pleame, mRNA, 2408 ntl	Homo sepiens phosphate cylidylytransferase 1, choline, beta isoform (PCYT1B), mRNA	Human mRNA for integrin elpha-2 subunit	Homo saplens S-antigen; retina and pineal gland (arrestin) (SAG), mRNA	Homo saplens KIAA0433 protein (KIAA0433), mRNA	Homo sepiens KIAA0433 protein (KIAA0433), mRNA	Homo sapiens RAN binding protein 7 (RANBP7), mRNA	Homo seplens chromosome 21 segment HS210004	Homo saplens chromosome 21 segment HS210004	Homo saplens MHC class 1 region	Homo saplens MHC class 1 region	Homo saplens interleukin 10 receptor, beta (IL10RB), mRNA	Homo sapiens cultin 4A (CUL4A) mRNA, complete cds
	_	EST	EST	100	3	호	EST	For	3	Ž	EST		NT	FN (	Z	M	EST	TN.	INT	N.	토	5	토	호	E	E	Ĕ	토	호	Ę	Ę	¥	Ę	Ę
Top Hit Acessian		2.0E-59 AW410698.1	2.0E-59 AW410698.1	7 (00700)	20E-69 Al631809.1	L11645.1	1.0E-59 BE286411.1	4 OF ED 4 4 7 4 9 4 9 4	W/ 40400.1	1.0E-59 AJ130894.1	1.0E-59 BE256814.1	1.0E-59 BE256814.1	11419830 NT	11428849 NT	11428849 NT	1.0E-59 AJ130894.1	8.0E-60 AW977845.1	4759159 NT	5174656 NT	5174656 NT	8.0E-60 AB029004.1	8 0E-80 S83 182 4	11420841 NT	8.0E-60 X17033.1	11428049 NT	- 11417118 NT	11417118 NT	5453997 NT	8.0E-60 AL163204.2	8.0E-60 AL163204.2	7.0E-60 AF055066.1	7.0E-60 AF055068.1	4504634 NT	7.0E-60 AF077188.1
Most Similar (Top) Hit BLAST E	Velue	2.0E-59	2.05-59	20.0	20E-59	2.0E-59	1.0E-59	02 20 0	1.05-03	1.05-59	1.0E-59	1.0E-59	1.05-59	1.05-59	1.0E-59	1.0E-59	8.05-60	8.0E-60	8.0E-60	8.0E-60	8.0E-60	8.05-60	8.0E-80	8.0E-60	8.0E-60	8.0E-60	8.05-80	8.0E-80	8.0E-60	8.0E-60	7.0E-60	7.0E-60	7.0E-60	7.0E-80
Expression Signal		234	2.34	1	8.98	4.02	18.92	8	9.08	1.18	1.07	1.07	0.85	0.54	0.54	98.6	229	2.85	265	2.66	0.94	1 04	0.89	237	288	12	1.2	0.68	4.65	4.65	30.34	69.13	1.17	1.04
ORF SEQ ID NO:						31428				34137	34319	34320	36222	38351	36352	34137	26768	27474	28217	28218	32389	32987	34285	34679	35687	36130		37873		37671	26760	26760	26822	28170
SE CONTRACTOR		24136	24136	3	20128	25836	13267	1007	B	(Q) (Q)	20825	20825	22768	22890	22890	20761	13824	14500	15197	15197	19173	19740	20803	21267	22257	22875	22675	23858	24138	24138	13816	13816	13874	15155
Probe SEQ ID		11180	11180		2873	12884	164	368	8	312	7988	7986	97/40	8983	<b>3966</b>	11201	784	1467	2182	2482	6094	96653	7962	8828	1608	8838	9288	10038	11182	11182	755	758	816	2138

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gie CAUI FILUDOS L'Aprosoci il cuito manchi	Top Hit Descriptor	Homo sapiens mRNA for KIAA0581 protein, partiel cds	Homo sepiens antiffine decarbacylase 1 (ODC1) mRNA	Homo sapiens ALR-like protein mRNA, partial cds	yr 204 r.f. Soeres fetal liver spicen 1NFLS Homo sapiens cDNA clone IMAGE: 205097 5' similar to contains. LTR5 repositive element;	y12704.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains	LTR5 repetitive element;	601658751R1 NIH_MGC_69 Homo sepiens cDNA done IMAGE:3886069 3"	Homo saplens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA	yg78h09.11 Soares fetal liver spleen 1NFLS Homo sapiens oDNA clone IMAGE.201963 5' similer to contains OFR repetitive element;	w152c07.x1 Sceres_NPL_T_GBC_S1 Hamo septens cDNA clane IMAGE-2359212.3	W152c07.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE-2359212.3	HF-BN0-ekt-g-07-0-UI.r1 NIH_MGC_60 Hamo septems cDNA clane IMAGE:3078348 5	UI-HF-BNO-ekt-g-07-0-UI.r1 NIH_MGC_50 Hamp sepiens aDNA dane IMAGE:3078348 5"	ST11498 Uterus Homo sapiens cDNA 5 end similiar to similar to retrovirus-related pol	hreft05x7 NCI_CGAP_KM11 Homo espiens cDNA clans IMAGE:3134913 3' shnifer to SW:RHOP_MOUSE Q61085 GTP-RHO BINDING PROTEIN 1;	Homo sapiens chromosome 21 segment HS21C078	Homo sapiens v-raf-1 murine leukernia viral oncogene homotog 1 (RAF1), mRNA	Homo sapiens v-raf-1 murine leutkernia viral oncogene homolog 1 (RAF1), mRNA	601336448F1 NIH_MGC_44 Hamo sepiens cDNA clane IMAGE:3690395 5	601336446F1 NIH_MGC_44 Home septens cDNA clone IMAGE:3680395 57	Homo sepiens prohibitin (PHB) mRNA	Homo saplens Xq pseudoautosomal region; segment 1/2	QV4-NN1149-250900-423-f01 NN1149 Hamo saplens cDNA	RGS-LT0023-200100-012-401 LT0023 Hamo sapients GDNA	d60H11.y6 NG_CGAP_Ktd3 Homo septens cDNA clone IMAGE:1534053 5' similar to SW:UDP_MOUSE	PEXIZA URIDINE PHOSPHORMASE;	Homo sapiens proline dehydrogenase (proline caddase) (PRODH) mRNA	Homo septens proline dehydrogenase (proline addase) (PRODH) mRNA	occida x1 Soares_Nih MiPu_S1 Homo sepiens cDNA clone IMAGE:1660337 3' shrilar to SW:FORM_MOUSE Q05860 FORMIN;	Homo sepiens protine dehydrogenase (proline coddase) (PRODH) mRNA
AUI FIUMS L	Top Hit Detabese Source	NT.		T.	EST HUMAN L	T	EST_HUMAN	T HUMAN		EST HUMAN	EST_HUMAN V	EST_HUMAN V	EST_HUMAN	EST HUMAN I	EST HUMAN		Г			T HUMAN	T HUMAN		П		EST HUNAN		T HUMAN			T_HUMAN	
Siligie	Top Hit Acession No.	7.0E-60 AB011153.1	4505488 NT	7.0E-60 AF284750.1	7 0F-80 H58041.1		7.0E-60 H58041.1	6.0E-60 BE964974.2	11421735 NT	6.0E-60 H52456.1	5.0E-80 AI807917.1	5.0E-60 AI807917.1	4.0E-80 AW 603208.1	4.0E-60 AW 503208.1	4.0E-60 AA299037.1	4.0E-80 BF196068.1	4.0E-60 AL163278.2	11433697 NT	11433597 NT	3.0E-80 BE562811.1	3.0E-60 BE562611.1	6031190 NT	3.0E-80 AJ271735.1	3.0E-60 BF365143.1	3.0E-60 AW836196.1		3.0E-60 AI792814.1	6174844 NT	5174844 NT	3.0E-60 Al040235.1	5174844 NT
	Most Similar (Top) Hit BLAST E Vatue	7.0E-60	7.0E-60	7.0E-80	7.05-80		7.0E-80	6.0E-80	6.0E-60	6.0E-80	5.0E-80	5.0E-60	4.0E-80	4.0E-80	4.0E-60	4.0E-80	4.0E-80	4.0E-80	4.0E-80	3.0E-60	3.0E-80	3.0E-60	3.0E-80	3.0E-80	3.0E-60				3.0E-60		3.0E-60
	Expression Signal	1.18	3.1	0.72	9.6	3	1.57	1.01	0.68	8.33	1.13	1.13	1.26	1.25	1.31	180	0.59	1.7	1.7	4.44	4.44	1.88	227	2.11	2.11		0.95	6.22	522	0.58	42
	ORF SEQ ID NO:	28806	30124	30519	4,53	3	38236		34483		26123	28124	28284	1_		20007		38127			27901		30308	31465			31263	35135	L	<u> </u>	35485
	Eggn SEQ ID NO:	15788	1	1_	<u> </u>	1_		15204	L	1	1.	1	1	1_	Ì_	1	1_	L		١.	1_	14910	17510	18554	18818	1_	18375	21713	L	l	Ш
	Probe SEQ ID NO:	2786	4208	4606	2000	3	11602	2180	8156	8780	2	2	2244	2244	2884	7678	888	11628	11628	1876	1876	- 1885	4485	5462	5724		7143	8746	8745	888	8

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rigie Exon Probes Expressed in bone Marrow	Top Hit Descriptor	601646227F1 NIH_MGC_60 Homo sapiens cDNA done IMAGE:3930690 5	ab07n04.r1 Stratagene lung (#837210) Homo sepiens cDNA cione IMAGE:840151 5' stratier to conteins LTR10.t1 LTR10 repetitive element;	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product	H. sapiens 41kDa protein kinase related to rat ERK2	Human bor protein mRNA, 5' end	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product	RC1+HT0288-031289-012-f02 HT0268 Homo saplens cDNA	Homo saplens interleukin 17 receptor (IL17R), mRNA	EST390114 MAGE resequences, MAGO Homo sapiens oDNA	Homo sapiens waf murine sarcoma viral oncogene homolog B1 (BRAF) mRNA	Homo seplens chromosome 21 unknown mRNA	UHHBW1-emis-e-05-0-UI.s1 NCI_CGAP_Sub7 Hamo sepiens cDNA clane IMAGE:3070852 3'	nn01ft12.y5 NCI_CGAP_Co9 Homo sepiens cDNA done IMAGE:1078486 5 striller to contains THR.tf THR	lepeauve etenenii.; Homo sanlans pro-alpha 2(1) callanan (CO) 142) cena camplais cda	Fernica-prince To Tape and Tape and Tape To Ta	Homo sapiens conflictroon releasing homone receptor 2 (CRHR2) mRNA	Homo sepiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA	EST181949 Jurkat T-cells V Homo saplens cDNA 5' end similar to similar to profflymosin, aighte	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to profrymosin, alpha	tb23409.x1 NCI_CGAP_Kid12 Homo septiens cDNA done IMAGE:2056185 3' similar to SW:GALR_RAT_ Q62805 GALANIN RECEPTOR;	UHH-BW1-emu-c-02-0-UI.s1 NCI_CGAP_Sub7 Homo sepiens cDNA clone IMAGE:3071210 3'	HS15BEST human adult teetis Homo sepiens CDNA done CAM_tEST16	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphortn) 6A (SEMAGA), mRNA	Homo septens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 9A (SEMAGA), mRNA	CARO-CT0013-290698-017-ft3 CT0013 Homo sepiens cDNA	CM0-CT0013-290639-017-ft3 CT0013 Homo sepiens cDNA
xon Probes Ex	Top Hit Database Source	EST_HUMAN 60	est_HUMAN LT	o¥I LN	F.	₩ F	H H	EST_HUMAN RC		EST_HUMAN ES		<u>오</u>	EST_HUMAN UF		EST HUMAN TOP				EST_HUMAN ES	EST_HUMAN ES		EST HUMAN UF	П	Г			EST_HUMAN CN	EST_HUMAN CA
alguic	Top Hit Acession No.	3.0E-60 BF102612.1	3.0E-60 AA485286.1	2.0E-60 AY008285.1	2.0E-60 Z11694.1	2.0E-80 M24603.1	2.0E-60 AY008285.1	2.0E-60 AW380450.1	57229	2.0E-60 AW978005.1	4757867 NT		2.0E-60 BF513458.1		2.0E-80 AI/91832.1		83044	4503044 NT	2.0E-60 AA311159.1		2.0E-60 Al308124.1	2.0E-60 BF512808.1			11991659 NT	11891659 NT	Į.	П
	Most Similar (Top) Hit BLAST E Value	3.0E-60	3.0E-60	2.0E-60	2.0E-60	2.0E-80	2.0E-80	2.0E-60	2.0E-60	2.0E-60	2.0E-60	2.0E-60	2.0E-80	0000	20190	200	205-80	20E-80	2.0E-80	2.0E-60	2.0E-80	2.0E-80	2.0E-60	2.0E-60 L36033.1	2.0E-60	2.0E-60	2.0E-60	2.0E-60
	Expression Signal	0.42	1.53	1.7	2.70	1.34	1.01	1.78	1.38	0.94	1.49	0.83	0.65		8,0	2 8	205	2.05	9.9	8.6	0.53	1.08	1.09	4.86	22	22	1.9	1.9
	ORF SEQ ID NO:	38411		20054	27428	27747	27758	28520	28637	28733	29557	29889		-	32074	76337	31279	31280	33630	33631	33756		34722	35618	36740	36741	38561	38562
	SEQ ID NO:	22944	25871	13163	14454	14784	14773	15495	15612	16716	16637	16975	17182	9	1000	10077	18359	18359	20288	20288	20401	20837	21307	22185	23281	23281	24985	24985
	Probe SEQ ID NO:	10017	12970	83	1421	1734	1743	2492	2814	2721	3592	3835	4161	3	3 5 5 5	2774	7027	7027	7317	7317	7434	788	8338	8218	10337	10337	12094	12094

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Top Fit	Top Hit Descriptor	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 6' flanking region and partial ods	Homo sapiens similar to HSPC0122 protein (H. sapiens) (LOC83504), mRNA	Hanio sapiens gene for AF-8, camplete ads	PM3-HT0805-270200-001-e06 HT0805 Hamo sepiems aDNA	AU143389 Y79AA1 Homo septems cDNA clone Y78AA1001854 5'	Homo sapiens chromosome 21 segment HS21C085	RC4-BT0311-141199-011-N06 BT0311 Homo septens cDNA	inco4e12.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.t1 L1 conceillus element	AVTEANST TO Home seniors CDNA clone TPGAED05 6	THAT CALL TENDENCE AND A CONTROL TO THE CONTROL OF	AUTISS44 NEMBAT Hand SEPTEMBAT CARE NEMBAT LOUGOS O	Homo saplens PHD finger protein 2 (PHF2) mrdNA	Homo sepiens PHD finger protein 2 (PHF2) mRNA	WIDSD10x1 NOLCGAP_Cos Homo septems cDNA clone IMAGE-2508555 3'	105510x1 NCL_CGAP_Cc3 Hamo sapiens cDNA clone IMAGE-2508555 31	Human endogenous retrovirus pHE 1 (ERV9)	n58g06.st NCI_CGAP_Lart Hamo sapiens cDNA clane IMAGE:1088218 3'	ys12e09.r1 Soares fetal liver episen 1NFLS Homo sapiens cDNA clone IMAGE:214600 5' similar to SP:C40H1.1 CE00109 OVARIAN PROTEIN ;	ys12e09.r1 Soares fetal liver spleen 1NFLS Homo sepiens dDNA clone IMAGE:214600 5 similar to	H. CAMPILL CONTROL TO THE TABLE	Trans septem ranco process (ranco), sinava	FIGURE SERVICE FANCED, INTO SERVICE FANCED SERVICES	601300838F1 NIH MGC ZI Homo sapiens CLYA CICHE IMAGE 303348U 0	601300938F1 NIH MGC 21 Hamo sapiens G.MA dame IMAGE:3635480 b	Hamo sapiens PRO2014 mRNA, complete cds	601108238F1 NIH_MGC_16 Homo septens cDNA clone IMAGE:3350145 5	m88h09.s1 NCL_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:10888973'	Homo segiens soutre carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product	AU130689 NT2RP3 Hamo sepiens cDNA clone NT2RP3001263 5	ig-beta/B23=CD79b (alternatively spliced) [human, B cells, mRNA Partial, 375 m]	Human autosomal dominant polycystic (ddney disease protein 1 (PKD1) gene
Top H≢t	Database Source		N.			EST_HUMAN			EST_HUMAN	NAMIN TOT	T		HOWAN			EST_HUMAN	EST_HUMAN		EST_HUMAN	EST HUMAN		- HOMEN			П	EST HUMAN			EST_HUMAN	Į.	EST HUMAN	NT	NT
	No.	11418192 NT	2.0E-80 AF088757.1	11418068 NT	2.0E-80 AB011399.1	1.0E-80 BE178588.1	1.0E-60 AU143389.1	1.0E-60 AL163285.2	1.0E-80 BE084410.1	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1.0E-00 AAZ44041.1	1.0E-00/AV/34061.1	9.0E-61 AU119344.1	4885546 NT	4885546 NT	8.0E-81 AW006478.1	8.0E-81 AW008478.1	X57147.1	8.0E-61 AA583968.1	171226.1		- 11	1706870 N	1/0/88/0//	6.0E-61 BE408310.1	G.0E-61 BE409310.1	6.0E-61 AF119860.1	8.0E-61 BE257400.1	6.0E-61 AA596033.1	6.0E-61 AY008285.1	6.0E-61 AU130689.1	6.0E-61 S79249.1	6.0E-61 U24498.1
Most Similar		2.0E-80	2.0E-80/	2.0E-60	2.0E-80/	1.0E-80	1.0E-60/	1.0E-80	1.0E-80	10 1	1.0E-00/	1.05-001	9.0E-81/	9.0E-61	9.0E-61	8.0E-81	8.0E-61	8.0E-61 X57147.1	8.0E-81	8.0E-81 H71225.1		8.0E-51 H/1220.1	7.0E-61	7.0E-81	8.0E-61	8.0E-61	6.0E-61	8.0E-61	8.0E-81	6.05-61	8.0E-64	6.0E-61	8.0E-81
· .	Signal	1.38	1.82	18.9	2.38	78.0	1.48	1.34	0.98		8 8	8	1.85	0.48	0.46	1.17	1.17	1.00	87.0	1.47	1	1.47	0.67	. 0.67	261	2.17	13.5	6.0	2.32	0.91	8.07	3.08	1.83
C I	D NO:					26512	20873	30896	l			30000	27095	35450	35451	28694			34604	38400		38401	1				L		27682	284/80	L	32452	}
Exam	SEQ ID	25330	25800	25411	25421	13594	169630	18008	21249		20074	20122	14145	22027	22027	15674	15674	16020	21186	24807	Į.	- (	13234	13234	13361	13870	14359	14666	14687	15154	46370	L	Ш
Probe	SEQ ID	12847	12771	12773	12789	223	3920	498 888	8280		8 3	22	1101	1908	<b>1</b> 908	2878	2878	2862	8227	11926		11926	138	128	285	812	1324	1834	1655	782	3317	6147	7565

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	Top Hit Descriptor	Hamo sapiens general transcription factor 2-4 (GTF2) mRNA, complete cds	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA	Homo septens protein phosphetase 1, regulatory subunit 10 (PPP1R10) mRNA	Homo saplens chromosome 21 segment HS21C079	Hamo sepiens 959 lib config between AML1 and CBR1 on chromosome 21q22; segment 1/3	AU140307 PLACE2 Hamo sepiens cDNA clone PLACE2000302 6	Homo septens DKFZP588B023 protein (DKFZP588B023), mRNA	AV731140 HTF Hamo sapiens aDNA clane HTFARB01 6"	AF150190 Human mRNA from od34+ stem cells Homo sapiens cDNA cione CBDAGB04	Hamo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA	QV2-HT0513-060400-147-401 HT0513 Homo sepiens cDNA	QV3-HT0513-060400-147-d01 HT0513 Homo septens cDNA	yx53d11.s1 Soares fetal Inver spisen 1NFLS Homo sapiens cDNA clone IMAGE:246453 3' similar to	gb:L25444 60S RIBOSOMAL PROTEIN L35A (HUMAN);	yy03f11.r1 Scares melanooyla 2NbHM Homo sapiens cDNA done IMAGE:270189 5	Homo septens ATPase, H+ transporting, tysosomal (vacuolar proton pump) non-catalytic accessory protein	1A (110/116/O) (ATPGN1A), mRNA	AV694317 GKC Hamo septems cDNA clane GKCEL G06 5	Homo sapiens mRNA for KIAA0536 protein, partial cds	UHTF-BNO-ekd-f-12-0-UI1 NIH_MGC_50 Hamp sepiens cDNA dane IMAGE:3076774 5	Homo sapiens polymenase (RNA) III (DNA directed) (39kD) (RPC39), mRNA	Homo sapiens ribosomal protein L44 (RPL44), mRNA	QV0-BN0042-170300-162-f10 BN0042 Hamo septens cDNA	Homo sapiens chromosome 21 segment HS21C003	Homo sapiens origin recognition camplex, subunit 2 (yeast homolog)-like (ORC2L) mRNA	Human polymorphic trinucleotide repeat in X-finked retinitis pigmentosa (RP3) gene region	Homo sapiens zona pellucida gi)coprotein 3A (sperm receptor) (ZP3A), mRNA	xn11b09.y1 NCI_CGAP_LI5 Homo septens cDNA clone IMAGE:2683369 6' similar to contains element MSB1 receitting element.	MINTER STREET WILL AND ON Home continue a INNA above INNACE SERVERY FO	VITZ/3613F1 NIT MIGG ZU FIGHT SEDIENS CLINA CICTE IMMUSE.301460/ 5	Homo septens KJAA0808 gene product (KJAA0806), mrtna	Human monoantine coldase A (MAOA) mRNA, complete cds	Homo sepiens TRAF family member-essociated NFKB activator (TANK) mRNA
	Top Hit Deleberse Source					NT	NT N	EST_HUMAN /		EST_HUMAN	EST_HUMAN_		EST HUMAN			EST_HUMAN	EST_HUMAN			T_HUMAN	¥	EST_HUMAN			EST_HUMAN	. TA				147.61	Т	HOMAN			
	Top Hit Acessian No.	AF035737.1	8922990(NT	TN 0662298	4506008 NT	5.0E-61 AL163279.2		1	4.0E-61 7661637 NT		3.0E-61 AF150190.1	TN 6282288	2.0E-61 BE168410.1						11426168 NT	AV694317.1	2.0E-61 AB011108.1	2.0E-81 AW500258.1	11421778 NT	11419729 NT	AW995328.1	AL163203.2	5453829 NT	1.0E-61 U32657.1	TN 6905909	7	AW02/201.1	BE386363.1	682319		4769249 NT
	Most Similar (Top) Hit BLAST E Value	6.0E-81	SOE-61	5.0E-81	5.0E-61	50E-81/	5.0E-61	4.0E-61	4.0E-61	4.0E-61	3.0E-81	20E-81	20E-91	20E-61		2.0E-61 N53039.1	2.0E-61 N39397.1		2.0E-61	20E-81	2.0E-61	2.0E-81	2.0E-81	2.0E-61	2.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61		10-20:1		1.0€-91	1.0E-61	1.0E-81
	Expression Signal	1.87	1.14	1.14	3.18	1,96	1.87	1.17	0.51	227	0.65	1.74	3.4	3.4		1.34	1.25		0.92	1.07	1.27	1.61	2.88	6.91	1.39	1.85	98.0	96.0	4.69		1.02	1.58	0.87	1	1.02
	ORF SEQ ID NO:	34189	26246	28247	27699	20020		27.788	32190		35154	26463	27213	27214		27684		<u> </u>	32891	35785		36692	37031		31701		26778		27899	1	18241	28831	28363	30198	30381
	SEQ ID	20822	13321	13321	14719	16106	17045	14803	18999	25143	21731	13571	14256	14255		14706	15646		19628	22334	22741	23207	23534	24183	26583	13509	13833	14813	14900		225	15906	16436	17317	17494
ſ	SEQ SEQ S	7878	ষ্ট	X	1688	8	<del>4</del> 008	1774	<b>59</b> 13	12348	8764	480	1217	1217		1674	2849		9999	6966	888	10282	10012	11230	13042	435	774	1784	1875		8	2846	3387	4288	4468

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Table 4
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ngie Exon Probes Expressed in bone marium	Top Hit Descriptor	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA	Homo sepiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA	Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA	Homo sepiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA	Homo sepiens eukaryotic translation hittetion factor 2B, subunit 2 (beta, 3910) (EIF2B2), mRNA	Homo sepiens 265 protessame essociated ped1 homolog (POH1), mRNA	Homo sepiens mRNA for KIAA1263 protein, partial cds	H.sepiens flow-sorted chromosome 6 Hindlll fragment, SC8pA16D3	H.sapiens flow-corted chromosome 6 Hindll  fragment, SC8pA16D3	df58g04.y1 Martan Fetal Cochlea Hamo sepiens cDNA clane IMAGE:2487751 5	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA	Hamo sepiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA	Homo sapiens calcineum binding protein 1 (KIAA0330), mRNA	Homo sapiens calcineum binding protein 1 (KIAA0330), mRNA	Hamo sepiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sepiens neurofibromin 2 (blisteral accustic neuroma) (NF2) mRNA	Homo sepiens mRNA for KIAA1476 protein, partial cds	Homo sepiens mRNA for KIAA1476 protein, partial ods	Human cyclophilin-related processed pseudogene	wa33f04.xt NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2288803 3' similar to contains THR.t2 TUD provether clonest:	I in reportation with the second MSM COSA		EST178374 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5 end	RC0-BN0284-800500-031-e05 BN0284 Homo sepiens cDNA	RC0-BN0284-300500-031-e05 BN0284 Homo saplens cDNA	Homo sapiens mannosidase, beta A, tysosomal (WANBA) gene, and ubiquitin-contugating enzyme E2D 3	(UBE2D3) genes, complete cds	QV4-BT0257-081189-017-e03 BT0257 Hamo septens cDNA	Homo sepiens intersectin 2 (SHXIO1B) mRNA, complete ods	Homo sapiens ADP/ATP carrier protein (ANT-2) gens, complete cds
Xon Propes E	Top Hit Defebase Source									INT	EST_HUMAN								N	NT	M	Natur Tora	NAMOE IS	Ž		EST_HUMAN			뒫	T_HUMAN	N	٤
albuix	Top Hit Acession No.	4606978 NT	11420654 NT	11421041 NT	7857057 NT	7857057 NT	11429973 NT	4.0E-62 AB033089.1			4.0E-62 AW023559.1	11418088 NT	11418192 NT	11418322 NT	11417862 NT	11417862 NT	11430460 NT	4557794 NT	1	3.1	G2858.1		3.0E-62/Ai632/33.1	2.0E-62 AL163284.2	2.0E-82 AA307490.1	2.0E-62 BF329911.1	2.0E-62 BP329911.1		2.0E-62 AF224869.1	2.0E-62 BF330678.1	1.0E-62 AF248540.1	78810.1
	Most Similar (Top) Hit BLAST E Vetue	4.0E-62	4.0E-82	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62 Z78768.1	4.0E-62 Z78786.1	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62	3.0E-82	3.0E-62	3.0E-82	3.0E-62 X52858.1		3.05-62/	205-62	2.0E-82	20E-82	20E-62		2.0E-62	2.0E-62	1.0E-62	1.0E-62
	Expression Signal	1.63	2.53	208	269	259	0.93	585	3.05	3.05	1.57	3.39	1.3	1.86	18.77	19.77	3.07	0.68	1.02	1.02	3.52		3. 3.	278	0.68	4.47	4.47		4.96	20.5	1.88	12.74
	ORF SEQ ID NO:	32318	32748	33696	34219	34220	34893	36594	37830	37831	38083	38176		31706	31703	31704	31717	26114	29029	29030					34470	35520		ļ			27044	
	SEQ ID	19115	(9/495	20347	20839	20839	21479	22184	24303	24303	24536	25090	25803	25505	25500	<u></u>	L	13192	16116	16116	16755	L_	- 1		21079	22088	Ł		23465		14091	14580
	Probe SEO ID NO:	6032	6428	7377	7898	7896	8511	9188	11353	11363	11598	12287	12491	12871	12924	12924	12877	76	3050	3059	3712		888	1235	8142	9127	8127		10533	11996	1045	1547

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Single Exon Probes Expressed in Borre Marrow	Top Hit Descriptor	Hamo sepiens manoamine addase A (MAOA), nuclear gene encoding mitochandrial protein, mRNA	Homo sapiens (L2-inducible T-cell kinase (ITK), mRNA	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds	Galtus galtus Dach2 protein (Dach2) mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C068	wm55g11.x1 NCI_CGAP_Ut2 Hamo septens cDNA clane IMAGE:2439908 3'	nc6s102.ri NCL CGAP_PH Hano sepiens cDNA done IMAGE:745947 similar to gb:Y00361 603 RIBOSOMAL PROTEIN (HUMAN);	Hamo sapiens G protein-coupled receptor 51 (GPR51), mRNA	Hamo sapians chranosome 21 segment HS21C078	Homo sapiens mRNA for KIAA0707 protein, pertial cds	Homo sapiens mRNA for KIAA0707 protein, partial cds.	CM2-BT0595-190100-072-a09 BT0595 Homo septens aDNA	CM3-BT0595-160100-072-e09 BT0595 Hamo septens cDNA	UI-H-Bi1-abq-e-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens dDNA clone IMAGE:2712482 3'	UI-H-BI1-abq-e-02-0-UI.s1 NCI_CGAP_Sub3 Homo septens aDNA clane IMAGE:27124823"	2184b01.s1 Sceres_bests_NHT Homo sepiens cDNA clone IMAGE:744649 3' similar to contains L1.t1 L1 necessities element:	Homo seniens mRNA for KIAA0717 protein, pertial cds	Human Met-dRNA-1 gene 1	Homo sapiens zinc finger protein 144 (Mel-18) (ZNF144), mRNA	Homo sepiens hepetboelhular carcinoma antigen gene 620 (LOC63928), mRNA	601485656F1 NIH_MGC_69 Hamo sapiens aDNA alane IMAGE:3888253 5"	01485656F1 NIH_MGC_69 Homo sepiens dDNA dane IMAGE:3888253 5	Human DNA topoisomerase I mRNA, partial cds	Homo sepiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA	Homo sepiens gutamata-cysteine ligase (gamma-glutamylcysteine synthetase), catalyfic (72.84D) (GLCLC)	MRNA	Homo sepiens Down syndrome candidate region 1 (DSCR1), mRNA	Homo sepiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cas	Homo sepiens RHCE mRNA for Rh blood CE group antigen paypeptide, complete as	601301627F1 NIH MGC 21 Hame capiens a INA dens IMAGE:3636103 5	Hamo sapiens chranosome 3 subekamenc region
Xon Probes E	Top Hit Dafathese Source					NT	EST_HUMAN V	EST_HUMAN F		NT . TN	NT.	Į.	EST_HUMAN		EST_HUMAN	EST_HUMAN	CCT LIBIAN	7				T_HUMAN	EST_HUMAN							$\neg$	T HUMAN	Į.
Single	Top Hit Acession No.	4557734	5031810 NT	8.0E-63 AF198349.1	8.0E-63 AF198349.1		7.0E-68 AI872137.1	ı	11526484 NT	4.0E-63 AL163278.2	4.0E-63 AB014607.1	4.0E-63 AB014807.1	4.0E-63 AW 750372.1	4.0E-63 AW7503721	4.0E-63 AW134709.1	4.0E-63 AW 134709.1	1 000000	4.0E-62 AAGCS000.1	Innato 1	AND FOR INT	11545810 NT	BE876158.1	3.0E-63 BE876158.1	2.0E-63 U07804.1	4885226 NT		4557624 NT	7657042 NT	2.0E-63 AB030388.1	2.0E-63 AB030388.1	2.0E-63 BE410739.1	2.0E-63 AF109718.1
	Most Stmilar (Top) Hit BLAST E Value	8.0€-63	8.0E-63	8.0E-83/	8.0E-63	8.0E-63	7.0E-88 /	6.0E-63/	5.0E-63	4.0E-63	4.0E-83	4.0E-63/	4.0E-63	4.0E-63	4.0E-83	4.0E-63	20,	3000	S OF AR	200	3.05-88	3.0E-63	3.0E-63	2.0E-63	2.0E-63		2.0E-63	2.0E-63	2.0E-63	2.0E-63	2.0E-63	2.0E-63
	Expression Signal	1.1	2.49	3.42	3.42	3.76	1.67	22.22	0.63	0.7	1.18	1.16	2.82	2.02	2.12	2.12	,	84.1	4 BK	- 14 - 29 - 4	32.29	0.51	0.51	1.91	1.91	,	3.06	1.7	4.18	4.18	1.33	277
	ORF SEQ ID NO:	28382	28416	29443	29444	30203			35822		28764	28785	32917	32918				Seven		20102	32954	38460	36461					26838		27578	Ш	29271
	Exam SEQ ID NO:	15360	15391	16521	16521	17323	13982	18515	22192	16383	16861	16861		1	24410	24410			L	70/01	_L_	L	L		13300		13570	13885		14602	Ш	16351
	Probe SEQ ID NO:	2354	2383	3475	3475	4294	88	6412	8228	3332	382	388	888	888	11467	11467		13023	3 25	7	<b>3 3 3 3 3 3 3 3 3 3</b>	10084	1006	8	88		88	128	1569	1569	1781	3288

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Probe SEQ ID	Ean SEQ ID	ORF SEQ	Expression	Most Similar (Top) Hit	Top Hit Acession	Top Hit Detabese	Too Hit Descriptor
Ö	Ö	Ö Q	Signer	BLASTE Value	o Z	Source	
3926	16965	29878	3.64		2.0E-63 L39891.1	ᅜ	Hamo sepiens palycystic Iddney disease essociated protein (PKD1) gene, camplete cds
<b>199</b>	17818	30810	98'0		2.0E-63 AF111167.2	<u> </u>	Homo sapiens jun dimertzstion protein gene, partial cds; cfos gene, complete cds; and unknown gene
5188	18197				2.0E-63 BE146928.1	EST_HUMAN	QV4HT0222-011199-018-g01 HT0222 Homo sapiens cDNA
5232	18240	31112	1.59	2.0E-63	6912617 NT	N	Homo sapiens glutaminyf-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA
5334	25835	31192	0.57	2.05-63	11410429 NT	¥	Homo sepiene similar to ectorucleotide pyrophosphalasse/phosphodiesterese 3 (H. sepiens) (LOC83214), mRNA
9889	19071		2.49		2.0E-63 BF373641.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sepiens cDNA
9869	19071	32271	2.49		2.0E-83 BF373541.1	EST_HUMAN	QV1-FT0170-040700-285-005 FT0170 Homo sepiens cDNA
6310	19381	32820	88.0	2.0E-63	11421940 NT	Ŋ	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6310	18381	32821	0.83	2.0E-63	11421940 NT	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
							Human germline T-cell receptor beta chain Doparnine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3,
0989	19913		1.23	2.0E-83	2.0E-63 U66059.1	TN	ICKBVBS/P, ICKBV/SSAZI, ICKBVISSZAII, ICKBVBSZAZPI, ICKBV/SZAINAI, TCRBVISSB/ISS
6911	19963	33259	0.81	2.0E-63	2.0E-63 AB032369.1	NT	Homo sapiens MIST mRNA, pertial cds
6911	19963	33260	1870	2.0E-63	2.0E-63 AB032369.1	IN	Homo sapiens MIST mRNA, partial cds
7278	20012	. 33315	1.48		8910365 NT	NT	Homo sapiens Cerbonic anhydrase-related protein 10 (LOC56834), mRNA
7278	20012		1.48			IN	Homo sapiens Cerbonic anhydrase-related protein 10 (LOC56934), mRNA
8028	20885	34391	0.82		2.0E-63 AB046844.1	NT	Homo sapiens mRNA for KJAA 1624 protein, pertial cds
8878	21845	29292	3.8		2.0E-63 AL163210.2	NT	Hamo sapiens chramosame 21 segment HS21C010
9409	22374		1.08		11420849 NT	TN	Homo sepiens kinesh family member 3B (KIF3B), mRNA
9400	22374	35811	1.06		11420949 NT	NT	Homo septens kinesin family member 3B (KIF3B), mRNA
10289	23224	38707	0.98	2.0E-63	2.0E-63 AL163218.2	MT	Homo sapiens chromosome 21 segment HS21C018
11088	24058	37582	13.74		2.0E-63 N78945.1	EST HUMAN	zb18b05.s1 Sceres fetal Jung NbHL19W Homo sepiens cDNA clone IMAGE:302385 3' similer to cocx17208 40S RIBOSOMAL PROTEIN S4 (HUMAN);
11127	24087	37614	232		2.0E-83 AF099810.1	Т	Homo esplens neuredn III-alpha gene, pertial cds
11127	24087	37615	2,32	2.0E-63	2.0E-63 AF089810.1	NT	Homo sapiens neurewin III-alpha gene, pertial cds
12381	25747	31515	8.02	2.05-63	11418185 NT	NT	Homo seplens accritiase 2, mitochondriai (ACOZ), mRNA
1515	14647	27518	0.93	1.0€-63	1.0E-63 F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo septens cDNA clone o-zvd11
1515	14547	27519	6 <b>6</b> 0	1.0E-63	1.0E-63 F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4370	17397	30278	3.4	1.0E-83	1.0E-63 F08485.1	HUMAN	HSCZVD111 normalized infant brain cDNA Homo sepiens cDNA clone c-zvd11
4370	17397	30277	3.4	1.0E-63		I_HUMAN	HSCZVD111 normalized infant brain eDNA Homo sapians cDNA clone o-zvd11
5428	18529	31408	1.08	1.0E-63	1.0E-63 AJZ71736.1	¥	Homo sapiens Xq pseudoautosomal region; segment 2/2

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Single Exon Probes Expressed in

gle Exon Probes Expressed in Bone Marrow	Top Hit Descriptor	QV0-ST0215-060100-083-509 ST0215 Homo sapiens cDNA	UHHBI3-ath-02-0-Ui.s1 NCI_CGAP_Sub5 Homo sepiens aDNA clane IMAGE-3088783 3"	U.H.H.BI3.eft.h.02.0-UI.s1 N.CI_CGAP_Sub5 Hamo sepiens aDNA clane IMAGE:3088763 3"	Homo sapiens chromosome 21 segment HS21CO47	Hamo sepiens chranosame 21 segment HS21 0007	UIHIF-BK0-ead-b-09-0-ULr1 NIH_MGC_36 Homo saplens cDNA clone IMAGE:3053153 6	tm50b07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161525 31	601155232F1 NIH_MGC_21 Hamo septens cDNA clone IMAGE:3138038 5	601508968F1 NIH_MGC_71 Hamp septems aDNA dane IMAGE:3910336 5	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA	yb88b02.r1 Strategene lung (#837210) Hamo sepiens cDNA clane IMAGE:78179 5	601311455F1 NIH_MGC_44 Hamo sepiens aDNA dane IMAGE:3833204 5	Homo saplens thimet oligopeptidase 1 (THOP1) mRNA	Homo saplens thimet oligopeptidase 1 (THOP1) mRNA	Homo sapiens IQ motif containing GTPese activating protein 1 (IQGAP1) mRNA	Homo sapiens EWS, gar22, mp22 and barn22 genes	w651607.x1 NCI_CGAP_GC8 Hamo seplens cDNA clone IMAGE:2309220 3° similar to gb:M15182 BETA- GLUCURONIDASE PRECURSOR (HUMAN);	wb51e07.xt NCI_CGAP_GC8 Homo septems cDNA done INAGE:2339220 3' similar to gb:M15182 BETA-	COCCONDANG TRECORSON (TOWNS)	wv13e03.x1 NCI_CQAP_Brr23 Hamo sapiens cDNA clane IMAGE-2529436 3'	wv13e03.x1 NCI_CGAP_BmZ3 Homo septens cDNA clone IMAGE_2529436 31	Homo sapiens MCP-1 gene and enhancer region	Homo sapiens MCP-1 gene and enhancer region	Homo sapiens protetn kinase C befa-II type (PRKCB1) mRNA, complete cds	Homo sapiens calcitonin receptor (CALCR), mRNA	Homo sapiens calcitonin receptor (CALCR), mRNA	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA	Homo sapiens acetyl-CoA synthetase (LOC55802), mRNA	Homo sapians progressive ankylosis-like protein (ANK) mRNA, complete cds	thic (human, brain, mRNA, 2715 nt)	Homo sepiens stromal antigen 3 (STAG3), mRNA	Homo sapiens stromal antigen 3 (STAG3), mRNA
kon Probes Ex	Top Hit Detabase Source	Ħ	EST_HUMAN  UI	EST_HUMAN  U	NT TA	NT TN	EST_HUMAN UI	EST HUMAN TO	EST HUMAN 60	T_HUMAN		EST_HUMAN   yb	T_HUMAN				¥	EST_HUMAN G	T	7	HUMAN	EST HUMAN W	H	Ŧ										
Single E	Top Hit Acession No.	1.0E-63 AW 682268.1 E	1.0E-63 AW451950.1	1		1.0E-63[AL163207.2 [N	9.0E-64 AW401433.1 E	9.0E-64 AJ478186.1	8.0E-64 BE280796.1	8.0E-64 BE885755.1 E	18177		1.1	4507490 NT	4507490 NT	4506786 h		6.0E-64 Al651992.1		1	1	6.0E-64 AW026445.1 ·   E			M3975.1	11422189 NT	11422189 NT	11525879 NT	11525879 NT	11420565 NT	6.0E-64 AF274753.1	378475.1	11420197 NT	11420197
	Most Similar (Top) Hit BLAST E Vatue	1.0E-63	1.0E-83/	1.0E-63	1.0E-63	1.0E-63/	9.0E-64	9.0E-64	8.0E-64	8.0E-64	8.0E-64	8.0E-64 T80651.1	7.0E-64	7.0E-84	7.0E-64	7.0E-64	7.0E-84 Y07848.1	6.0E-64		6.0E-64 /	8.0E-64	8.0E-84	6.0E-64 Y18933.1	6.0E-64 Y18933.1	6.0E-64 M13975.1	6.0E-64	6.0E-64	6.0E-64	8.0E-64	6.0E-64	6.0E-64	6.0E-64 S76475.1	6.0E-64	6.0E-64
	Expression Signal	97.84	0.72	0.72	2.94	5.18	99.0	4.61	2.71	3.25	822	2.63	9.0	3.2	32	0.0	4.78	3.88		3,86	4.25	4.25	2.43	2.43	6.33	0.71	0.71	2.85	2.85	7.07	1.78	2.44	4.48	4.48
į	ORF SEO ID NO:	32140	32855	32856			32370	34579		32569	-			30678	30679	34430	36794	27748		27749	29105	29108	31973	31974	31888	32200	32210	33764	33785	36091	36254	36473	37605	37606
ļ	Exan SEQ ID NO:	18953	19594	19594	24783	25859	19159	21169	14094	18336	25034	25070	16586	17783	17783	21032	23315	14765		14765	16186	16196	18798	18788	18819	19015	19015	20412	20412	22635	22800	23003	24081	24081
	Probe SEQ ID NO:	5864	8534 1	6531	8816	13020	82028	8199	<b>\$</b>	6263	12187	12239	3540	4763	4763	808	10303	1736		1735	3139	3139	6703	5703	5725	6289	2828	7448	7446	2888	<b>888</b>	10076	11121	11121

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		WAGE:25294363'	WAGE 2529436 3'			•					VA, pertial cds		E:3944397 5	•		NNA clone GEN-569E02 5'	₹.3943 <i>577 6</i>				ONA clone IMAGE:3073161 5"		complete cds	complete cds	E:3047975 5' similar to gb:L08069 DNAJ	E:3047975 5' similar to gb:L08069 DNAJ			Ą	A		AAGE:1031151 3'	
	Top Hit Descriptor	wr13e03.x1 NCI_CGAP_Brn23 Hamo sepiens dDNA clane IMAGE:2529436 St	wv13e03.x1 NCI_CGAP_Bm23 Hamo sepiens dDNA clone IMAGE.2529436 3'	Homo sepiens interleukin 10 receptor, beta (IL10RB), mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unionown mRNA	Homo sepiens mRNA for KIAA0903 protein, partial ods	Human I(3)mbt protein homolog mRNA, complete ods	Hamo septens KIAA0618 gene product (KIAA0618), mRNA	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA	Homo sapiens putative transcription factor CR63 (CR63) mRNA, pertial cds	Homo sepiens mRNA for KIAA0908 protein, pertial cds	80150382F1 NIH_MGC_7 Homo sepiens cDNA clone IMAGE:3944397 5	RC3-ST0197-120200-015-003 ST0197 Homo sepiens cDNA	RC3-ST0197-120200-015-803 ST0197 Homo sepiens cDNA	C18895 Human placenta cDNA (TFujiwara) Homo sapians cDNA clone GEN-569E02 6	601539565F1 NIH_MGC_7 Homo eaplens cDNA clone IMAGE:3943577 6	AV711714 DCA Hamo sapiens cDNA clone DCAAMC01 57	AV711714 DCA Homo sapiens oDNA done DCAAMC01 5	H.sapiens isoform 1 gene for L-type calcium channel, exon 28	UHHF-BP0p-eix-c-05-0-ULr1 NIH_MGC_51 Homo sepiens cDNA clone IMAGE:3073161 57	RC8-FN0019-280600-011-G11 FN0019 Homo septens cDNA	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds	bb7zh12.y1 NIH_MGC_12 Hamo sapiens cDNA clone IMAGE:3047975 5' sImilar to gb:L08069 DNAJ  PROTEIN HOMOLOG 2 (HUMAN);	bb72tf12.y/ NIH_MGC_12 Hamo sepiens cDNA clone IMACE:3047975 5' similar to gb:L08069 DNA. PROTEIN HOMOLOG 2 (HUMAN);	Homo sepiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	EST389483 MAGE resequences, MAGO Homo sepiens cDNA	EST389483 MAGE resequences, MAGO Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS210027	af08408.s1 Scares_tastis_NHT Homo sapiens cDNA clone IMAGE:1031151 3	Homo sapiens el F4E-like cap-binding protein (4EHP) mRNA
مالات محمد المحم مالات	Top Hit Database Source	EST_HUMAN	EST_HUMAN	Ν	NT	NT	NT	NT	M	NT	Ϋ́	Ŋ	EST_HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Ŋ	EST HUMAN	EST_HUMAN	NT	NT	EST HUMAN	EST HUMAN	M	K	EST HUMAN	EST_HUMAN	Mī	EST_HUMAN	N.
Culbino.	Top Hit Acession No.	8.0E-64 AW026445.1	6.0E-64 AW026445.1	11526198	5.0E-64 AF231919.1	6.0E-64 AF231919.1	5.0E-64 AB020710.1	5.0E-64 U89358.1	7662205 NT	7862205 NT	5.0E-64 AF017433.1	5.0E-64 AB020710.1	4.0E-84 BE794607.1	4.0E-64 AW813783.1	4.0E-64 AW813783.1	C18895.1	3.0E-64 BE794381.1	3.0E-64 AV711714.1	3.0E-84 AV711714.1	226273.1	3.0E-64 AW500881.1	3.0E-64 BF370000.1	3.0E-64 AF248953.1	3.0E-64 AF248953.1	3.0E-64 BE206521.1	3.0E-64 BE206621.1	2	2	7	3.0E-84 AW977384.1	3.0E-64 AL163227.2	2.0E-64 AA609940.1	4757701 NT
	Most Similar (Top) Hit BLAST E Value	6.0E-64	6.0E-64	6.0E-84	5.0E-64	5.0E-64	5.0E-64	5.0E-64	5.0E-64	5.0E-64	5.0E-64	5.0E-64	4.0E-84	4.0E-64/	4.0E-64	3.0E-64 C18895.1	3.0E-64	3.0E-64	3.0E-84	3.0E-64	3.0E-84	3.0E-84	3.0E-64/	3.0E-64	3.0E-64	3.05-64	3.0E-64 /	3.0E-64	3.0E-64/	3.0E-84	3.05-84/	2.0E-64 /	2.0E-84
	Expression	1.73	1.73	97.6	3.66	3.66	0.03	1.7	3.52	3.52	7.14	0.93	0.57	1.66	1.55	6.32	0.72	1.85	1.85	1.35	0.64	278	1.78	1.78	273	2.73	1.54	1.54	8.0	80	1.87	0.95	1.2
	ORF SEQ ID NO:	29105	9016Z	31818	26829	26830	27345	27740	27483	27484	29834	30053	34460	37650	37651	28243	29244	29422	29423	32508	32786	32975	36201	35202	35225	35226	36177	36178	36278	36279	38471	27086	27401
	SEQ ID NO:	16196	16196	25172	13879	13879	14378	14754	14509	14509	17023	17164	24062	24122	24122	15223	16322	16503	16503	19274	19540	19699	21778	21778	21807	21807	22723	22723	22825	22825	24876	14134	14432
	Probe SEQ ID NO:	11358	11358	12398	82	821	1341	1724	2837	2837	3983	4132	8425	11164	1108	2208	3288	3457	3457	6200	6475	6641	6088	8808	. 8840	8840	9782	9782	9872	9872	11898	1090	1398

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	Ταρ Hit Descriptor	we87b01x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2462281 3' similar to contains element. L1 repetitive element;	Hamo saptens chramosame 21 segment HS210046	Hamo sapians chromosome 21 segment HS210046	EST370215 MAGE resequences, MAGE Homo sepiens cDNA	EST3702/16 MAGE resequences, MAGE Homo sapiens cDNA	AU124387 NT2RM2 Hamo sepiens aDNA clane NT2RM2002113 5	Homo sapiens englopoletin 4 (ANG4) mRNA, partial cds	602123474F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:4280395 5	or29603.x1 Sceres, total fetus_Nb2HFB_BW Homo septens aUNA done tward=16/6/1/3	H.sapians dopamine receptor D5 pseudogene 1, partial cds	Homo sepiens ataxin 2-binding protein 1 (A2BP1), mRNA	QV1-HT0413-010200-059-h12 HT0413 Homo sepiens cONA	Homo septens lymphocyte cytosotic protein 1 (L-plastin) (LCP1), mRNA	Homo sapiens lymphocyte cytosotic protein 1 (L-plastin) (LCP1), mRNA	Homo sapiens hypothetical protein SBBi67 (LOC57115), mRNA	AU132570 NT2RP4 Homo sapiens cDNA clane NT2RP4000109 5	2042882F1 NCI_CGAP_Bm67 Homo septens cDNA clone IMAGE:4180556 6	wn81b08x1 NCI_CGAP_Ut1 Hamo sapiens cDNA clone IMAGE:2462211 3	wn81b08.x1 NCL_CGAP_Ut1 Hamo septens cDNA clane IMAGE-2452211 3"	601185078F1 NIH_MGC_8 Homo septens cDNA done IMAGE:3542822 5	1185078F1 NIH_MGC_8 Homo septens cDNA clone MAGE:3542822 5	Homo saplens period (Drosophila) homolog 3 (PER3), miQNA	CHR220101 Chromosome 22 evan Hamo sepiens cDINA crane C22_132 5	Homo sepiens chromosome 21 unknown mRNA	ausoco1x1 Schneider fetal brain 00004 Homo sapiens cONA cione IMACE-2519136 3' similier to db:1.21696 .cds.1 PROTHYMOSIN ALPHA (HUMAN);contains element MSR1 repetitive element;	Homo saplens synaptojanin 1 (SYNU1), mRNA	Homo sepiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein,	JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaplophysin genes,	complete cds; and L-type calcium channel a>	Homo sepiens TRIAD3 mRNA, pertial cds	Homo sepiens TRIAD3 mRNA, pertial cds	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mKNA
igle Exult Flobes Express	Top Hit Databese Source	EST_HUMAN L1	FN FN	NT He	EST_HUMAN ES	EST HUMAN ES	T_HUMAN	ヿ	T	EST_HUMAN 02	H		T_HUMAN				EST_HUMAN A	П		EST_HUMAN W		EST HUMAN 60		T HUMAN	¥	EST HIMAN OF			<u>5</u>				
Siligio E	Top Hit Acession No.	2.0E-64 Al927030.1	2.0E-64 AL163246.2	2.0E-64 AL163246.2	1	1				1	2.0E-64 M77185.1	11431054 NT	2.0E-64 AW606785.1	11434008 NT	11434008 NT	11423508 NT	2.0E-84 AU132570.1	2.0E-84 BF528114.1				2.0E-64 BE269660.1	3567387		1.0E-64 AF231919.1	1 0F-84 A1979419 1	207334			1.0E-64 AF198779.1			TN 6232268
	Most Similar (Top) Hit BLAST E Vatue	2.0E-64/	2.0E-84	2.0E-84	20E-84	2.0E-84	2.0E-64	2.0E-64	2.0E-84	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-84	20E-84	2.0E-64	2.0E-84	2.0E-84	2.0E-64	2.0E-84	2.0E-64	2.0E-84	2.0E-64	2.0⊑-64	1.0E-64	1 0F.84	10E-64		_	1.0E-64	1.0E-64	1.0E-64	1.0E-64
	Epression Signal	206	3.13	3.13	29.0	0.67	22	1.38	4.02	1.5	3.88	0.57	0.58	5.60	5.69	0.43	96.0	3.74	4.59	4.59	1.89	1.89	1.47	3.64	1.48	CH 7.P	0.81			5.73	1.38	1.38	2
	ORFSËQ ID NO:		28560	28561	29748	29749	32424	32681	32969	33080	33208	34442		35400	35401	35899			37866	37867	38301	38302	31844		26279	20026				29492	29962	29563	29870
	Exan SEQ ID NO:	15533		L	<u> </u>	16841	19189	19438	19690	19800	19912	L		_	<u> </u>	L	1.	L	24337	24337		24716	Z15Z	8883	13355	44072		L		16568	16643		16957
	Probe SEQ ID NO:	888	2536	2538	3801	3801	6121	6370	6632	8745	6885	818	8164	9016	8016	9485	9896	11114	11391	11391	11833	11833	12316	12744	258	į	\$0.24			3522	3598	3598	3917

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Destabase Source	Top Hit Descriptor
10424		38831	0.68	1.0E-64	1.0E-64 AA042975.1	EST_HUMAN	2463008.s1 Scares_pregnant_uterus_NbHPU Homo septems cDNA clone INAGE:4865673
12288			2.03	1.0E-64	1.0E-64 AL163246.2	N.	Homo saplens chromosome 21 segment HS21C046
2284		12882	1.64	9.0E-65	9.0E-65 X89211.1	IN	H.sapiens DNA for endogenous retroviral like element
2284	15297		1.64	9.0E-66	9.0E-66 X89211.1	MT	H. sapiens DNA for endogenous retroviral like element
11863	24745		36.25	9.0E-65	9.0E-65 BF330678.1	EST_HUMAN	QV4-BT0257-081189-017-e03 BT0257 Homo saplens cDNA
11837	24720	38305	12.7	8.0E-65	8.0E-66 A1929244.1	EST HUMAN	eu58h07x1 Schmelder fetal brain 00004 Homo saplens cDNA done IMAGE:25100053' similar to SW:RLZ1_HUMAN P46778 60S RIBOSOMAL PROTEIN L21.:
10515	23437	36836	2.13	7.0E-65	7.0E-65 BE081653.1	EST HUMAN	QV2-BT0635-240400-162-c02 BT0635 Homo septens cDNA
1059	14105		2.73	6.0E-65	6.0E-65 AV721898.1	EST_HUMAN	AV721898 HTB Hamo sapiens cDNA clone HTBBZC09 5
1938	14962		12.23	6.0E-65	6.0E-65 AA560829.1	EST_HUMAN	nj86410.s1 NCI_CGAP_P11 Homo sepiens cDNA clone IMACE:988379 similer to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
6721	19777	33056	0.87	6.0E-65	6.0E-65 AA503892.1	<b>EST_HUMAN</b>	nh37b07.s1 NCI_CGAP_Pr5 Homo septems cDNA clone IMAGE:954517
9606	22064	35489	2.49	6.0E-85	6.0E-85 AW083252.1	EST_HUMAN	xx07b09x1 NCI_CGAP_Co21 Homo sepiens cDNA clone IMAGE:2583545 3' similar to TR:Q63308 Q63308 LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORF'S. ;contains L1.b2 L1 repetitive element;
8365	22330	35759	4.16	8.0E-85	8.0E-85 AA427878.1	EST HUMAN	zw53b08.s1 Soares_total_fetus_Nb2HF8_9w Homo sepiens cDNA clone IMAGE:773747 3'
8365		85760	4.18	8.0E-86	8.0E-86 AA427878.1	EST_HUMAN	ZW53b08.s1 Scares_total_fetus_Nb2HF8_9w Homo sepiens cDNA clone IMAGE:773747 3'
9429	22383	35832	1.08	8.0E-85	6.0E-65 A1085314.1	EST_HUMAN	qf18h05x1 NCI_CGAP_Bm25 Homo saplens cDNA clone IMAGE:17504253*
9429		35833	1.08	6.0E-85	6.0E-65 Al085314.1	EST_HUMAN	qf18h05x1 NCI_CGAP_Bm25 Homo seplens cDNA clone IMAGE:17504253'
11220			2.59	8.0E-65	6.0E-65 BE567816.1	EST_HUMAN	601340485F1 NIH_MGC_63 Hamo septens cDNA dane IMAGE:3682877 67
11378			1.51	8.0E-85	6.0E-65 BF340825.1	EST_HUMAN	602037721F1 NCI_CGAP_Bm64 Hamo saplens cDNA clone IMAGE:4183677 5
1825	_1	38294	1.8	6.0E-85	6.0E-85 AL163210.2	F	Homo sapiens chromosome 21 segment HS21C010
835		26617	1.92		AF06460	된	Homo sapiens KE03 protein mRNA, partial cds
1355		27359	122	5.0E-85		F	Homo sepiens KIAA0156 gene product (KIAA0156), mRNA
1355	14390	27360	122	5.0E-65	7881951 NT	¥	Homo saplens KIAA0156 gene product (KIAA0156), mRNA
28		28200	1.61	6.0E-85	5.0E-65 AB033768.1	N	Homo sapiens hPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
3269		29245	. 2.18	5.0E-65		NT	Homo saplens ubiquitin specific protesse 13 (iscreptidase T-3) (USP13) mRNA
3269		29246	2.13	5.0E-85		NT	Homo eaplens ubiquitin specific protesse 13 (tscpeptidase T-3) (USP13) mRNA
7052		33381	1.18	5.0E-85	4504606 NT	NT	Homo saplens interferon-related developmental regulator 1 (IFRD1), mRNA
10833		37253	1.28	5.0E-85	5.0E-65 AF009668.1	M	Multiple scienceis associated retrovirus polyprotein (pol) mRNA, partial cds
<del>2</del> 8	13296	26224	2.33	4.0E-65	4.0E-65 AL120419.1	EST_HUMAN	DKFZp781G108_r1 761 (synonym: hamy2) Homo sepiens cDNA clone DKFZp781G108 5
747	13808	26748	1.29	4.0E-65	4.0E-65 A1266468.1	EST_HUMAN	qm48e01.x1 Soares_placenta_8b08weeks_2Nb+P8b08W Homo sepiens cDNA done IMAGE:1891800 3*

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Single Exon Probes Expressed in Bone Marrow

		≅1891800 3″															ription factor								ntains element			ntains element		(A), mRNA	
Top Hit Descriptor		qm46e01.x1 Scares_placenta_8to9weeks_2NtHP8to9W Homo sepiens cDNA clone IMAGE:1891800 3'	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA	Homo sapiens ribosomal protein L34 (RPL34) mRNA	RC2-BN0033-160200-013-e03 BN0033 Homo septens cDNA	Homo sapiens mRNA for KIAA1267 protein, partial cds	Homo sapiens mRNA for KIAA1267 protein, partial cds	Hamo sepiens axysteral binding protein-related protein 3 (ORP3) mRNA, complete ads	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats	Hamo sapiens hypothetical protein FL/22087 (FL/22087), mRNA	Human 3',5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds	Human 3',5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds	Human MAP kinase kinase 6 (MKK6) mRNA, complete cds	Homo saplens nel (chicken)-like 2 (NELL2), mRNA	Homo sapiens nel (chicken)-tike 2 (NELL2), mRNA	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA	Homo sapiens WEE1 gene for protein Idnase and pertial ZNF143 gene for zinc finger transcription factor	AV738764 CB Hamo sapiens cDNA done CBCCBE05 67	Homo saplens PRO1474 mRNA, complete cds	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA	DKFZp761G108_r1 781 (synanym: hamy2) Hamo sapiens cDNA clane DKFZp761G108 5	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA	Homo sepiens pre-B-cell colony-enhancing factor (PBEF) mRNA	H.sapiens HZF9 mRNA for zinc finger protein	ov2303.s1 Scenes_testis_NHT Homo sapiens cDNA cione IMAGE:1638173 3' stratiar to contains element.	Homo servines mRNA for KTAA0235 protein partial cds	Homo sapiens faminin, beta 1 (LAMB1), mRNA	ACTABLE AS CAME DE HE MAT Home canions of NA chara MACE 1838173 S' challer in contains element	MSR1 repetitive element;	Homo sapiens rabb GTP asse activating protein (GAP and centrosome-essociated) (GAPCENA), mRNA	601479686F1 NIH_MGC_68 Homo saplens cDNA clone IMAGE:3882405 5
Top Hit Database Source		EST_HUMAN	KT	. !	EST_HUMAN	N	NT	NT	NT	KT	M	NT	NT	Z	F	¥	IN	EST HUMAN	¥	¥	EST_HUMAN	IN	NT	NT	NYFU GT LOO	ESI HUMAN			EST_HUMAN	N.	EST_HUMAN
Top Hit Acessaron No.		4.0E-65 AI286468.1	4826735 NT	4506636 NT	4.0E-65 AW 993185.1	4.0E-65 AB033083.1	4.0E-65 AB033083.1	4.0E-65 AY008372.1	M19879.1	11545780 NT	140372.1	140372.1	J39656.1	5453765 NT	6463766 NT	11429127 NT	4.0E-86 AJ277548.2		4.0E-65 AF119846.1	4826735 NT	4.0E-65 AL120419.1	5031976 NT	5031976 NT	C78932.1		3.0E-65 All000882.1	TANDADED INT	The same	3.0E-65 A1000692.1	6912385 NT	3.0E-65 BE787366.1
- III	varue	4.0E-85	4.0E-65	4.0E-65	4.0E-65/	4.0E-65 /	4.0E-65 /	4.0E-65	4.0E-65	4.0E-65	4.0E-65 U40372.1	4.0E-65 U40372.1	4.0E-65 U39656.1	4.0E-65	4.0E-65	4.0E-65	4.0E-66/	4.0E-85/	4.0E-85/	4.0E-85	4.0E-65	3.0E-85	3.0E-65	3.0E-65 X78932.1	0 000	3.DE-65 AIGUUGSZ	20.00	200	3.0E-65	3.05-65	3.0E-65
Expression Signal		84	1.51	15.66	25.0	4.17	4.17	0.62	0.84	2.48	0.58	95.0	0.81	0.78	0.78	1.34	2.65	289	8.02	1.79	1.6	3.16	6.62	22.13	Ţ	77.	200	3	1.61	133	1.42
ORF SEQ ID NO:		26749	27077		28825	32585	32588	33595	33638	33748	34124	34125	34452		Ĺ			111118	37918	77072	L						1007		29688		
Exan SEQ ID NO:		13808	14124	14515	17011	18351	18351	20281	20285	20396	20740	20749	21055	2114	2144	22465	23885	24251	24378	14124	13286	13214	13214	15819	L	1	10001	2	16776	17700	1 1
Probe SEQ ID		747	<u>1</u>	1482	3971	6273	6273	7280	7324	7429	7.077	1811	8118	8174	8174	9501	10946	11301	11434	12808	13091	26	88	1236		1840	306	2000	3734	4670	10429

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Top Hit Descriptor Source	Homo sepiens methylene totrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA	EST_HUMAN QV1-DT0069-110200-067-510 DT0069 Homo sepiens cDNA	EST_HUMAN   EST377546 WAGE resequences, MAGI Hamo expiens cDNA		[Homo expiens methylane tetrahydrafolate dehydrogenase (NAD+ dependent), methanyltatrahydrafolate cyclohydrolase (MTHFD2), mfNA	Homo sepiens hypothetical protein FLJ20116 (FLJ20116), mRNA	Human endogenous retrovirus pHE.1 (ERV9)	EST HUMAN   UIH-BW1-enr-e-10-0-UI.s1 NCI_CGAP_Sub7 Homo septens CDNA clone IMAGE:3070747 3'	Homo sepiens mRNA for KIAA0886 protein, partial cds	Homo sapiens solute carter family 25 (mitochondrial cartier, edenine nucleotide translocator), member 5 (SLC25A6), nuclear gene encoding mitochondrial protein, mRNA	Homo sapians solute carrier family 25 (mitochondrial carrier, adentine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA	yzZ7g12_r1 Sceres_multiple_sclerosis_ZNbHMSP Homo septems cDNA clone IMAGE:284328 6' chriller to SW.HzBr_T1GCA P35088 HISTONE H2B.1/HzB.2 [2] PIR-B56812;	yz77g12_r1 Soares_multiple_sclerosis_ZNbHMSP Homo eaplens cDNA clone IMAGE:284328 5' stmiler to EST_HUMAN SW:H2B1_T1GCA P35068 HISTONE H2B.1/H2B.2 [2] PIR:B56812;		Homo sapiens TGF(bets)-Induced transcription factor 2 (TGIF2), mFNA	Homo sapiens KIAA0649 gene product (KIAA0849), mRNA	Homo sepiens mRNA for KJAA0892 protein, partial ods	Homo sapiens protein kinase C beta-li type (PRKCB1) mRNA, complete cds	Homo sepiens NIPSNAP, C. elegans, homotog 1 (NIPSNAP1), mRNA			Homo expiens mRNA for FLJ00045 protein, partial cds			Homo expiens motybdenum cafactor biosysthesis protein E (MCBPE) mRNA, complete cds
Top Hit Acessicn No.	11428843 NT	4.0E-66 AW939119.1	4.0E-66 AW965473.1 E	J78168.1 NT	11428843 NT	11421638 NT	67147.1 NT	3.7	4.0E-66 AB023215.1 NT	4502098 NT	4502098 NT				11141880 NT	7682223 NT	3.0E-68 AB020699.1 NT	413975.1 NT	11417946 NT	11417946 NT	02211.1 NT	3.0E-68 AK024453.1 NT	11417118 NT	3.0E-66 7019480 NT	VF155659.1
Most Similar (Top) Hit BLAST E Vakue	4.0E-68	4.0E-86	4.0E-66	4.0E-66 U78168.1	4.0E-88	4.0E-88	4.0E-68 X67147.1	4.0E-88	4.0E-66/	3.0E-68	3.0E-88	3.0E-86 N55323.1	3.0E-86 N66323.1	3.0E-86 N55323.1	3.0E-86	3.0E-66	3.0E-66	3.0E-66 M13975.1	3.0E-66	3.0E-66	3.0E-66 X92211.1	3.0E-66	3.0E-88	3.0E-68	3.0E-86/
Expression Signal	3.80	82.0	4.69	7.18	0.98	6.46	1.46	1.75	1.8	5.80	5.89	1.07	1.07	1.07	4.78	6.79	0.78	0.79	1.49	1.49	4.07	0.7	0.62	0.69	28'0
ORF SEQ ID NO:	31887	32109	31266	33652	31887	34789	34859	37512	38248	27432	27433	28027	28028	28029	28729	28101	31579	31920	32143	32144	33985	36290	38474	36841	37315
Earl SEQ ID NO:	18726	18925	18368	20309	18728		<u> </u>	L	L	<u> </u>	<u>L</u>	1	L	l	16742		L	18763	18956	18956	20620	22836	23004	23355	Ш
Page SEQ ID NO:	9836	5835	7036	7338	7897	8413	8472	11020	11706	1424	1424	188	1888	1986	2718	3134	5542	2999	2867	5867	7660	8883	10077	10433	10889

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ngle Exon Probes Expressed in Bone Marrow	Top Hit Descriptor	Homo sepiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA	Homo sapiens celotneurin binding protein 1 (KIAA0330), mRNA	Homo eapiens Misshapen/NIK-related kinase (MINK), mRNA	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA	Homo sepiens critim recognition complex, subunit 5 (yeast homotog)-like (ORCSL) mRNA, and translated products	Homo sepiens origin recognition complex, subunit 5 (yeast homolog)-tite (ORCSL) mRNA, and translated	products	Homo sapiens chromosome 21 segment HS21C101	H.saplens pseudogene for the low affinity IL-8 receptor	H.saplens pseudogene for the low affinity IL-8 receptor	Homo saplems hypothetical protein FLJ20309 (FLJ20309), mRNA	Novel human gene mapping to chomosome 1	Homo sapiens HLA-B gene for human leucocyte antigen B	Homo sepiens HLA-B gene for human leucocyle antigen B	EST380930 MAGE resequences, MAGJ Homo septems cDNA	EST380930 MAGE resequences, MAGJ Homo sapiens cDNA	y/68-02.rt Sceres_multiple_sclerosts_ZNbHMSP Homo sepiens cDNA clone IMAGE-277828 5	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA	AV717817 DCB Hamo septems aDNA clane DCBADC07 5"	AV717817 DCB Hamo sepiens aDNA clane DCBADC07 5'	AV717817 DCB Hamo sapiens aDNA dane DCBADC07 6'	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5	802152986F1 NIH_MGC_81 Hamo saplens cDNA clans IMAGE:4294151 5	IL2-NT0101-280700-118-E04 NT0101 Homo saplans cDNA	ILZ-NT0101-280700-118-E04 NT0101 Homo septens cDNA	RC5-BN0183-010900-034-G06 BN0193 Homo saplens cDNA	aa80e04.s1 NCI_CGAP_GCB1 Hamo sepiens cDNA dane (MAGE:8272623"	2857e12.r1 Soares retina N2b4HR Homo sepiens dDNA done IMAGE:3631185	AV748749 NPC Hano sapiens aDNA dane NPCBVA05 5'	AV748749 NPC Hamo saplens cONA clane NPCBVA05 5	ho47h02.x1 Sceres_NPL_T_GBC_S1 Hamo sepiens cDNA clane IMAGE:3040565 31
ia Exon Probes Ex	Top Hit Database Source									1) IN	NT.			± EN			EST_HUMAN E	EST HUMAN Y				EST HUMAN A	EST HUMAN A	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN F	EST_HUMAN	EST HUMAN 2			EST HUMAN
Single E	Top Hit Aoesston No.	5453949 NT	11417862	7857334 NT	7857334 NT	4505524 NT		4505524 NT	1.2			8923290 NT	2.0E-66 AL117233.1	2.0E-66 AJ133267.2	2.0E-66 AJ133267.2	2.0E-66 AW968854.1	2.0E-66 AW968854.1	2.0E-66 N45480.1	11418318 NT	1.0E-66 AV717817.1	1.0E-66 AV717817.1	1.0E-88 AV717817.1	1.0E-66 AV717817.1	1.0E-66 BF873088.1	1.0E-88 BE765232.1	1.0E-66 BE785232.1	1.0E-66 BF328623.1	1.0E-66 AA688858.1	1.0E-66 AA018828.1	1.0E-88 AV748749.1	1.0E-66 AV748749.1	1.0E-66 BE044595.1
	Most Similar (Top) Hit BLAST E Value	3.05-88	3.0E-88	2.0E-88	2.0E-88	2.05-68		2.0E-66	2.0E-86	2.0E-86 X65859.1	2.0E-86 XB5859.1	2.0E-88	2.0E-86	2.0E-66/	2.05-66	2.0€-66	2.0E-66	2.0E-68	2.0E-68	1.0E-66	1.0E-86	1.05-86	1.0E-66	1.0E-88	1.05-86	1.0E-68	1.0E-88	1.05-96	1.0E-66	1.0E-86	1.0E-68	1.0E-68
	Expression Signal	5.1	1.38	1.94	1.94	0.7		0.7	2.18	2.33	1.39	62.0	60	38.62	38.62	0.82	0.82	2.88	2.61	1.58	1.58	3.69	3.69	5.82	1990	9.0	1.09	42	0.7	6.0	6.0	0.44
	ORF SEQ ID NO:	38306	31847	28082	26083	26015		26016	27867	28279	28965	29501	29727	30598	30599	32191	32192	35585		28885	28886	28885	28886	31468	32164	32155			36176	37153		37429
	Exan SEQ ID NO:	24721	25629	13173	13173	13117		13117	14869	15265	16044	16578	16819	17708	17708	L	19000	22165	26941	15963	15963	15963	15963	18557	18964	18984	1	21768	22722	23859	23659	23913
	Probe SEQ ID NO:	11838	13109	ន	ଞ	422		422	1843	2241	2986	3532	37777	4685	4685	6914	5914	9498	12614	2802	2804	4412	4412	5455	68875	5875	7125	8804	9781	10737	10737	10993

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Top Hit Descriptor	Homo sapiens jun dimerization protein gene, pertial cds; cfos gene, complete cds; and unknown gene	EST380820 MAGE resequences, MAGJ Hamo saplens cDNA	Homo sapiens Ran GTP ase activating protein 1 (RANGAP1), mRNA	84/76402,x1 Sdinetian fetal brain 00004 Homo sapiens CINA clone IMAGE:2782083 S' similar to gb::MS7104 ATP SYNTHASE COUPLING FACTOR 8, MITOCHONDRIAL PRECURSOR (HUMAN);	EST86812 Teetis I Homo sapiens cONA 5' end similar to similar to C. elegans hypothetical protein, cosmid 2K363	258005.11 Scares fetal liver_spieen_1NFLS_S1 Home sepiens cDNA clone IMAGE:416049 6	zh680517 Soares febal liver spisen 1NFLS S1 Homo sapiens cDNA cione IMAGE:416049 5	Homo septens thosital 1,9,4-triphosphate 5/8 ldnase (ITPK1), mRNA	Homo saplens inosital 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA	8u75d02x1 Schneider fetal brein 00004 Homo sapiens cDNA cione IMAGE:2782083 3' similar to gb:1437104 ATP SYNTHASE COUPLING FACTOR 8, MITOCHONDRIAL PRECURSOR (HUMAN);	Homo sapiens zinc finger protein 304 (ZNF304), mRNA	Homo sepiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA	Homo saplens adaptor-related protein complex 2, beta 1 eubunit (AP2B1), mRNA	Homo sapiens ATPasa, H+ transporting, lysosomal (vacuoler proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6N1A), mRNA	Homo saplens mitochondrial carrier family protein (LOC55972), mRNA	Homo septens mitochondrial cernics family protein (LOC55972), mRNA	Homo saplens latent transforming growth factor bata binding protein 2 (L.T.BP2) mRNA	Homo sapiens retinaldehyde dehydrogenase 2 (RALDH2), mRNA	Human cytochrome oxidase subunit VIa (COX6A1P) psaudogene, complete cds	Homo sepiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sepiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens gene for AF-8, complete cds	Homo sapiens calcium channel, voltage-dependent, abha 2/deita subunit 1 (CACNA2D1), mRNA	H.saplens mRNA for acetyl-CoA carboxylasa	Homo expiens mRNA for transmebrane receptor protein	Homo sapiens PMP89 gene, exans 3,4,5,8 & 7	Homo septens refinchiastoma 1 (including osteosercoma) (RB1) mRNA	Homo septens Synepsin III (SYN3) mRNA, and translated products	Homo sepiens Synapsin III (SYN3) mRNA, and translated products
Top Hit Detablese Source	NT H	T HUMAN		EST_HUMAN AT		Τ	Γ			HUMAN												NT H			H IN				
Top Hit Acession . No.	1.0E-66 AF111167.2	1.0E-68 AW968744.1	11418177 NT	7.0E-67 AW 162232.1				7857243	7857243 NT	7.0E-67 AW162232.1	10190895 NT	11425572 NT	11425572	4865084 NT	11419212 NT	11419212 NT	4557732 NT	836044	U82486.1	11430460 NT	11430460 NT	AB011399.1	11421527 NT	6.0E-67 X88968.1	6.0E-67 Z17227.1	6.0E-67 Y14320.1	4506434 NT	4507332 NT	4507332
Most Similar (Top) Hit BLAST E Value	1.0E-66	1.05-68	9.0E-67	7.0E-67	7.05-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.05-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	79-30.7	7.0E-67	6.0E-67	6.0E-67	6.0E-67	6.0E-67	6.0E-67	6.0E-67
Epression Signal	2.47	1.69	276	2.51	1.2%	1.19	1.19	1.02	1.02	2.78	960	1.82	1.82	1.14	1.13	1.13	0.69	6.73	2.45	1.92	1.82	1.86	1.44	1.19	1.7	206	1.16	1.33	1.33
ORF SEQ ID NO:	37767	38322		28425					28087			L	32717	33233	34216	34217	35055	35681	38458	38619		31789		26548	26802				
Exan SEQ ID NO:	24240	24736	25170	13483	L		14690	L	15067	13480	18273	19469	19469	18837	20836	i.	1	1	i.	25019	25019	26323	25561	13631	13855	14313	16238		16497
Probe SEO ID NO:	11280	11863	12398	8	\$	1553	1558	848	88	282	818	<u>§</u>	9401	888	7883	7893	8888	8284	11885	12169	12169	12639	13009	\$	788	1278	3183	3451	3451

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	Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C001	Homo saplens chromosome 21 segment HS21C001	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA	Homo sepiens DKFZp434P211 protein (DKFZP434P211), mRNA	Hamo saptens B-ATF gene, complete cds	Homo sepiens B-ATF gene, complete cds	Hamo septiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA	yn02d11.rt Soares adult brain N2b4HB557 Homo saplens cDNA cione IMAGE: 107233 3	ojzeotsus NCL_CGAP_Kid3 Homo sepiens oDNA clone IMAGE:1463288 3' simitar to SW:233A_HUMAN 006730 ZINC FINGER PROTEIN 33A ;	RCD-HT0834-150900-02603 HT0934 Homo saplens cDNA	And the Coat SS1 Home septems abid done IMAGE:12384723' similar to TR:010385 010385	PRO-POL-DUTPASE POLYPROTEIN;	EST37803 Embryo, 9 week Homo sapiens cDNA 5' end	MR3-SN0068-040500-008-f01 SN0068 Homo sapiens cONA	Hamo septens chramosame 21 segment HS210079	Heff0537 NCL CGAP_Kid11 Hano sapiens dDNA clane IMAGE:3134913 3' similier to SW:1410P_MOUSE. 061085 GTP-RHO BINDING PROTEIN 1;	om18b07.s1 Sozres_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:15413653	hw16g08.x1 NCI_CGAP_Lu24 Homo septiens cDNA clone IMAGE:31831363' stmilar to WP:F23H11.9	CE09817;	QV4-ST0234-181199-037-f05 ST0234 Homo saplens cDNA	Hamo sepiens double strended RNA activated protein kinase (PKR) gane, excris 28, 2, 3, and 4	ba72g05,y1 NIH_MGC_20 Homo saplens cDNA clone IMAGE:2805976 5' similar to 1K:094892 084692 KIAA0798 PROTEIN ;	ba72g05.y/ NIH_MGC_20 Homo sepiens cDNA clone IMAGE:2805976 6' straitar to TR:094862 094892.	(MANUSOFINO)	Homo sapiens hypometical protein curozcusus (Lukacusus), minnak	Homo sepiens hypothetical protein d./4620/23.2 (U./4620/23.2), mr.v.A	Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cas	Homo sapiens developmentally regulated GTP-binding protein 1 (LHCs1), mixing	Zu91g01.s1 Soares, testis, NH I Hamo septens a JNA dane IMAGE: (40352.5	Hamb septers arrandsanter 21 segment nozivitivo
	Top Hit Defebase Source	H IN	1NT				NT IN	H IN	П	EST HUMAN	EST HIMAN	T	T	EST_HUMAN	EST_HUMAN	EST HUMAN	Į.	EST HIMAN	Т	Т		T HUMAN		EST_HUMAN		HOMAN					EST HUMAN	٦.
	Top Hit Acession No.	6.0E-67 AL163201.2		7857020 NT	T857020 NT	6.0E-67 AF016898.1	Ļ	1	3.1		4 NE. 47 A 1733873 1			4.0E-67 AA714294.1		1.1	Γ	2 OF 47 DE106088 1	3.0F-87/AA927874.1		20E-67 BE348354.1	5.1		2.0E-67 BE303037.1		2.0E-67 BE303037.1	11422948 NT	11422948 NT	AF309581.1	758795	-	2.0E-67 AL 163300.2
	Most Similar (Top) Hit BLAST E Vatue	8.0E-67/	6.0E-67/	8.0E-67	6.0E-67	8.0E-67	8.0E-67	5.0E-67	5.0E-67	4.0E-67 R90819.1	70 20 4	1000	4.00-0/	4.0E-67	3.0E-67	3.0E-67	3.05-67	20 05 87	3.05.67		2.0E-67	2.0E-67	2.0E-87	2.0E-67		20E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	20E-67
	Expression Signal	67.0	67.0	3.56	3.56	800	0.99	202	13.10	225	8	8 5	1.18	1.48	1.16	2.52	188	7.4	2 X		260	6.48	188	1.28		128	6.0	60	1.18	1.38	3.78	2.7
}	ORF SEQ ID NO:	30069	30070	30647	30648	34121	31122	29212		27335	ok.	80.5	1		28820	30634	L		coere	†	28217			27872	_		28291	28282	L			Ц
	SEQ ID	17183	17183	17754	17/54	18250	18250	16290	24279	4388	100	200	21685	24347	L	17743	17773	1	24538		13291	13902	14151		1_	14925	15265	١_	1_			Ш
	Probe SEQ ID NO:	4450	4153	1 25	\$7.5	6242	5242	3235	41328	1331	}	8	873	11403	282	4773	47.53		222	8	6	88	1107	Ş		1901	2251	2251	2394	2438	3481	4027

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ngie Exon Probes Expressed in Bone Marrow	Top Hit Descriptor	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sepiens chromosome 21 unimown mRNA.	Homo sapiens mRNA for KIAA1431 protein, partial cds	Homo saplens retinoblastoma-binding protein 2 (RBBP2) mRNA	Т	Homo septens RAB3A interacting protein (rabins)-like 1 (RAB3IL1), mRNA	Homo septiens RAB3A Inferacting protein (rabins)-like 1 (RAB3IL1), mRNA	Homo septems transcription factor NRF (NRF), mRNA	Homo sepiens transcription factor NRF (NRF), mRNA		Homo saplens sedlin (SEDL) gene, exon 4	Homo sepiens serine carbooppeptidase 1 precursor protein (HSQP1), mRNA	Home sepiens serine carboxypeptidase 1 precursor protein (HSGP1), mRNA	Homo saplens DKFZP586L0724 protein (DKFZP586L0724), mRNA	Hamo sepiens mRNA for KIAA0145 protein, partial cds	Homo sapiens mRNA for KIAA0146 protein, pertial cds	Homo septens mRNA for KIAA1485 protein, partial cds	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA	Hamo explens protein tyrosine phosphalase type IVA, member 1 (PTP4A1) mRNA	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds	Mus muscutus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds	q038N02.x1 Scares_fetal_king_NbHL19W Homo sepiens cDNA clone IMAGE:1950291 3' shrillar to contains	T		F	7715f02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3284747 3' similar to TR:080828 080828		Homo sapiens gene for ectivin receptor type IIB, complete ads			Homo sepiens UDP-N-ecety-elpha-D-gelectosamine:polypeptide N-ecetygelactosaminytransferase 8 (GetNAo-T8) (GALNT8), mRNA
Xon Prot	Top Hit Detabase Source	NT	Į.	Į.	Ĭ	NT	<b>EST_HUMAN</b>	Ž	F	W	TN.	SWISSPROT	NT	ΙN	ΝT	IN	IN	ĮŅ.	Ţ	IN	ΝŢ	Į	ΙN	NAMIN TOO	EST HIJMAN	EST HUMAN	¥		EST_HUMAN	¥	EST_HUMAN	EST_HUMAN	5
Single	Top Hit Acession No.	5.0E-68 AF231919.1	5.0E-68 AF231919.1	5.0E-68 AF231919.1	5.0E-68 AB037852.1	TN 7969284	5.0E-68 AL157845.1	7019612 NT		11421388 NT	11421388 NT	4.0E-68 P04408	AF157063.1			TN 6891887	4.0E-68 D63479.2	D63479.2	4.0E-68 AB040918.1			1	3.0E-68 AF236082.1	9 OE 40 A1947373 4	3 0F-88 F78784 1	3.0E-68 AW939485.1	2.0E-68 D00522.1		2.0E-68 BE675768.1	2.0E-68 AB008681.1	2.0E-68 R45088.1	2.0E-68 BF035318.1	11625737 NT
	Most Similar (Top) Hit BLAST E Vælue	5.0E-68	5.0E-88	5.0E-68	5.0E-68	5.0E-68	5.0E-68	5.0E-68	5.0E-68	4.0E-68	4.0E-68	4.0E-68	4.0E-68	4.0E-68	4.0E-88	4.0E-68	4.0E-88	4.0E-68	4.0E-68	4.0E-68	4.0E-68	3.0E-68	3.0E-68	9 OE 80	305-88	3.0E-68	20E-68		2.0E-68	2.0E-68	2.0E-68	2.0E-68	2.0E-88
	Expression Signal	4.72	4.72	1.23	3.08	8.0	0.75	0.67	0.67	0.94	0.94	7.63	0.67	5.5	5.5	0.72	5.91	5.91	283	1.55	1.65	502	0.83	27.2	28	1.99	812		0.75	1.86	9.21	4.51	0.61
	ORF SEQ ID NO:	28827	26828	28799	29133		30429	33236	33237	28555	28558		32368	33485	33486	34278	35790	35791	35944	37821	37822	28630	31164		37788				29987	30623		33289	
Ī	SEQ ID	13878	13878	15783	16218	17239	17543	19941	18941	15535	15535	18026	19156	20163	20163	20887	22360	22360	22498	24295	24295	16716	18303	24435	37.88	25725	18821		17092	. 17729	20081	20000	20392
	Probe SEQ ID NO:	828	0Z8	7784	3162	4210	4518	6880	6889	2532	2532	5011	6075	6833	6833	7946	9395	9395	8533	11345	11345	3673	2289	0047	10963	13012	2873		4055	4708	7059	7265	7425

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Ingre Extri Frons Expressed in Done manow	Top Hit Detabase Source	EST_HUMAN	SWISSPROT FORMIN 4 (LIMB DEFORMITY PROTEIN)		EST_HUMAN		INT	1 EST HUMAN		EST HUMAN	62349 NT			18869 NT	NT Itomo espiens MIF2 suppressor (HSMT3) mRNA, complete ods	NT Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5	NT Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5											Homo sepiens glutamate-cysteine ligase (genima-glutamytoysteine synthetase), regulatory (30.84D) (GLCLR)	12000	LV.	I EST HUMAN	NT	GES12 NT		
High Land	Top Hit Acession Da	2.0E-68 BF336745.1 EST		4606222 NT	.1	1		1.1		1.0E-68 AA897343.1 [EST_	7662349 NT	11436716 NT	11418869 NT	11418869 NT				11418431 NT	11418431 NT	4505222 NT	11430460 NT	11418213 NT	5031978 NT	5031976 NT	5031980 NT	5031980 NT	4757867 NT	1100000	2		-	8.0E-69 AJ237744.1 NT	9966912 NT	8.0E-89 A/192784.1 EST	
<u> </u>	Most Similar (Top) Hit BLAST E Vatue	2.0E-68	2.0E-68 Q05859	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-08/	1.0E-88	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68 L.76416.1	1.0E-68 U50319.1	1.0E-88 U50319.1	1.0E-68	1.0E-68	1.0E-88	1.0E-68	1.0E-88	9.0E-69	9.0E-89	9.0E-89	9.0E-89	9.0E-09	100	8.UE-08	9.0E-69/	9.0E-69	8.0E-69	7.0E-69	8.05-89	
	Expression Signal	0.61	0.67	0.75	17.65	1.27	1.27	1.04	1.01	0.69	1.8	0.56	1.48	1.48	3.37	2.13	2.13	1.73	1.73	2.19	2.07	1.61	5.15	5.15	0.76	0.76	76.0		7.02	0.83	5.51	1.77	5.65	15.42	
	ORF SEQ ID NO:	33916	35898	28120		28301	28302	28781	29975	30857	31378	34270	37884	37885	37725	38131	38132	38449	38450	28120			28040		L					31120			32802		1
	SEQ ID	20558	22266	13186	13390	16277	15277	15759	17075	18078	18498	20880	24153	24153	24203	24668	24588	24852	24862	13196	25896	25563	13142	13142	14075	14075	17186	Ι.		18249	24189	16446	18552	1	١
	Probe SEQ ID NO:	7585	<b>1088</b>	8	887	2283	2268	2767	4037	2066	5395	888 888	41188	1198	11250	11831	11631	11975	11976	12790	13005	13057	Ø	Z	1029	1029	4155		4175	5241	11238	3397	6487	80	

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	Top Hit Descriptor	qe62701.x1 Sceres_feta_lung_NbHL19W Homo sapiens cDNA cione IMAGE:1743801 3' similar to gb:L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);	od60a03.s1 NCL_CGAP_GCB1 Hamo septens cDNA clane IMAGE:1372300 3'	wm26h11 x1 NCI_CGAP_Ut4 Hamo septens aDNA done IMAGE:2437125 3'	601344705F1 NIH .MGC_8 Hamo sapiens aDNA clane IMAGE:3677641 5	wh57b08.x1 NCI_CGAP_Kid11 Homo saplens dDNA done IMAGE:2384819 3' skniler to TR:055137 OKS437 ACM_CDA THIOFSTERASE	Homo sepiens letent transforming growth factor beta binding protein 2 (LTBP2) mRNA	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA	AU119634 HEMBA1 Homo sapiens cDNA clone HEMBA1006283 5	601110371F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3351352 5	Homo sapiens Smad- and Off-Inferacting zinc finger protein mRNA, partial cds	Homo sapiens lymphatic vessel endothelial hyaturonan receptor 1 (LYVE-1) mRNA	ye48h04.rl Scares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:121015 5	ye48h04.r1 Scares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:121015 5	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA	Human type ii iL-1 receptor gene, exon 1B	Homo sepiens dNT-2 gene for mitochondrial 5(3)-decoynthonucleotidase (dNT-2 gene), econs 1-6.	Homo sapiens sperm surface protein (HSS), mRNA	Homo sepiens stoot chein L-3-hydroxyecy-CoA dehydrogenase precursor (HADHSC) gene, ruckear gene encoding mitochondrial protein, complete cds	Homo sepiens arm-repeat protein NPRAP/heurojungin (CTNND2) mRNA, pertiel cds	Homo sapiens TRAF6-binding protein TGBP mRNA, complete cds	UI-H-BIT-ac/#-g-01-0-UI.s1 NCI_CGAP_Sub3 Hamo septens cDNA clane IMAGE:2715840 3'	EST8807 HSC172 cells II Hamo sapiens cDNA 5 end similer to similar to ribosomal protein S18	Homo sapiens hypothetical protein FL/20276 (FL/20275), mRNA	H.sapiens mRNA for N-acetylglucosamide (beta 1-4)-galactosyltransferase	Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor	(MIF)-related protein	Homo sepiens SEC10 (S. cerevisiae)-like 1 (SEC10L1), mRNA	Homo sepiens ribosomal protein S15a (RPS15A), mRNA	EST88807 HSC172 cells II Homo sepiens cDNA 6 end similar to similar to ribosomal protein S18	Homo sepiens HGC8.2 protein (HGC8.2), mRNA
-	Top Hit Database Source	EST_HUMAN gt	EST_HUMAN   00	EST_HUMAN W	EST HUMAN G	W NAMIU TOTAL	- 1000 E		EST_HUMAN A	EST_HUMAN 6	H		EST_HUMAN   N	EST_HUMAN   y		H					F	EST_HUMAN U	EST_HUMAN E		노	=	NT (A			THUMAN	
,	Top Hit Acession No.		5.0E-69 AA826039.1	4.0E-69 AI873630.1	4.0E-69 BE561063.1		57732	4557732 NT	4.0E-69 AU119634.1		1	5728910 NT			11418185 NT		3.0E-69 A.1277557.1	11426786 NT	3.0E-69 AF095703.1		3.0E-69 AF268075.1	-		8923248 NT	3.0E-69 X13223.1			5730036 NT	11432120 NT		11419157 NT
	Most Similar (Top) Hit BLAST E Value	6.0E-69	5.0E-69	4.0E-69	4.0E-69	W 20 7	405-69	4.0E-69	4.0E-69	3.0E-89 (	3.0E-69	3.0E-69	3.0E-69 T96234.1	3.0E-69 T96234.1	3.0E-69	3.0E-69 U1417B.1	3.0E-69	3.0E-69	3.0E-69	3.0E-69	3.0E-69	3.0E-69	3.0E-69	3.0E-69	3.0E-89		3.0E-69 X06233.1	3.0E-69	3.0E-69	3.0E-69	3.0E-69
1	Expression Signal	15.42	1.04	1.27	1.38	u u	277	2.77	0.55	3.2	2.56	0.83	0.83	0.83	1.79	0.54	0.58	9.0	0.82	1.52	8.4	1.05	1.38	0.5	29.		59.4	0.71	3.29	1251	7.34
	ORFSEQ ID NO:	34575			32130	88	3 25	33123	35662	26432	26595				38613	31983		31257	33918	33977	34128	35111		35722	36164			36597	37483		
	SEQ ID NO:	21165	22280	13592	25646	2000	888	19838	22231	13489	13679	16394	17639	17639	18330	18806	20195	ı	ł	20611	20752	21683	Ĺ.	L	22709		22844	L.:	23969		Ш
	Probe SEQ ID NO:	8185	8325	523	5855	9	2 8	6783	9286	88	614	2386	4618	6286	5314	5712	6972	7038	7597	7651	7800	87.15	9120	8328	89/6		9891	10188	11003	11180	12300

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Top Hit Descriptor	Homo septens KIAA0553 protein gene, complete cds; and alphallb protein gene, partial cds	Homo sepiens KIAA0553 protein gene, complete cds; and alphalib protein gene, partial cds	Homo septens KIAA0553 protein gene, complete cds; and alphalib protein gene, partial cds	Homo septens KIAA0553 protein gene, complete cds; and alphalib protein gene, partial cds	H100444F1 NIH_MGC_18 Hamp sepiens aDNA dane IMAGE:3350074 6	zw71g02.r1 Soares_testis_NHT Homo saptens cDNA clone IMAGE:781682 5	zm28g01.r1 Strategene pancress (#687208) Homo sapiens cDNA clone IMAGE:527088 5	Rattus norvegicus brein specific cortactir-binding protein CBP90 mRNA, partial cos	601301284F1 NIH MGC 21 Homo sepiens cDNA clone IMAGE:3835/81 5	601675788F1 NIH JAGC_21 Hamo septens aDNA dane IMAGE:3808532 5	601675788F1 NIH_MGC_Z1 Homo explems cDNA clone IMAGE:3858532 5	QV0-1T0010-031199-046-c07 1T0010 Hamo septems cDNA	Homo saptens KIAA0716 gene product (KIAA0716), mRNA	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA	Homo saplans mRNA for KIAA1147 protein, partial cds	Homo septens mRNA for KIAA1147 protein, pertial cds	601278532F1 NIH_MGC_39 Homo septems cDNA clone IMAGE:3610614 5	601278532F1 NIH_MGC 39 Homo sepiens CDNA clone IMAGE:3610614 5	TCBAP1E2978 Pediatric pro-B cell acute lymphobles6ic leukemia Benkor-HGSC project≃1 CBA Homo septens cDNA cione TCBAP2678	TCBAP1E2878 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo saplens	CUNA CODE I CCAP 20/0	Homo septems mixtwa for NiAAU/0/ protein, partiel cos	60/2043782F1 NCL CGAP BINDT Hamo septems alina ciate IMAGE:41613/20 0	Homo sapiens keretin 8 (KRT8) mRNA	607762802F1 NIH MGC 20 Hamo septiens aDNA clane IMAGE:4025785 6	w/84608.X1 Source, NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:2360390 3' straiter to contents Atu	repositive desirant contains element mir repositive element	nc13d12_r1 NG_CGAP_PT Homo septens d.N.A. done IMAGE:1008023	Homo septems DGSH mRNA, 3' end	tm89f01 x1 NCI_CGAP_Bm25 Homo sepiens cDNA clane IMAGE_2165305 3	tm89f01 x1 NCL CGAP Bm25 Hamo sepiens cDNA clane IMAGE:2785306 3	ZISTOATI NCI CGAP GCB1 Homo septens cONA ctore IMAGE:713239 5	Homo septiens tumor suppressor detegg in oral carder-related 1 (DOC-1R) mixira.
Top Hit Database Source	NT F		H	TN TA	HUMAN		EST_HUMAN   z		EST_HUMAN 6		EST HUMAN 6	HUMAN			±.	NT TA	EST_HUMAN 6	EST_HUMAN 6	EST HUMAN		HUMAN		EST_HUMAN		EST_HUMAN C		7	T HUMAN	TN.		╗	LHUMAN	
Top Hit Acession No.	2.0E-69 AF160252.1	2.0E-69 AF160262.1		2.0E-69 AF160252.1							1.0E-69 BE902501.1	1	7662263 NT	7682263	1.0E-69 AB032973.1		1.0E-69 BE531007.1		1.0E-89 BE245070.1				1.0E-69 BF528429.1	4504918 NT	1.0E-69 BF125887.1			3.1		7.0E-70 AI497807.1		7.0E-70 AA282955.1	5031668 NT
Most Similiar (Top) Hit BLAST E Value	2.0E-69	2.0E-69 A	2.0E-69 A	2.0E-69 A	2.0E-69 B	2.0E-69 A	2.0E-69	1.0E-69	1.0E-69	1.0E-69	1.0E-69	1.0E-69	1.0E-89	1.0E-69	1.0E-89	1.0E-69	1.0E-89	1.0E-69	1.0E-69		1.0E-69	1.05-69	1.05-69	1.0E-89	1.0E-69		1.05-69 /	8.0E-70	8.0E-70 L77568.1	7.05-70	7.05-70	7.0E-70	7.0E-70
Expression Signal	1.06	1.08	4.75	4.76	1.48	3.8	26'0	2.69	6.73	0.78	0.78	4.09	1.4	4:1	2.78	2.78	0.62	0.62	4.31		4.31	1.48	0.53	278	1.80		B.78	1.61	2.11	228	2.26	1.87	2.97
ORF SEQ ID NO:	E SE	28412	28411	28412	27824		36289	27728		32474	32475	33092	33544		33453	33464	33396	33397	36952			83028	37198		38167				30314			27969	
Esen SEQ ID NO:	13477	13471	1347	13477	14928	15916	21888	14744	18069	18243	19243	1	l	20215	20137	20137	20087	20087	22456		23468	23553	23700	<u> </u>	L	l_	25331	15890	1_	14857	1_		15095
Probe SEQ ID NO:	128	138	\$	ई	1802	2856	8800	1714	5050	9168	9168	82/9	2889	6882	7011	ğ	7065	7085	10534		10634	10831	40T78	11219	12234		12648	2339	4401	<u>\$</u>	1880	1947	2078

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Top Hit Descriptor	Homo sepiens adenylate cyclase 3 (ADCY3) mRNA	Hown seniors MIST mRNA partial cels	HOURS OF THE STATE	MID SEPTION INC. I MANY, PAIN WE WAS THE SEC AMONG THE	Homo experts gare encoding spiraing technical or 1, extres 20	Homo eapiens thin immunoglobulin domain protein (myonim) (1110.), mr.cvv.	Homo sepiens mRNA for KIAA (294 protein, partial cots	Homo sepiens mRNA for KIAA1294 protein, pental cos	Human displacement protein (CCAAT) mRNA	Human displacement protein (CCAAT) mFtVA	Human PBX3 mRNA	Human PBX3 mRNA	Homo sapiens phospholipid scrambase 1 gene, exth 1 and 9 mandring region	Homo sepiens karyopherin bela Zb, transportin (TRVZ), mrKVA	Homo sapiens karyophenin beta 20, transportin (TRAV2), mrdNA	Homo sapiens glubaneis-cysteins ligase (gamms-glubamyloysteine syntheisse), catsydc (72,840) (GLCCC) mRNA	Homo sepiens NDST4 mRNA for N-descetylase/N-euffohransferase 4, complete cds	Homo sepiens NDST4 mRNA for N-descetylese N-sufformatenese 4, complete cos	Homo sepiens HTR (histone cell cycle regulation defective, S. cerevisias) handog A (HIRA), mRNA	Hamo sepiens HIR (histone cell cycle regulation defective, S. cerevisias) hamalog A (HIRA), mRNA	Human kappa-Immunoglobulin germ line pseudogene variable region (subgroup V Kappa I)	Human kappa-immunoglobulin gerin line pseudogene variame region (subgroup v kappa )	Hamo sepiens emylaid beta (A4) precursor protein (protesse nexin-II, Alzheimer disease) (APP), mRNA	Human Ku (p70/p80) subunit mRNA, complete cds	Homo sepiens CMP-IX-ecolyineurantiric acid synfrase (LOCSSWO7), miXIVA	Homo sapiens KIAA0782 gane product (KIAA0782), mPOA	Homo sepiens KiAA0702 gene product (KIAA0782), mMVA	MR3-HT0487-150200-115-608 HT0487 Homo espiens GDNA	ESTUS928 Fetal brain, Stratagene (cata838230) Homo septens CLIVA done Fil BUNZO	CAR-UNXXXX-OTICSXX-105-gus Unitary from Septems at IVA	CARA-UNKOUG-010300-100-guis Umiduus Homo Sapienis Curin
Top Hit Database Source										N		H	F			,		Y.				N T						HUMAN	7	7	EST HUMAN
Top Hit Acession No.	TM POTTACA					7306							7.0E-70 AF163715.1	11525984 NT	11525984 NT	4657624 NT	7.0E-70 AB036429.1		11628319 NT	11528319 NT	7.0E-70 Z00040.1		4502168 NT	8.0E-70 M30838.1	TM 6682389	7662307	7662307	5.0E-70 BE100034.1	4.0E-70 T06037.1	4.0E-70 AW783228.1	AW786228.1
Most Similar (Top) Hit BLAST E	10 A	21.0	7.05-70/	7.0E-70/	7.0E-70	7.0E-70	7.05-70	7.0E-70	7.0E-70 M74099.1	7.0E-70 M74089.1	7.0E-70 X59841.1	7.0E-70 X59841.1	7.0E-70	7.05-70	7.06-70	7.05-70	7.96-70	7.06-70	7.0E-70	7.0E-70	7.0E-70	7.0E-70	6.0E-70	8.0E-70	8.0E-70	5.0E-70	5.0E-70	5.0E-70	4.0E-70	4.0E-70	4.0E-70
Expression Signal	18,	87.	5.30	6.36	238	0.74	243	243	4.26	4.26	2.78	279	3.51	205	205	80	0.0	9.0	236	2.36	13.63	34.82	. 238	4.7	1.17	1.78	1.78	2.62	1.24	0.78	0.78
ORF SEQ ID NO:		30105	31602	31603	33346	34379	35162	35163								1				38397	١	1			L		L		1		
SEQ ED		1683	18657	18657	20044	ł.	21741	21741	22038	22038	22475	22475	2113	21138	21138	1	L	23583	24804	24804	25882	25605	1	Ĺ	L	1_	1	1	<u> </u>		Ш
Probe SEQ ID		2	5560	2560	7110	8045	87774	8774	222	2708	8512	9612	0878	9816	8	1	1001		11828	11623	12883	13071	33	2147	2516	2560	25.50	12243	8918	1989	6961

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· Top Hit Descriptor	Homo sapiens cytoplasmic dynah intermediate chain 1 mRNA, complete cds	Homo sapiens stalytransferase 6 (N-acetyliacosamthide alpha 2,3-sialytransferase) (SIAT6), mRNA	Homo septens cysteinyl-tRNA synthetase mRNA, complete cds, afternatively spitoed	Human guarine nucleotide binding protein alpha-subunit gene (G-e-alpha), excris 4 and 5	Homo sapiens amylo-1,6-glucosidese, 4-abha-glucanotransferase (glycogen debranching enzyme, glycogen	SECREGE GESSES (yps III) (YOUL) III AND AND A HAMA SEVIEWS CONA CHARA MACE 192882 5	Т	Homo septens dynactin pos strount (LOCO) 104, mrava	Homo sapiens calclum-binding transporter mtKNA, partial cos	Homo sapiens mRNA for KIAA1216 protein, partial ods	Homo septens hypothetical protein FL/20450 (FL/20450), mrkNA	Homo septens hypothetical protein FLJ20450 (FLJ20450), mRNA	Homo septens eukaryotto translation initiation factor 3, subunit 6 (48td) (EIF3S6) mRNA	Homo saplens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Hamo sepions transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamytransferase) (1 GM3)	Ī		٦			Т		$\neg$	$\neg$		xx2401.x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2814049 3' similar to TR:054730 CAA720 TRANSPI ANTABILITY ASSOCIATED PROTEIN 1;	T	٦
Top Hit Databesse Source	Z	F	¥	TN	1		EST HUMAN	Ę	Į	MT	IN	NT	NT	TN	IN		Į,	EST_HUMAN	EST HUMAN	<b>EST_HUMAN</b>	EST HUMAN		EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	MAN IST	NAME TO T	EST HUMAN
Top Hit Acessian No.	2.0E-70 AF123074.1	11422642 NT	2.0E-70 AF288207.1	20E-70 M21741.1		11423599 NT		28355	2.0E-70 AF123303.1	2.0E-70 AB033042.1	8823420		TN 023520 NT		11430460 NT		4507476 NT	1.0E-70 W85795.1	1.0E-70 AA442292.1	1.0E-70 AV738538.1	0 0E. 74 A 1443B7D 1		9.0E-71 A1143870.1	9.0E-71 AI654903.1	9.0E-71 AI654903.1	8.0E-71   AA171451.1		8.UE-/1 AW 2/3020.1	7.0E-71 AA442Z30.1
Most Similar (Top) Hit BLAST E Vætue	2.0E-70	2.0E-70	2.0E-70	20E-70		2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	20E-70	20E-70		1.0E-70	1.0E-70	1.0E-70		0.05.74	TANKS					1	1	1
Expression Signal	11.3	1.44	0.58	5.38		0.45	0.76	0.95	1.42	0.49	3.11	3.11	11.5	2.84	2.64		3.08	0.78	0.64	8.8	1.0		7.1	1.98	3.67	360		0.45	8.17
ORF SEQ ID NO:	33168	34223	33956	34629		34952		35835	36918	Ŀ	37884			Ŀ						37767	L	24.65%	32345	33587	33587		1		33923
Exan SEQ ID NO:	19878	18421	L	2720			21973	22487	L	L.	L	1_		L		١.	16453	_	L	<u> </u>	<u> </u>	2018	19435	20253	20253			23887	
Probe SEQ ID NO:	6824	7.80	7883	8251		8564	2006	8524	10497	10083	11408	11408	11958	12837	12887		3,50	8838	10158	4384		8	6054	7231	11852	25		10967	7601

. Table 4 Single Exon Probes Expressed in Bone Marrow

ORF SEQ Expression (Top) Hit Top Hit Acession Database ID NO: Signal RLASTE No. Source	35412 1.61 7.0E-71 AA705457.1 EST_HUMAN	38168 1.76 7.0E-71 AL163210.2 NT	28258 8.79 5.0E-71 AF056322.1 NT	30068 1.1 5.0E-71 AW818405.1 EST_HUMAN	32264 2.02 6.0E-71 4502740 NT	33162 1.15 5.0E-71 11641408 NT	33341 0.72 5.0E-71 7682209]NT	31243 0.64 5.0E-71 AB033106.1 INT	31244 0.64 5.0E-71 AB033106.1 NT	33671 0.69 5.0E-71 11431590 NT	34075 1.82 6.0E-71 M38106.1 NT	34304 0.84 5.0E-71 11528446 NT	34340 22.85 5.0E-71 AF072810.1 INT	36256 0.61 5.0E-71 5453777 NT	35257 0.81 5.0E-71 5453777 NT	2.45 5.0E-71 X13467.1 NT	37803 7.5 6.0E-71 11438514 NT	38020 2.01 6.0E-71 11438069 NT	38624 1.81 5.0E-71 11417862 NT	26145 1.04 4.0E-71 4607592 NT	28363 66.4 4.0E-71 AF157628.1 NT	28384 56.4 4.0E-71 AF157828.1 NT	28873 1.9 4.0E-71 4505880 NT	30372 4.75 4.0E-71 AF056322.1 INT	30821 6.04 4.0E-71 7657602 NT	1.34 3.0E-71 AU135734.1 EST HUMAN		37538 2.84 3.0E-71 AA567683.1 EST_HUMAN	27231 6.66 2.0E-71 AL163206.2 INT	31374 8.35 2.0E-71 D87462.1 NT	31375 8.35 2.0E-71 D87462.1 NT	8392  31236  0.57  2.0E-71 AL042439.1   EST_HUMAN   DKFZp434D17Z1_r1 434 (synonym: hiss3) Homo sapiens dONA done DKF-2p434D17Z1 5
SEQ ID ORF						19873 3		_	18398				l								13439 2	13430 2	15956 2	17485 3	L		_	24014		18496 3		18392 3
SEO ID NO:	9208	11858	822	4145	988	6819	738	7467	7107	7353	7783	7874	2008	88	8888	10271	11325	11525	12198	\$	320	350	7887	453	5022	8888		11051	482	5383	5383	7160

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ORF SEQ Expression (Top) Hit Acession Detabese ID NO: Signal BLAST E No. Source	35762 0.5 2.0E-71 BF196586.1 EST_HUMAN Q92165 PUTATIVE FOUR REPEAT ION CHANNEL.;	37382 4.19 2.0E-71 AF095703.1 NT encoding mitochandrial profein, complete cds	4.19 2.0E-71 AP0-5703.1 NT	3.41 2.0E-71 BE018477.1 EST HUMAN	2.27 2.0E-71 R55828.1 EST_HUMAN	7.13 2.0E-71 T95489.1 EST_HUMAN	1.0E-71 A1077827.1 EST_HUMAN	1.68 1.0E-71 7706281 NT	M	9.86 1.0E-71 AF012872.1 INT	1.29 1.0E-71[AB017007.1 ]NT	28132 1.29 1.0E-71 AB017007.1 NT Homo capiens PMS2L16 mRNA, partial cds	4.81 1.0E-71 7657153 NT		29573 5.11 1.0E-71 AF246219.1 INT Homo septems SNARE protein kinase SNAK mRNA, complete cds	22619 1.18 1.0E-71 BE122850.1 EST_HUMAN clone 02_15 © similar to Homo septems chances 1.9		1.18 1.0E-71 BE122850.1 EST HUMAN		N	30531 0.68 1.0E-71/H23178.1 (EST_HUMAN ) ym56h10.11 Soares Infant brain 1NIB Homo sepiens cDNA clone IMAGE:52528 5	26182 NT	1.28 1.0E-71 AB011131.1 NT	12.67 1.0E-71 U80753.1 NT	0.76 1.0E-71 AF105287.1 NT	2.14 1.0E-71 11425430 NT	4.49 1.0E-71
	35762	37382	37383	37539	38377		28626	26946	27096	27347	28131	28132	28714	29672	29573	29619	-	29620	29707	30409	30531	33266	33598	33857	34871	34890	35177
	22324	23870	23870	24016	24788	25121	13705	13993	14146	14378	15111	15111	15699	16855	16855	16705	-	16705	16798	17522	17843	18968	20284	20498	27454	21477	21758
Probe Exam SEQ ID SEQ ID NO: NO:	8359	L	1	1	L	12315	88	8	1102	13 24 3	2094	2094	2703	10	3810	2882	1	3662	3764	4497	\$22	98	82	7533	8	8509	8

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ORF SEQ Expression (Top) Hit Top Hit Acession Databese Signal BLAST E No. Source	35178 4.49 1.0E-71 8922811 NT	36897 0.83 1.0E-71 S72393.1 INT	36767 9.49 1.0E-71 AY007643.1 NT	3.08 1.0E-71 AV761217.1 EST_HUMAN	37336 1.52 1.0E-71 11433142 NT	2.43 1.0E-71 AV761217.1 EST_HUMAN	37706 2.12 1.0E-71 11418903 NT	37973 2.27 1.0E-71 11417191 NT	37974 2.27 1.0E-71 11417191 NT	3.13 1.0E-71 AB011399.1  NT	w495g03.x1 NCI_CGAP_Lu19 Homo sepiens cDNA clone IMAGE:2423188 3' similar to TR:O88705 O86705	28415 1.23 9.0E-72 AI857835.1 EST_HUMAN	32538 0.89 8.0E-72 BF036752.1   EST_HUMAN	37927 2.55 8.0E-72 11424480 NT	37928 2.55 8.0E-72 11424480 NT			30057 1.24 7.0E-72 4601868 NT Homo septens aconttess 2, mitochondrial (ACO2), muclear gene encoding mitocondrial protein, mRNA	30058 1.24 7.0E-72 4501868 NT	33646 2.87 7.0E-72 S41694.1 NT	1.52 7.0E-72 F28259.1 EST_HUMAN	4.9 6.0E-72 AL163246.2 NT	26102 4.86 6.0E-72 BF383707.1 EST_HUMAN	28103 4.86 5.0E-72 BF333707.1   EST_HUMAN	28102 13.05 5.0E-72 BF333707.1   EST_HUMAN	28103 13.05 6.0E-72 BF333707.1  EST_HUMAN	2.75 5.0E-72 L11645.1 NT	14 33427 1.65 5.0E-72 AU128584.1 EST HUMAN AU128584 NIZRP2 Homo septens GUNA clane NIZRPZ 2003/01 5
													L															
SEO D SEO D SEO D	21756		7 23280		1_			11 24424	1 24424		19780	13480	L		L.			07171	07170	_			L			13184		38 20114
Probe SEQ ID NO:	8789	888	10367	4042B	10801	11137	11228	11481	11481	12681	407	407	6232	11444	11444	1144	4139	4139	4130	200	12800	8727					1141	7138

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	Top Hit Descriptor	EST188312 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 6 end similar to similar to FAC1	au80c03.y1 Schnetder fetal brain 00004 Horno septens cDNA clone IMAGE:2782564 6' similiar to TR:099785 089785 HYPOTHETICAL 32.4 KD PROTEIN ;contains element MSR1 repetitive element;	AV724632 HTB Homo sapiens cDNA clone HTBAKB01 5	MR4-BT0598-070800-005-005 BT0598 Framo Saprems GUNA	MR4-B10588-010880-005-005 B10389 Frain September Culva	QV1-BI0632-280800-342-810 BI0632 main septems conv.	iomo sepiens hypometical protein to 100/1220.2 (50/100/1220.2), illinoso	Homo sapiens zinc finger protein 2.1-7-80 (2.1-80) mirkin, autamativas spirod, cumpros con	y483401.17 Soares fetal liver spicen 1NFLS Homo expens GUNA GOTB INVACE: 1157 02.5 Stilling to SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN;	Homo sapiens hect domain and RLD 2 (HERC2), mRNA	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mKNA	RC3-LT0023-200100-012-d11 LT0023 Homo sepiens CLIVA	RC3-LT0023-200100-012-411 LT0023 Homo septens cDNA	467-002.x1 Soares, febal_inver_spleen_1NFLS_S1 Homo sepiens cDNA clone INAGE::1849730.3 similar to TR:Q14498 Q14498 SPLICING FACTOR. [1] ;contains Alu repetitive element.contains element L1 repetitive	element;	SEC2609.51 NCI_CGAP_GCB1 Homo sapiens cDNA done INAGEC141213 3 smiller to 514.54 1 LATAN CATOR DRECLIRSOR.	AND CHICKCHICASI INCOCETATION CONTRACTOR CONTRACTOR STATES OF AN ANTICOCETATION OF CHARGOT IN STATES OF A PARTY OF CHARGOT IN STATES OF	RECORDS 1 NG CGAP GCB1 Hamb expense curve date invented to the senior of the precipitation of	y 128803.71 Sogres fetal ther spiech Tinth's frams square and the limited throughout.	yd29d09.af Scarce fetal liver spicent TNFLS Frome septens curve cause invested to	Homo septens WEE1 gene for protein kinase and partial ZNF143 gene for zino finger transcription factor	Homo saplens pre-B-cell colony-enhancing factor (PBEF) mRNA	and 3a06.s1 Scenes testis JNHT Hamo explens CDNA done 13102303'	Human chondrottin sulfate protectatycan versican V0 splice-variant precursor peptide mRNA, complete cds	Human chondroitin sulfate proteogrycen versioen V0 spiloe-varient precursor peptide mRNA, complete ods
אוואופ בייטון גומסס באוווים	Top Hit Deterberse Source	EST_HUMAN			П	П	T_HUMAN		LN.	T_HUMAN		FN	EST_HUMAN	EST_HUMAN		EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Ę	Ę	EST_HUMAN	Ę	Ę
Bigino	Top Hit Acessian No.	6.0E-72 AA316832.1	6.0E-72 AW161274.1				5.0E-72 BE926845.1	<b>§</b>	4.0E-72 AF170025.1	T87947.1	TN 28867 NT	TN 6923689 NT	4.0E-72 AW 836230.1	4.0E-72 AW836230.1		4.0E-72 AI248796.1		4.0E-72 AA465388.1	4.0E-72 AA465388.1	4.0E-72 H79421.1	4.0E-72 T81910.1	4.0E-72 AJZ77548.2	5031976INT	3.0E-72 AA723823.1	3.0E-72 U16306.1	3.0E-72 U16306.1
	Most Similer (Top) Hit BLAST E Velue	6.0E-72	6.0E-72	5.0E-72	5.0E-72	5.0E-72	5.0E-72	4.0E-72	4.0E-72	4.0E-72 T87947.1	4.0E-72	4.0E-72	4.0E-72	4.0E-72		4.0E-72		4.0E-72	4.0E-72	4.0E-72						
	Expression Signal	0.55	4.14	0.58	2.74	2.74	2.52	1.12	0.75	. 0.83	128	124	0.49	0.48		124		45.1	1.54	609	1.72	4.28		123	1	5.57
	ORF SEQ ID NO:	34500				39068			31677	<u> </u>		l				37208	ŀ	38115							27.152	
	Econ SEQ ID NO:	24194	2005	23244	24511	24511	26929	17877	18837	19785	20500	23069	22870	22870		23707		24554	1 _	L.	L		L	1		1
	Probe SEQ ID NO:	8463	8	10320	11573	11573	12389	88	55. 65.	e e	2830	10143	40750	3775	3	10788		11616	11616	11857	11988	49790	27.2	7 8	1159	1150

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ngie Exon Probes Expressed in Bone Marrow	Top Hit Descriptor	Human gamma-aminobutyric acid transaminase mRNA, partial cds	Human gamma-aminobutyric acid transaminase mRNA, partial cds	TCAAP1E1252 Pediatric acute myelogencus leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1252	Homo sapiens 959 to config between AML1 and CBR1 on chromosome 21422, segment 3/3	Homo sapiens hypothetical protein FL/20585 (FL/20585), mRNA	TCR V delta 2-C alpha ≐T-cell receptor delta end C alpha fusion gene {atternatively spliced, splice junction} [humen, precursor B-cell line REH, mRNA Partial, 211 m]	Homo sapiens hypothetical protein (FLJ1127), mRNA	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds	Homo sepiens protein methyltransferase (JBP1) mRNA, complete cds	EST371747 MAGE resequences, MAGF Homo sapiens cDNA	Homo sepiens semaphorin W (SEMAW) mRNA	Hamo sepiens growth factor receptor-bound protein 10 (GRB10) gene, exan 5	Homo sepiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5	Homo sepiens mRNA for KIAA1081 protein, partial cds	Homo sepiens mRNA for KIAA1081 protein, pertial cds	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA	Homo sapiens basic transcription factor 2 p44 (bt/Zp44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and eurwival motor neuron protein (anni) genes, complete cds	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA	Homo sepiens S100A12 gene for Celgranulin C, exxon 2 and joined cds	Homo sapiens CD37 antigen (CD37), mRNA	Homo sapiens CD37 artigen (CD37), mRNA	Homo septens ADP-ribosylation factor binding protein GGA3 (GGA3) mRNA, complete cds	Homo sepiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA	601890418F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5	601890419F1 NIH_MGC_17 Hamo sapiens cDNA clone IMAGE:4131461 5	e/28609.s1 Soares_testis_NHT Homo sepiens cDNA clone 1391609 3' similar to gb:X02067 H.sepiens mRNA for 7SL RNA pseudogene (HUMAN);	Rattus norvegicus putative phosphate/phosphoencipyruvate translocator mRNA, complete cds	Homo sapiens vacuciar protein scriing 41 (yeast homolog) (VPS41), mRNA	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mKNA
Xon Probes E	Top Hit Detabase Source	¥	Z	EST HUMAN	Ī		-		LN TN	LNT TN	T_HUMAN		NT IN		LN.	LN.		- LN		IN.			NT		T HUMAN	EST_HUMAN	EST_HUMAN			
	Top Hit Acession No.			-		23548		11416196 NT	3.0E-72 AF167672.1		3.0E-72 AW959677.1	4759093 NT			3.0E-72 AB029004.1	3.0E-72 AB029004.1	4826987 NT		5031892		11424091 NT	11424091 NT	3.0E-72 AF190864.1	11428671 NT	3F308560.1	20E-72 BF308560.1	2.0E-72 AA789277.1	20E-72 AF182714.1	7657676 NT	11321578 NT
	Most Strater (Top) Hit BLAST E Vetue	3.0E-72 U80226.1	3.0E-72 U80226.1	3.0E-72	3.0E-72	3.0E-72	3.0E-72 S77589.1	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72 U80017.1	3.0E-72	3.0E-72	3.0E-72 11	3.0E-72	3.0E-72	205-72	20E-72	20E-72	20E-72	20E-72	1.0E-72	1.0E-72
	Expression Signal	0.71	0.71	1.45	13.29	2.41	2.52	3.77	1.31	1.31	1.02	1.06	1.91	1.91	4.78	4.78	3.89	1.87	1.07	7.09	3.23	3.23	3.56	1.53	0.62	0.62	2.4	6.47	3.76	1.24
	ORF SEQ ID NO:	27193	27194	27528	28062	29265	28778	30492	30710	30711	31037	-	32386	32387	32600	32801	33103	34160	34898	37220	38383	38384	38546	32362		35853	l _	31745		33046
	SEQ ID	14238	l	i	16148	16345	16876	17598	17817	17817	18158	l	19171	1917	18362	18362			1	L	1	24783	l	19150		22415				19767
	Probe SEQ ID NO:	1188	128	1623	3000	3282	3886	4576	4800	4800	5140	<b>3699</b>	6092	6092	98239	06239	2929	888	8516	10797	11912	11912	12078	88	9451	9451	11092	12726	5861	6711

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Top Hit Descriptor	AV729428 HTC Homo sepiens cDNA clone HTCAAF071 6	H.seplens SH3GLP2 pseudogene, 5' end	Homo sepiens chromosome 21 segment HS210048	RC3-NNC068-270400-011-c04 NN0068 Homo sepiens cDNA	Homo septens BASS1 (BASS1) mRNA, pertial cds	RC3-NN0068-270400-011-c04 NN0066 Homo sepiens cDNA	Human beta globin region on chromosome 11	Homo septens caspase 8, apoptosis-related cysteine protease (CASP8) mPNA	Homo sepiens Perkinson disease (autosomal recessive, juvenile) 2, perkin (PARK2), transcript variant 3, mRNA	Homo saptens Parkinson disease (autosomai recessive, juventie) 2, parkin (PARK2), transcript variant 3,	THACKA	Mus musculus rhohao-interacting citron kinase (Crit) mRNA, complete cos	Mus musculus rho/rac-interacting citron kinase (Crity) mRNA, complete cds	Homo sepiens mRNA for KJAA1591 protein, partial cds	Homo sepiens interleukin 4 receptor (IL4R), mRNA	Homo sepiens Interleukin 4 receptor (IL4R), mRNA	Human peripheral myelin protein 22 mRNA, complete cds	Hamo sapiens mRNA for KIAA1329 protein, partial cds	Gallus gallus Decht2 protein (Decht2) mRNA, complete cds	Gallus gallus Dacht2 protein (Dacht2) mRNA, complete cds	Homo sapiens glufathione synthetase (GSS) mRNA	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA	Homo sapiens supervilin (SVIL), transcript variant 1, mRNA	Homo sapiens KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2 (KIAA1080), mRNA	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA	Homo septens galactosyloeremidese (Krabbe disease) (GALC), mRNA	Homo sapiens mRNA for KIAA1059 protein, pertial cds	RC3-NN0068-270400-011-c04 NN0068 Homo sepiens cDNA	AU121585 MAMMA1 Homo septens cDNA clone MAMMA1000490 5	CM/1-HT0282-111199-042-h10 HT0282 Homo septems CUNA	gg61b07.r1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:1839637 6' stratter to contains etement MER22 repetitive element;
Top Hit Detribase Source	EST_HUMAN	NT	M	EST HUMAN	FA	EST_HUMAN	NT	NT	Ę		Į.	NT	NT	NT	TN	NT	TN	IN	NT	NT	NT	M	F	     	Z	NT	¥	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	Ļ		3.0E-73 AL163248.2	3.0E-73 AW898081.1	1	۲.	101317.1	4502582 NT	T668639 NT		7665539 NT	1	20E-73 AF086824.1	.1	11431471 NT	11431471 NT		1	1	2.0E-73 AF198349.1	4504168 NT	11496980 NT	11496980 NT	11431598 NT	4557812 NT	4657812 NT	2.0E-73 AB028982.1	2.0E-73 AW898081.1	1.0E-73 AU121585.1	1.0E-73 BE151283.1	1.0E-73 A147427.1
Most Smiller (Top) Hit BLAST E Vellue	3.0E-73 AV729428.	3.0E-73 X99660.1	3.0E-73	3.0E-73	2.0E-73 A	2.0E-73	20E-73 U01317.1	20E-73	20E-73		2.0E-73	2.0E-73	20E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73 MD4048.1	20E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	20E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73/	2.0E-73	1.0E-73	1.0E-73	1.0E-73
Expression Signal	0.55	1.66	1.35	1.97	1.9	2.85	1.58	3.89	7.0		0.77	0.7	0.7	6.38	1.52	1.52	0.59	0.77	0.55	0.65	1.12	1.69	8.	140	264	264	181	1.81	281	12	1.47
ORF SEQ ID NO:	35504				26868			28170	29527		28528	32802	32903	32964	33206	33207	34427		L.	L									27814		
SEQ ID	77022	24011	25667	25569	13908	14985	15318	_	1		16607	19637	19637	19685	18911	1891				22843					L				L		<u>L</u> i
Probe SEQ ID	8	11047	13017	1302 1202	882	1983	2308	3188	388		88	6577	129	1298	8388	888	8082	8080	0686	0586	10788	10863	10863	11107	11395	41395	11420	12681	1788	6495	9857

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ight Lives Lybrasses in Color in the Color i	Top Hit Descriptor	601276071F1 NIH_MGC_20 Hamo sapiens cDNA clane IMAGE:3617105 5	Homo sepiens CD39-like 4 (CD39LA) mRNA	Ce2+/calmodulin-dependent protein kinase IV kinase isoform (rats, brain, mRN4, 3429 nt)	Ce2+fcalmodulin-dependent protein kinase IV kinase isorom (rats, brain, mxVvA, 3429 m)	Homo sapiens NKGZD gene, excm 10	Homo sapiens chromosome 21 segment HSZ10046	60164928471 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3832897 5	601191927F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE.3333655 5	Homo sapiens S164 gene, partia cds, PS1 and hypothetical protein garies, compliete cds, and S171 gene, partial cds	xn78g07.x1 Soares_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:2700636 3'	601283521F1 NIH_MGC_44 Homo septens cDNA clone IMAGE:3605453 5	601283621F1 NIH_MGC_44 Hamo sepiens cDNA clane IMAGE:3605453 5	UI-H-BIO-earh-h-03-0-UI,s1 NCI_CGAP_Sub1 Homo sepiens cONA cione IMAGE 2708386 3	UI-H-BIO-eah-h-03-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA cione IMAGE:2708365 3	hr64e11.x1 NCI_CGAP_Ktd11 Homo sapiens cDNA clone IMAGE:3132332 3	hr54e11.x1 NCI_CGAP_K411 Hamo sapiens aDNA clane IMAGE:3132332.3	Homo sapiens DEAD/H (Asp-Git-Ala-Asp/His) box polypeptide 11 (S.cerewislae CFL1-like helicase) (DDX11) mRNA	Homo sapiens DEAD/H (Asp-Gtu-Ale-Asp/His) box polypeptide 11 (S.cerev/stas CHL-Hie helicase) (DDX11) mRNA	Homo seplens actin filament associated protein (AFAP), mRNA	df17c09.y1 Morton Fetal Cochlea Homo saplens cDNA clone IMAGE:2483704 5'	PMIO-CT0288-271099-001-H07 CT0289 Hamo sepiens cDNA	Homo sepiens phosphatidylinositid giycan, class L (PIGL), mRNA	H. sapiens mRNA for TPCR16 protein	Homo sepiens VAMP (vesicle-associated membrane protein)-associated protein A (3540) (VAFA) invova. end translated products	Homo sapiens interleukin 4 receptor (IL4R), mRNA	Homo sapiens interleukin 4 receptor (IL4R), mRNA	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA	Homo sepiens KIAA0716 gene product (KIAA0716), mRNA	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA	H.saplens mRNA for HIP-
	Top Hit Detablese Source	EST_HUMAN 6		NT				╗	EST HUMAN	<u> </u>	EST_HUMAN >			EST_HUMAN I			EST_HUMAN				T HUMAN	EST_HUMAN		¥							¥
Pigillo	Top Hit Acession No.	1.0E-73 BE385477.1	· 4557426 NT			1	2	+	7.0E-74 BE266305.1	6.0E-74 AF109907.1	.1	1		1.1	.1	1	1	4758135 NT	4758135 NT	11056013 NT	5.0E-74 AW020986.1		11425417 NT	<b>39670.1</b>	IN SARTOSA.	14434A74 NT	14431474 NT	T882263 NT	7662263 NT	-	5.0E-74 Y09420.1
1	Most Similar (Top) Hit BLAST E Vatue	1.0E-73	8.0E-74	8.0E-74 S83194.1	8.0E-74 S83194.1	7.0E-74 AJ001689.	7.0E-74 AL163246.	7.0E-74	7.0E-74 E	6.0E-74	8.0E-74 /	6.0E-74	6.0E-74	8.0E-74/	8.0E-74/	6.0E-74	6.0E-74	8.0E-74	8.0E-74	6.0E-74	5.0E-74	6.0E-74	6.0E-74	5.0E-74 X89670.1	K 0E-74	E 05 74	A 05-74	5.0E-74	5.0E-74	5.0E-74	5.0E-74
	Expression Signal	21	1.47	1.84	1.84	4.43	.201	2.25	4.84	5.19	1.03	7.92	7.82	1.12	1.12	1.28	1.28	4.18	4.18	3.08	2.09	3.68	1.78	12.05	1.22	12.0	274	2.18	0.54	3.05	4.06
	ORF SEQ ID NO:	37455	28742	32308	32307	27989	28311	36051	31734	27120	27639	28357	28358	28852	28853	28679	29680	30955		L	26917		31482				20000				37570
	SEO ID NO:	23904	13803	19704	19104	14987	16390	22602	26417	14168	14684	15335	15335	15834	15834	16768	16788	18075			13961	L		L	70007	L	Page 4	Ш		L.	ш
	Probe SEQ ID NO:	11779	742	203	1209	1988	888	8898	12784	1124	\$	222	2324	2875	2875	3726	3728	5065	FOR S	2430	908	2713	5481	2887			200	5 60%	708	8371	11087

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Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor	H, sapiens mRNA for HIP-1	Homo sapiens DNA for amyloid precursor probin, complete ods	Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo sepiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	Homo septems DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	Homo sepiens probessome (prosome, mecropein) subunit, beta type, 1 (PSMB1) mRNA	Homo septems proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mPNA	Homo eapiens mRNA for KIAA1168 protein, partial cds	Homo sapiens PLP gene	Homo sepiens PLP gene	Homo sapiens chromosome 21 segment HS21C047	Homo sapiens KIAA0569 gane product (KIAA0569), mRNA	Homo sepiens mRNA for transmebrane receptor protein	Homo sapiens mRNA for KIAA1476 protein, partial cds	EST13131 Thymus tumor III Homo sepiens cDNA 5 end similar to similar to ribosomal protein L37	EST01132 Subtracted Hippocampus, Stratagene (cat. #839206) Homo sapiens cONA clone HHCPF91	no17g05.s1 NCI_CGAP_Phe1 Hamo sepiens cDNA clane IMAGE:110098437	Hamo sapiens glyceraddehyde-3-phosphata dehydrogenasa (GAPD), mRNA	Homo sapiens giyoeraidehyde-3-phosphate dehydrogenase (GAPD), mRNA	Human endogenous retrovirus HERV-K-T47D	wo51e07.x1 NCI_CGAP_Lu28 Homo septens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-85, ;contains element MER22 repetitive clement ;	Homo sapiens epidermal growth factor receptor (avian erythrobiastic leukennia viral (werb-b) oncogene	homolog) (EGFR) mRNA	Homo saptens epidermal growth factor receptor (avian erythroblastic leutemia viral (v-erb-b) oncogena boundary (cross) mPNA	Indiada) (Edity) Index	1.2.1 1.0 Collaboration equation	Novel human gene mapping to chomosome 22	Novel human gene mapping to chomosome 22	Human platelet glycoprotein IIb mkNA, 3' end	RC6-HT0678-220500-011-C03 H10678 Hamo septems GUNA
Top Hit Database Source	N.	NT	H	¥	5	¥	NT	NT	٦	NT	NT	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	MT	NT	EST_HUMAN		¥	į.	- Iı	ESI HOMAIN	K	ĮN.	Į.	EST_HUMAN
Top Hit Acession No.	709420.1		4.0E-74 AB028942.1	4.0E-74 AB026898.1	4 OF-74 AB026999 1	4506192 NT	4506192 NT	4.0E-74 AB032894.1	4.0E-74 AJ006976.1	4.0E-74 AJ006978.1	4.0E-74 AL163247.2	7662183 NT	17227.1	4.0E-74 AB040909.1	3.0E-74 AA300378.1	3.0E-74 M78984.1	3.0E-74 AA601483.1	7669491 NT	7669491 NT	20E-74 AF020082.1	20E-74 Al960528.1		4885198 NT	0012001	N SECTOR	2.0E-74 Al557280.1	2.0E-74 AL355092.1	2.0E-74 AL355092.1	2.0E-74 J02963.1	2.0E-74 BE711134.1
Most Similar (Top) Hit BLAST E Value	5.0E-74 Y09420.1	4.0E-74 D87675.1	4.0E-74	4.0E-74	405-74	4.0E-74	4.0E-74	4.0E-74	4.0E-74	4.0E-74	4.0E-74	4.0E-74	4.0E-74 Z17227.1	4.0E-74	3.0E-74	3.0E-74	3.0E-74	20E-74	20E-74	20E-74	2.0E-74		2.0E-74		2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74
Expression	4.06	1.85	5.8	22	2.2	238	2.38	1.51	18.0	6.46	1.23	2.06	0.99	0.74	21.61	2.57	2.69	58.94	58.94	6.0	1.32		3.54		3.54	3.02	3.67	3.67	0.83	2.03
ORF SEQ ID NO:	37571							l								36208							27606				30833		30838	
SEQ ID	24048	13374	13909	L	L	15103	15103	15159	15441	16164	17125	17609	17887		1_	22755		14012	14012		<u></u>	1	14631	l	1		18055		1	25847
Probe SEQ ID NO:	11087	85	88	1979	g,	2086	888	2442	2434	3107	<u>\$</u>	4587	4848	6055	988	2228	10703	898	88	1173	1249		1599		1599	2600	5042	5042	5046	5896

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Most Similar  Expression (Top) Hit Top Hit Acession Delabase Signal BLAST E No. Source	1.93 2.0E-74 11439587 NT	1.93 2.0E-74 11439587 NT	2.58 2.0E-74 11439587 NT	2.58 2.0E-74 11439587 NT	1.14 2.0E-74 BF030788.1 EST_HUMAN	1.35 2.0E-74 AB037816.1 NT	8.08 2.0E-74 AL 163204.2 NT	1.72 2.0E-74 5453965 NT	3.11 2.0E-74 AA196181.1 EST_HUMAN	2.22 1.0E-74 7857334 NT	3.95 1.0E-74 AW816405.1 EST_HUMAN	1.1 1.0E-74 8922829 NT	8.18 1.0E-74 X02344.1 NT	2.15 1.0E-74 4508020 NT	2.21 1.0E-74 AL163246.2 NT	3.56 1.0E-74 AB002059.1 (NT	2.83 1.0E-74 4758697 NT	0.79 1.0E-74 4504116 NT	0.79 1.0E-74 4504116 NT	5.75 1.0E-74 AL163268.2 NT	0.98 1.0E-74 BE083080.1 EST_HUMAN	0.71 1.0E-74 BE467769.1 EST_HUMAN	1.36 1.0E-74 D83327.1 NT	0.97 1.0E-74 M89914.1 NT	1.17 1.0E-74 11417977 NT	1.1 1.0E-74 BE549105.1 EST_HUMAN	1.1 1.0E-74 BE549105.1 EST_HUMAN	3.86 1.0E-74 AF214562.1 NT	0.71 1.0E-74 BF351951.1 EST_HUMAN	0.55 1.0E-74 AJ261550.1 NT	0.55 1.0E-74 AJ251550.1 NT	1.51 1.0E-74 11420549 NT	568 1.5 1.0E-74 AB007941.1 INT Homo sapiens mitting for NIAAU47.2 protein, partiel cos
	1.93	1.93	2.58	2.58	1.14	1.35	8.08	1.72	3.11	22	3.95	1:	8.18	2.15	22	3.56	2.83	0.79	0.79	5.75	96'0	0.71	1.36	76.0	1.17	1.1	1.1	3.86	0.71	0.55	0.55	1.51	1.5
Boan ORF SEQ ID NO:	25650 32280	25650 32281		25650 32281			22765 36220		,	13175 26086	13426 26348		ŀ						16983 29899				18226 31100	19916 33210		21360 34767							24971 38568
Probe SEQ ID NO:	1_		7209	<u> </u>		L	Ŀ			L	L		L	L	L		L	L	L	L	4082	4296	5217	£		<b>8394</b>	L	9157	9486	10600	10800	10847	12100

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	Top Hit Descriptor	Homo sepiens mRNA for KIAA0581 protein, partial cds	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cas	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds	Hamo sepiens DNA for emyloid precursar protein, complete cds	Homo sepiens KIAA0971 protein (KIAA0971), mRNA	Homo septens adeptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA	Homo septens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA	Homo sapiens cytopiasmic dynein intermediate chain 1 mRVA, complete cds	Homo sepiens cytoplasmic dynein intermediate chain 1 mRWA, complete cds	Homo septens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA	Homo sepiens Oncogene TIM (TIM) mRNA	Homo sepiens Oncogene TIM (TIM) mRNA	Homo sepiens snail 1 (drosophila homdog), zinc finger protein (SNAI1), mRNA	Homo sepiens Drosophila Kelch like protein (DKELCHL), mRNA	Homo septems synucketh, alpha (non A4 component of amyloid precursor) (SNCA), mKNA	Homo sepiens brefeldin A-inhibited guanine nucleotide eachange protein 1 (BIG1), mRNA	Homo saplens brefeldin A-Inhibited guartine nucleotide-exchange protein 1 (BIG1), mKNA	AV734880 cdA Homo septens cDNA clone cdABED02 5	qog1e02.x1 NCI_CGAP_Kid5 Homo capiens cDNA clone IMAGE:1915688 3' similar to TK:Q66388 Q65386 POL/ENV GENE ;	agoodo2x1 NCI_CGAP_UM Hamo sapiens cDNA clone IMAGE:2832707 3' similar to contains PTR7.t1	PTR7 repetitive element;	H.saplens ERCC2 gene, exons 1 & 2 (pertial)	601157633F1 NIH_MGC_21 Hamo sapiens cDNA clone IMAGE:3504272 6	601437130F1 NIH_MGC_72 Hamo sapiens CDNA clane IMAGE:3822333 5	RC5-B10640-020300-031-H03 B10640 Homo septens curva	RC5-810640-020300-031-H03 B10640 Homo septens CUNA
-	Top Hit Detabase Source	INT IN		ĮŽ	N.					NT N	7		•										EST_HUMAN /	EST HUMAN	1	EST HUMAN	M		Т	T	EST_HUMAN
	Top Hit Acession No.	3.0E-75 AB011153.1					7662421 NT	11420956 NT	20956	3.0E-75 AF123074.1	3.0E-75 AF123074.1	11628319 NT	11528319 NT	7662209 NT	7862209 NT	4885632	4885632	11420804 NT	11420222 NT	11436430 NT		6715588 NT	2.0E-75 AV734680.1	2 0E-76 AI311783.1		1.0E-75 AW168135.1		1.0E-75 BE279301.1	1.0E-75 BE894192.1	1.0E-75 BE082528.1	3E082528.1
	Most Straiter (Top) Hit BLAST E Vatue	3.0E-75	3.0E-75 M72393.1	3.0E-75 M72393.1	3.0E-75 M72393.1	3.0E-75 D87675.1	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	2.0E-75	2 OF-75		1.0E-75	1.0E-75 X52221.1	1.0E-75	1.0E-75	1.0E-75	1.0E-76
	Expression Signal	1.13	0.95	98.0	0.78	1.03	0.71	1.15	1.15	0.51	0.51	1.78	1.78	4.47	4.47	2.82	2.82	1.21	0.85	4.18	1.73	1.73	1.41	2.58		7.79	3.35	0.85	7.0	0.76	0.78
	ORF SEQ ID NO:	28477	28334	29335	29706	30118	30379	31179	31180	32891	32892	33479	33480	33858	33857	34204	34206	35730	36431	37341	38552	.38553		35405		28346		30630			34166
	SEQ ID	16258	16411	18411	16794	17228	17492	18429	18420	19714	19714	20159	20159	20313	20313	20828	20828	22301	22964	23828	24857	24857	18850	22080		15323	16015	17738			
_	Prefe SEQ ID NO:	88	88	338	ន្ទ	4197	4488	2323	833	1000	00057	6835	8835	2	8	\$	<b>28</b>	8838	10037	10908	12085	12085	2766	8	3	2311	7887	4718	5224	7843	8

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Top Hit Descriptor	### ### ### ### ### ### ### ### ### ##	601900234F1 NIH_MGC_19 Hamo septens cDNA clone IMACE:4123878 5	601900294F1 NIH_MGC_19 Hamo sapiens cDNA clone IMACE:4129878 5	ac77b08.s1 Strategene lung (#837210) Homo septens cDNA clone IMAGE:968599 3'	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively ispliced	601457130F1 NIH MGC_72 Hamo septiens aDNA clane IMAGE:3922303 67	wb30b10.x1 NCI_CGAP_GC8.Homo sepiens cDNA clone IMAGE:2307163 3' strailer to TR:O75235 O75235 TRAP1;	WESD510-X1 NCI_CGAP_GC8 Homo sepiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1 :	285507.s1 Scares fetal liver spleen 1NFLS. S1 Homo sapiens cDNA clone IMAGE:4475413'	Human fentitin Heavy subunit mRNA, complete cds	Homo saplens H factor 1 (complement) (HF1) mRNA	Homo sapiens H factor 1 (complement) (HF1) mRNA	Homo sepiens mediator (Sur2), mRNA	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA	Homo sapiens sertine/threcatine kinase 2 (STK2), mRNA	Homo sepiens mitochondrial carrier family protein (LOC55972), mRNA	Homo septens AIN-1 protein (LOC51151), mRNA	Hamo sepiens mRNA for KIAA1544 protein, partial cds:	Human adenosine deeminase (ADA) gene, complete cds	Homo sapiens baculoviral IAP repeat-containing 6 (BIRC6), mRNA	Home septens calcineum binding protein 1 (KIAA0330), mRNA	Homo sepiens ditydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo- gutanase complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA	Homo sapiens cAMP-specific phosphodiestensse 8A (PDE8A) mRNA, partial cds	Hamo septens lymphocyte antigen 75 (LY75) mRNA, and translated products	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA	Home sapiens sepiapterin reductase (7,8-difrydrobtopterin:NADP+ oxtdoreductase) (SPR) mRNA	601312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3858757 5	801142253F1 NIH_MGC_14 Homo saplens cDNA clone IMAGE:3508029 5
Top Hit Databerse Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Į.	EST HUMAN	EST HUMAN	EST HIMAN	EST HUMAN	Z	¥	MT	L	NT	N.	N.	F	LN.	NT	N	K	Ę	NI	K	N N	ᅜ	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	1.0E-75 AA388270.1	1.0E-75 BF313646.1	1	1.0E-75 AA664377.1		-	9.0E-76 Ales2848.1	0 0E-78 A 105/204/8 1	9.0F-76 AA702415.1		4504374 NT	4604374 NT	7706724 NT	11421442 NT	11436215 NT	11419212 NT	11416961 NT	AB046764.1		10442821 NT	11417882 NT	5016092 NT	7.0E-78 AF056490.1	505052	4507184 NT	4507184 NT	.1	6.0E-76 BE273201.1
Most Similar (Top) Hit BLAST E Vatue	1.0E-75	1.0E-75	1.0E-75	1.0E-75	1.0E-75	1.0E-75	9.0E-78	90 OF 78	9.0E-78	9.0E-78	8.0E-76	8.0E-76	8.0E-76	8.0E-76	8.0E-78	8.0E-76	8.0E-76	8.0E-76	8.0E-76	8.0E-76	8.0E-78	7.0E-78	7.0E-78	7.0E-76	7.0E-76	7.0E-78	8.0E-78	6.0E-76
Expression Signal	12.42	4.03	4.03	3.79	2.13	1.72	223	200	880	37.43	86.0	98.0	1.28	4.70	1.41	76.0	0.64	0.45	1.41	4.09	229	1.41	28.65	8.23	4.52	4.62	12.96	2.36
ORF SEQ ID NO:		36179			37840	ı				36670					34049	34141	35030	328656	37161	37518		28782						37469
E SEQ ID	21724	22724	22724	24182		ı	13168	49466	15,482	23188	13990	13990	15979	1		1	Į į	22417	23666	2300A	25408	13836	16358	16364	L		ı	23948
Probe SEQ ID NO:	8767	83/6	8268	11220	11428	12438	84	97	3676	10281	788	788	282	96239	73	7816	8838	8453	10744	11028	12767		3305	3311	4390	4399	1238	11783

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Source	П	EST HUMAN EST368823 MAGE resequences, MAGE Homo septens cDNA	EST_HUMAN   qe77h12x1 Soares_fetal_lung_NbHL19W Homo saplens cDNA clone IMAGE:1745083 3'	7 Homo sapiens glucoldnese (GCK) gene, excn 2	Homo septens distribution and metalloprotease domain 10 (AL/AM10) mit VA	Homo sepiens tousled-like kinase 1 (TLK1) mRNA, complete cds	Homo septens culin 1 (CUL1) mRNA	Homo septens ubquitin specific protesse 18 (USY18), miting	Homo sepiens EGF-like repeats and discolain I-like domains 3 (EUIL3), mixwa		HOMAN	Homo septens protein kinase C beta-li type (PRKCB1) mKNA, complete cas	H. sepiens mRNA for ubiquitin hydrolase	H. sepiens mRNA for ublquitin hydrolese	Homo sapiens 3-hydroxylsobutynyl-Coenzyme A hydrolase (HIBCH), mRNA	Homo sepiens 3-hydroxylsobutynyl-Coenzyme A hydrolesse (HIBCH), mRNA	Hamo septens sarting near 5 (SNX5), mRNA	Hamo septiens sorting neatin 5 (SNX5), mRNA	Human mRNA for KIAA0209 gene, partial cds	Human mRNA for KIAA0289 gene, partial cots	Homo septens SET domain and martner transposase fusion gene (SETMAR) mitting	Homo capiens SET domain and mariner transposace fusion gene (SE IMAR) mitAMA	yu64g01.r1 Weizmerin Olfectory Epitheflum Homo septems cDNA clone IMAGE:238608 6' similer to EST_HUMAN SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY265 - ;	yu64g01.r1 Wetzmann Offactory Eptithetium Homo septems cDNA clone IMAGE:238608 5 similar to EST_HUMAN SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5-;	П		EST_HUMAN PMS-MT0078-080800-005-503 MT0078 Homo saplens cDNA	EST_HUMAN AV764617 MDS Hamo saplens cDNA clane MDSBTF10 5	EST_HUMAN RC3-BN0053-170200-011-H01 BN0053 Homo sapiens cDNA	Hamo sapiens CYP17 gene, 5' end	Homo sapiens CGI-79 protein (LOC61634), mRNA	Hamo sapiens mikina tor Kura 1413 protein, partial cus
Top Hit Acessian	4504600 NT	6.0E-77 AW957753.1 ES	6.0E-77 Al204068.1 ES	5.0E-77 AF041015.1 NT	4567250 NT	6.0E-77 AF162668.1 NT	4503160 NT	8394518 NT	5031680 NT	5031680 NT	5.0E-77 AL043953.1 EST	A13975.1	(98296.1 NT	X98296.1 NT	11428849 NT	11428849 NT	11421928 NT	11421928 NT	5.0E-77 AB002297.1 NT	6.0E-77 AB002297.1 INT	5730038 NT	5730038 NT	3.0E-77 H65167.1 ES			3.0E-77 AI017333.1 ES	-	-	1.	2.0E-77 L41825.1 NT	7706315	2.0E-77 AB037836.1 NT
Most Similar (Tap) Hit BLAST E Value	6.0E-77	6.0E-77	6.0E-77	5.0E-77	5.0E-77	6.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77 M13975.1	5.0E-77 X98296.1		5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	3.0E-77	3.0E-77	3.0E-77	3.0E-77	3.0E-77	3.0E-77	3.06-77	20E-77	2.0E-77	2.0E-77	2.0E-77	2.0E-77
Expression	4.64	20.18	3.97	234	1.41	1.03	0.96	0.64	0.92	0.92	3.64	0.84	0.52	79.0	122	1.22	3	3	0.82	0.82	1.26	1.26	0.71	0.77	0.68	0.68	3.68	1.88	231	1.01	2.46	2.28
ORF SEQ ID NO:	282383	27/138	27551		27367	28709	28786					33499		33886	Ċ	35105				37277	28015	28016				L						28620
Exam SEQ ID NO:	13358	14187	14578	14276	14398	15691	15766	16580	17752	17752	17990		ı	ı	L	21679	L		23777	77762		15010		l			L		L			16898
Probe SEQ ID NO:	282	114	1545	1240	1382	2692	2774	3534	4732	4732	4075	<u>268</u>	75,48	7849	8711	8711	8628	8288	10857	10857	1989	1989	10862	10652	10068	90	41222	1354	1428	2102	2113	2600

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Top Hit Descriptor	Homo sapiens mRNA for KIAA1415 protein, partial cds	ho43b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens dDNA clone IMAGE:3040113 3' similier to SW:GAG2_HUMAN P10284 RETROVIRUS-RELATED GAG POLYPROTEIN ;	w.22g02.x1 NCI_CGAP_Bm62 Homo sepiens cDNA clone IMAGE:2260466 3° similer to TR:085245 065245 F21E10.7 PROTEIN. ;	tw22g02x1 NCI_CGAP_Bm52 Homo septens cONA clone IMAGE:2260466 3' similar to TR:065245 065245 F21E10.7 PROTEIN.;	ns68g12.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29. [1] ;contains element MSR1 repetitive element;	tw22g02.x1 NCI_CGAP_Brn52 Homo sepiens cDNA done IMAGE:2290466 3' striiter to TR:085245 085245 F21E10.7 PROTEIN. ;	tw22g02x1 NCI_CGAP_Bm52 Homo sepiens cDNA clone IMAGE:2260466 3' similar to TR:065245 065245 F21E10.7 PROTEIN. ;	601119852F1 NIH_MGC_17 Hamo septens cDNA done IMAGE:3029436 5	601476802F1 NIH_MGC_68 Hamo sapiens aDNA done IMAGE:3879505 5	at74a09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311 Q13311 TAX1-BINDING PROTEIN TXBP161. [1];	qy70c09x1 NCL_CGAP_Bm25 Hamo sapiens cDNA clone IMAGE:2017380 3° similar to WP:F28D11.1 CE05765 LOW DENSITY LIPID RECEPTOR-RLATED PROTEIN ;	Human protein kinase C substrate 80K-H (PRKCSH) gene, exxn 7	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7	601895183F1 NIH_MGC_19 Homo sapiens cDNA done IMAGE:4124541 5	601805183F1 NIH_MGC_19 Homo sepiens cDNA clone IMAGE:4124541 5	Homo sapiens mRNA for KIAA1278 protein, pertial ods	Homo sepiens mRNA for KIAA1276 protein, partial cds	Homo septens amyloid beta (A4) precursor protein (protesse nexin-li, Alzheimer disease) (APP), mRNA	Homo sepiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA	Homo sepiens amykoid beta (A4) precursor protein (proteese nexin-II, Abzheimer disease) (APP), mRNA	Homo sapiens amyloid beta (A4) precursor protein (protease nean-II, Alzheimer disease) (APP), mRNA
Top Hit Detabase Source	Ę	EST_HUMAN	EST_HUMAN (	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	NT	EST_HUMAN	EST_HUMAN		IN				
Top Hit Acession No.	20E-77 AB037836.1			2.0E-77 Al613519.1	2.0E-77 AA653025.1	20E-77 Al613519.1				2.0E-77 Al833003.1	2.0E-77 AI362707.1			2.0E-77 BF310349.1	2.0E-77 BF310349.1	1.0E-77 AB033102.1	1.0E-77 AB033102.1	4502168 NT	4502166 NT	4502166 NT	4502166 NT
Most Similar (Top) Hit BLAST E Velue	20E-77	2.0E-77	2.0E-TT	2.0E-77	2.0E-77	2.0E-77	20E-77	20E-77	20E-77	2.0E-77	20E-77	2.0E-77 U50321.1	20E-77 U50321.1	2.0E-77	2.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77
Expression Signal	228	1.25	0.68	0.68	2.32	0.65	0.65	2.06	1.62	14.21	0.75	5.64	5.64	0.5	9.0	0.94	0.94	1.33	1.33	231	2.31
ORF SEQ ID NO:	78621				30713	30357			l	33704	35264			36763	36754		26069	26294	26295	26891	26892
Exam SEQ ID NO:	15898			ł	17819			1				Ŀ		L	l _		13165	13368	13368	15853	15853
Probe SEQ ID NO:	2800	4064	4442	4442	4802	5158	5158	8065	883	7380	8874	8888	9888 888	10354	10354	\$	45	272	272	876	876

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Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor	,	Homo sepiens midNA for KIAA1101 procen, compress cas	Homo saplens 2,4-diencyl CoA reductase 1, minoriorizma (UECKII), minori	Homo sapiens CGI-80 protein (LOCS1628), mrdNA	Homo sepiens cAMP responsive element binding protein 1 (CREBT) mixtrA	Homo sapiens 959 to config between AML1 and CBK1 on chromosome Z1922; segment 1/3	Homo sepiens breast cancer 1, early onset (BRCA1), transcript versant BRCA1-earthe, minute.	qv09g04.x1 NCI_CGAP_Ktd8 Homo septens dDNA done IMAGET1881110 3	Homo sapiens cAMP responsive element binding protein 1 (CACED) mixina	Homo sapiens cAMP responsive element binding protein 1 (CRED1) minning	Homo sapiens chromosome 21 segment HSZTCU4/	Homo saplens dynactin 1 (DCIN1) gene, exons 27 and 20	Homo sepiens dynactin 1 (DCTN1) gene, exons 27 and 28	Human von Willebrand factor gene, exon 20	Homo saptens diaphanous (Drosophile, homolog) 1 (DIAPH1), mxWA	Homo saptens etastin (supravalvular acrtic stenosis, Williams-Beuran syndroma) (ELN), miXNA	Homo septens cultin 1 (CUL1), mRNA	Human mRNA for Iddney epidemal growth factor (EGF) precursor	H. septens DNA for Cane cGMP-PDE gene	H. sepiens DNA for Cone cCMP-PDE gene	Homo sapiens hu-GicAT-P mRNA for glucuronyfiransferase, complete cds	Homo sapiens hu-GicAT-P mRNA for glucuronyfiransferasa, complete cds	RC3-CT0254-280999-011-b05 CT0254 Homo septens cDNA	RC2-ET0023-080500-012-e05 ET0023 Homo septiens oDNA	RC2-ET0023-080500-012-605 ET0023 Hamo septems cDNA	AU118789 HEMBA1 Homo sepiens cDNA clone HEMBA1004354 5	AU118789 HEMBA1 Homo sepiens dDNA clone HEMBA1004304 b	602016826F1 NCL CGAP Brids Hamp septems CUNA date IMAGE. 4132211 3	Homo sepiens GDNF family receptor alpha 1 (GFRA1), mKNA	Homo sepiens hypothetical protein FLJ11316 (FLJ11316), mKNA	be54h03.ys NIH_MGC_10 Homo septems cDNA clone IMAGE:2800405 5 shriker to WP:Y4888A.8	CE22121;	Human collegenase type IV (CLC4) gene, excn 5	Homo sapiens Best's macutar dystroprty retained protein michtyk, parteal wis	dono saprens usinsioning giover races, boar maccos, con (100 m).
Ssion Top Hit Database Source						H		EST_HUMAN					TN.						N.	E		k	T_HUMAN		EST_HUMAN		EST_HUMAN /	EST_HUMAN				r_HUMAN	M		
Top Hit Acession No.		1.0E-77 AB029024.1	4503300 NT	TN6239NT	4758053 NT	1.0E-77 AJ220041.1	655332 NT	1.0E-77 AIZ73014.1	4758053 NT	4758053 NT	1.0E-77 AL163247.2	1	1.0E-77 AF086944.1		4885182 NT	5881412 NT	11420159	(04571.1			8.1	4.0E-77 AB029396.1	9.0E-78 AW753302.1	8.0E-78 AW947061.1	8.0E-78 AW947061.1	6.0E-78 AU118789.1	6.0E-78 AU118789.1	6.0E-78 BF344101.1	11432710 NT	11422486 NT		5.0E-78 AW673424.1	5.0E-78 M55586.1	5.0E-78 AF038536.1	11416585 NT
u	VENUE	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77 M25844.1	1.0E-77	1.0E-77	1.0E-77	1.0E-77 X04571.1	1.0E-77 X94354.1	1.0E-77 X94354.1	1.0E-77	1 0E-77	9.0E-78	8.0E-78	8.0E-78	6.0E-78	8.0E-78	8.0E-78	6.0E-78	5.0E-78					5.0E-78
Expression Signal		1.73	2.04	3.92	0.73	16.98	211	0.72	0.95	99.0	1.12	1.61	1.61	1.39	138	14.51	16.0	0.69	0.65	0 65	0.92	80	67	2.93	2.03	214	2.14	8.56	234	1.73		5.48	3.94		24.78
ORF SEQ ID NO:		28477	20028	30289	30438	30465	30589	30632	30438	30438		32324	32325	32471	10000		L	34373						1				L		26244		28590			31917
SEQ ID	<u> </u>	15455	16115	17408	17550	17575	12201	ı		1	ì	19120	19120		1	1	L		L	L	_	1						L		1	L	15570	1		18751
Probe SEO D	<u> </u>	2450	3058	4380	4525	AF. S	4680	477	0002	5219	5246	8038	8	8	CON	73.5	gCQZ	9040	000	3 8	2000	2000	10080	08580	083	8	8	33.55	67.72	3 8	7	2569	3308	5486	5655

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Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	EST385190 MAGE resequences, MAGB Hamo sepiens cDNA	Human lysosomal alpha-mannosidasse (manB) gene, exon 7	601648061F1 NIH_MGC_62 Hamo sapiens cDNA clane IMAGE:3831887 5	TCAAP1E0886 Pediatric acute myelogenous leukemia cell (FAB M1) Baykor-HGSC project=TCAA Homo sapiens cDNA cione TCAAP0886	TCAAP1E0886 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0886	DKFZp434N0323_r1 434 (synonym: hies3) Homo sepiens cDNA clone DKFZp434N0323 5	Novel human gene mapping to chomosome 22	w97b12.x1 NCI_CGAP_Kid11 Homo sepiens dDNA clone IMAGE:2485615 3' shrifar to SW:WAP_PIG 046655 WHEY ACIDIC PROTEIN PRECURSOR;	Hamo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds	Homo sapiens synoytin (LOC30816), mRNA	Homo sapiens phosphatidylinositid 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA	Homo sepiens phosphalidylinostici 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA	Homo sapiens SFRS protein kinase 2 (SRPK2), mRNA	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA	Homo sepiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mKNA	Homo sapiens ribosomal protein S8 kinase, 70kD, polypeptide 1 (RPSGKB1) mkNA	Homo saplens phosphatidylinosital 4-kinase 230 (pHK230) mRNA, complete cds	Homo sepiens phosphatidylinositol 4-kinase 230 (pl4K230) mRNA, complete cds	Homo sapiens X-ray repair complementing defective repair in Chinese hamstar cells 4 (XRCC4), mRNA	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo saplens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo saplens s-CaBP1 (CABP1) mRNA, complete cds	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)	Homo saplens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA	Homo sapiens gene for AF-6, complete cds	Homo sapiens eRF1 gene, complete cds	Homo sapiens eRF1 gene, complete cds	AU140604 PLACE3 Hamo sapiens cDNA clane PLACE3000373 6	Homo sapiens synapticlanin 1 (SYNJ1), mKNA
2001	Top Hit Detabese Source	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	N	EST_HUMAN	NT	NT	NT	NT	NT	LN	NT	NT	NT	NT	NT	Į,	N	NT	F	N	NT	NT	NT	NT	f.1 EST_HUMAN	NT
	Top Hit Acession No.	5.0E-78 AW953120.1	J60889.1	5.0E-78 BE960836.1	5.0E-78 BE241639.1	5 0F-78 RF241639 1		4.0E-78 AL355841.1	4.0E-78 AB85094.1	4.0E-78 AF107405.1	7656876 NT	4505806 NT	4505806 NT	11420732 NT	TN 6012897	7662409 NT	4506736 NT	4506736 NT	4.0E-78 AF012872.1	4.0E-78 AF012872.1	11417251 NT	11560151 NT	11580151 NT	ım	K05844.1	11024711 NT	4.0E-78 AB011399.1	3.0E-78 AF095901.1	3.0E-78 AF095901.1	3.0E-78 AU140604.1	4507334
	Most Similar (Top) Hit BLAST E Value	5.0E-78	5.0E-78 U60889.1	5.0E-78	5.0E-78	5.0F-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78 X05844.1	4.0E-78	4.0E-78	3.0E-78	3.0E-78	3.0E-78	3.0E-78
	Expression Signal	222	6.85	3.51	1.64	184	1.88	274	1.11	3.31	1.47	2.16	2.18	1.13	0.61	0.61	0.59	0.58	1.66	1.08	0.64	1.97	1.97	1.65	5.69	2.38	3.89	2.77	2.77	0.94	0.68
	ORF SEQ ID NO:	33681							27683	28360	30256	30719			32608	32809	33060	34052	35601	35602	36204								26190		29771
	SEQ ID NO:	20331	22402	22403	24562	24552	14182	14553	14688	15337	17377	17824	17824	18951	19369	18369	19781	20688	22171	22171	22761	23732	23732	24634	L	_	<u> </u>	<u>L</u> .	13265		16869
	Probe SEQ ID NO:	7367	8538	9639	11614	1189.4	1139	153	1656	8282	4350	4807	4807	2882	623	6297	67725	7733	8205	9205	87.23	10811	10811	11749	11883	12128	12797	162	162	3776	3829

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Table 4
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Single Exol Troposed of the Samuel State of th	Most Similar Top Hit Acession (Top) Hit Top Hit Acession (Top) Hit Ace	ID NO: Signal BLASTE No. Source	29771 0.79 3.0E-78 4507334 NT	5.79 3.0E-78 BE144758.1 EST HUMAN	37804 1.8 3.0E-78 BE166318.1 EST_HUMAN	4.1 20E-78 U04489.1 NT	1.43 2.0E-78 AA311872.1 EST HUMAN	34027 1.24 2.0E-78 AW 402308.1 EST_HUMAN	34028 1.24 2.0E-78 AW 402308.1 EST_HUMAN	34335 3.2 2.0E-78 BF689800.1 EST_HUMAN	34766 2.64 2.0E-78 AV714177.1 EST_HUMAN	35183 1.51 2.0E-78 AIS57509.1 EST_HUMAN	35184 1.51 2.0E-78 AI557509.1 EST_HUMAN	2780K 2 5 2 05-78 A197837.1 EST HUMAN	37040 2 03 2 0E-78 N66951.1 EST HUMAN	31357 3.22 1.0E-78 11417304 NT	31284 0.87 1.0E-78 AV648639.1 EST_HUMAN	2.95 1.0E-78 U52373.1 INT	31847 1.81 1.0E-78 11430480 NT	30838 3.81 9.0E-79 11625891 NT	30807 3.55 9.0E-79 BE000837.1 EST_HUMAN	31537	37785 3.249 9.0E-79 545445 NT	33109 0.87 9.0E-79 11430822 NT	1,06 9,0E-79 11424427 NT	34150 0.84 8.0E-78 11421735 NT	34151 0.84 9.0E-79 11421735 NT	34197 0.55 9.0E-79 D30858.1 NT	35079 0.5 9.0E-79 11417280 NT	35080 0.5 9.0E-79 11417260 NT	35821 5.53 9.0E-79 J02853.1 NT	35822 5.53 9.0E-79 J02853.1 NT	36218 0.68 9.0E-79 D87675.1 NT	
	ORF SEQ	ÖN Ö							<u> </u>							L			Ì	١							L							
		N S S	16869	L				1_		L.		1_		1	1_		L.			L	上	1_		1			l	1_			1_		L	
	Probe	SEC NO:	4131	40840	133	34.38	<u>}</u>	7,00	3	8003	8375	878	8785	1	44450	2024 - 1	7144	8499	12323	12774	4899	6507	6474	200	7573		2	7875	8889	8689	9418	9418	9735	10730

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Table 4
Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor		Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mrdVA, complete cos	Hamo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds	Hamo sepiens TRAFE-regulated IKK activator 1 beta UertA mRNA, complete cas	Hamo septens suppressar of white epricat hamolog 2 (SWAP2), mRNA	Homo sepiens suppressor of white eprical homolog 2 (SWAP2), mRNA	Homo sepiens KIAA1035 protein (KIAA1035), mRNA	Homo sepiens gamma-glutamytransferase 1 (GGT1), mRNA	Hamo septens chramosome 21 segment HS21C010	Homo sepiens period (Drosophilia) hamalog 3 (PER3), mRNA	60147276671 NIH_MGC_68 Harno sepiens cDNA clane IMAGE:3875657 3	284604.51 Sogres fetal liver spiesn 1NFLS_S1 Homo sepiens cDNA clone IMAGE:462568 3° similar to TR-0.15408 0.15408 NEUTRAL PROTEASE LARGE SUBUNIT ;	Hamo septens chromosome 21 segment HS21C082	Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA	Homo sepiens intersectin short isoform (ITSN) mRNA, complete cds	Homo sapiens cell-line tsA201a chloride ion current inducer protein I(Cin) gene, complete cds	Human zinc finger protein ZNF131 mRNA, partial cds	Homo septens MSTP016 (MST016) mRNA, complete cds	Homo sapiens mRNA for KIAA0892 protein, partial cds	601482143F1 NIH_MGC_68 Hamo sepiens cDNA clone IMAGE:3884554 5	601482143F1 NIH_MGC_68 Homo sepiens cDNA cione IMAGE:3884554 5	Homo sapiens netrin 1 (NTN1), mRNA	Homo sepiens netrin 1 (NTN1), mRNA	601112055F1 NIH_MGC_16 Hamo sapiens cDNA clane IMAGE:3352885 5	Homo sapiens mRNA for KIAA0820 protein, pertial cds	Homo sapiens mRNA for KIAA0820 protein, partial ods	Homo sepiens Bci-2-essociated transcription factor short form mRNA, complete cds	Homo sapiens tetratricopeptide repeat domain 3 (TTC3), mRNA	AV698115 GKC Hamo septens cDNA clane GKCAHE11 5	y48f03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208641 3'	601159415F2 NIH_MGC_53 Hamo sepiens aDNA dane IMAGE:3511107 5	Homo sapiens BCL2-like 2 (BCL2L2) mRNA	Homo sapiens Gardner-Rasheed feline sercoma viral (v-fgr) oncogene homolog (FGR) mRNA	Homo sapiens Gardner-Kasheed teline sarcoma Wrai (M-Igr) droogene norwooj (FGK) mivNA
Top 工程 Detablese		MT	IN	NT	IN	IN	H	LN.	NT	M	EST_HUMAN	EST HIMAN	M	¥	¥	N.	¥	NT	NT	EST_HUMAN	EST_HUMAN	NT	NT	<b>EST_HUMAN</b>	NT	M	NT	NT	EST HUMAN	EST_HUMAN	EST_HUMAN	NT.	NT	Į,
Top Hit Acession No.		9.0E-79 AF062346.1	9.0E-79 AF062348.1	8.0E-79 AY008273.1	72827	11423827	7862451 NT	11417877 NT	8.0E-79 AL163210.2	8567387 NT	7.0E-79 BE619648.1	6 OF 70 A A 6008/20 1	5.0E-79 AL 163282.2	8922325 NT	3.0E-79 AF114488.1	3.0E-79 AF232708.1	J09410.1	3.0E-79 AF110322.1	3.0E-79 AB020699.1	3.0E-79 BE789470.1	3.0E-79 BE789470.1	11426770 NT	11426770 NT	3.0E-79 BE256893.1	3.0E-79 ABO14520.1	3.0E-79 AB014520.1	VF249273.1	10835036 NT	3.0E-79 AV698115.1	2.0E-79 H63129.1	2.0E-79 BE379928.1	4757841 NT	4885234 NT	4885234
Most Similar (Top) Hit BLAST E	Value	9.0E-79	9.0E-79	8.0E-79	8.0E-79	9.06-79	9.0E-79	9.0E-79	8.0E-79	8.0E-79	7.0E-79	0. 30 A	5.0E-79	4 0F-79	3.0E-79	3.0E-79	3.0E-79 U09410.1	3.0E-70	3.0E-79	3.05-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.05-79	3.0E-79	3.05-79	3.0E-79	3.0E-79	2.0E-79	2.0E-79	2.05-79	2.0E-79	2.0E-79
Expression Signal		£.1	1.53	4.27	2.87	2.97	2.71	1.55	1.33	99.0	7.24	28.0	457	1.35	1.48	202	28	6.05	1.01	98'0	98'0	4.05	4.05	8.0	3.31	3.31	1.58	0.57	9.0	2.05	1.29	1.35	4.78	4.78
ORF SEQ ID NO:		37204	37205			l	38586		29708	31078	29242		38290	L	26331					32115	32116	32138	32139	33267	33294	33295					26622			
SEO ID	į	23706	1		24724	24724	24985	25556	16797	18204	16320	600	24707	18248	13405	14030			l		18931	18962		19961	L.	19997		L		L	L			14036
Probe SEO ID	<u> </u>	10784	40784	11408	11841	11841	12115	13000	3766	5185	3268	1	11824	340	313	86	3115	5435	5812	584	584	5883	<b>5883</b>	8008	7282	7282	8504	9758	10712	287	635	828	<b>388</b> 5	985

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Single Exon Probes Expressed in Bone Marrow

gie Exon Probes Expressed in Doire marion	Top Hit Descriptor	#128-07 x1 NCI CGAP Pr28 Hamp sapients aDNA clane IMAGE:27186853	TOTAL STATE OF THE	HOMO Septems Licensory gards 4 (License), included	Homo sapiens Dicktopr gene 4 (Dr.N4), mr.N.A.	Homo sapiens KIAA0703 gene product (KIAA0703), mraya	Homo sapiens phosphodiasterase 6A, cGMP-specific, rod, alpha (PUCOA), mixak	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, apna (PUPCOA), mixina	Hamo sepiens mRNA for Fes-essociated factor, FAF1 (Fet1 gene)	Homo sapiens chloride channel CLC4 (ClC4) mRNA, complete cds	Homo sapiens mRNA for Fas-associated factor, FAP1 (Par1 gene)	Homo saplens chromosome 21 segment NSZTCMVO	EST182926 Linket T-cells VI Homo septens CDNA 3' end similiar to similiar to C. eregans hyboureuch process, according to the septens hyboureuch process.	COSTIN DVSVS.13	OHO Septens A usua reporter of the control of the c	Homo sapiens mRNA for KIAAOSSO protein, partial cus	Homo sapiens membrane essociated calcium-independent phospholipase A2 gamma mRNA, complete cds	Homo sapiens Rino GTP ase activating protein 6 (ARHGAP6), transcript variant 4, mRNA	Homo seniens Rho GTP ass activating protein 6 (ARHGAP9), transcript varient 4, mRNA	Homo semients refinoblastorma-files 1 (p107) (RBL1) mRNA	1900 Carried and Personal House (F. 11006), mRNA	Hullis Sapratio injurational process H. (20275/FILE) mRNA	From Septems hypothetical produit is 120275 (F. 120275), mRNA	Harries septemblished ATPass H+ transporting Inspectment (vacuolar proton pump) membrane sector	essociated protein MB-9 (H. septens) (LOC83961), mRNA	H4(D:10S170)=putative cytoskeletal protein [human, tryroid, mRNA, 3011 fr]	H4(D10S170)=putative cytoskeletal protein [human, mytota, mrtvva, 3011 m.]	RC4-BT0310-110300-015-f10 BT0310 Hamp septems 42NA	RC4-BT0310-110300-015-110 BT0310 Homo septems curva	Homo sapiens p53R2 gene for riborucieotide reduciase, exon 9 and compress cos	Homo sapiens KIAA0879 protein (KIAA0879), mrava	Homo sapiens mixing for Kladucasa protein, per usi cues	Homo sapiens cannenn Eigh LAG seventiess Chipatricopera (Chipatricopera)	
XON PTODES EX	Top Hit Detabase Source	Т	NAMOL							노	F	NT		HOMAN		- LN	<u> </u>											EST_HUMAN	EST_HUMAN				1445	ESI_HUMAN
Single	Top Hit Acession No.		T	7657024 NT	7857024 NT	7682255 NT	4585863	4585863 NT	2.0E-79 AJZ71408.1			2.0E-79 AL163208.2			81769	2.0E-79 AB020637.1	2 NE-79 AF283613.1	7382479	TIM OF ACOUST	130247	4500442	11427428 NI	8923248 NT	8923248	11432184 NT	2.0E-79 S72869.1	2.0E-79 S72869.1	2.0E-79 BE064388.1	2.0E-79 BE064386.1	2.0E-79 AB036532.1	7662357 NT	AB020640.	11418322 NT	1.0E-79 BF363071.1
٠	Most Similar (Top) Hit BLAST E Vatue		20E-79/	2.0E-79	2.0E-79	20E-79	2.0E-79	20E-79	2.0E-79	20E-79	2.0E-79	2.0E-79		2.0E-79	2.0E-79	2.0E-79	2 OF-79	07.00.0	2.0E-19	2.0E-/8	2.0E-79	2.0E-79	2.0E-79	2.0E-79	2.0E-79	2.0E-79	2.0E-79	2.0E-79	2.0E-79	2.0E-79	2.0E-79	2.0E-79		
	Expression Signal		1.02	0.97	76.0	0.92	4.97	4.97	0.94	0.83	1.15	76.0		1.25	0.88	1.07	0.7		1./4	1.74	1.13	2.55	0.46	0.46	*	3.12	3.12	3.86	3.86	2.62	3.21	4.8	2.41	3.28
	ORF SEQ ID NO:			27819	27820	27914	28193	28194	28237	29887	30113	30628			32088		24778							35513	35749			1			31296	31837	31804	
	SEO ID		<del>1</del> 4082	14832	14832	14918	15174	15174	15217	18973	17224	17738		18848	18905					Ì				22084	222	1_	L	1_		L		L	25254	25668
	Probe SEQ ID NO:		1036	18	1804	1893	24.58	2 2	33.5	200	4193	4716		5754	5815	6371	5	327	7373	7373	8437	2988	9118	9118	0857	10452	40452	11368	11368	41666	12207	12283	12524	6739

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Ingle Excit modes Expressed in Done marrow	Top Hit Descriptor	tys7e08.x1 NCI_CGAP_U2 Homo sepiens cDNA clone IMAGE:2281286 3' similar to TR:0.28623 0.28623 TEKTIN C1.;	tys7e08.x1 NCI_CGAP_Ut2 Homo sepiens cDNA clone IMAGE-2281286 3' similer to TR-026623 0.26623   TEKTIN C1.;	601311517F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3632809 5	QV2-HT0540-120900-358-a05 HT0540 Homo septens cDNA	ai23e05.s1 Sogres_testis_NHT Hamo sepiens cDNA done 1343648 3'	at23e05.s1 Soares_testis_NHT Hamo sapiens cDNA clone 1343648 3*	601581652F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3836061 5	Homo sepiens solute center family 7 (cationic amino acid transporter, y+ system), member 8 (SLC/AB), mRNA	Homo sepiens solute cernier family 7 (cationic arritno acid transporter, y+ system), member 8 (SLC/AB), mRNA	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA	Homo sapiens triple functional domain (PTPRF Interacting) (TRIO), mRNA	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA	Callithrix jacchus olfactory receptor (CJA80) gene, partial cds	tf88d02x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' stmiler to SW:NUEM_HUMAN Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;	Homo sapiens NRD convertase mRNA, complete cds	Hamo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA	Homo sepiens mRNA for KIAA1165 protein, partial ods	Hamo sapiens mRNA for KIAA1155 protein, pertial cds	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)	Homo septens tubby like protein 3 (TULP3), mRNA	Homo sepiens KIAA0941 protein (KIAA0941), mRNA	Homo espiens dystrophin (DMD) mRNA, complete cds	Homo sapiens G protein-coupled receptor 31 (GFN51), mKNA
XOII LIODES	Top Hit Database Source	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	H	Į.	¥	K	F	F	NT	EST_HUMAN	¥	NT	NT	NT	Į,	NT	NT	NT	NT	NT	노
Siligle	Top Hit Acession No.	1.0E-79 Al613480.1	1.0E-79 AI®13480.1	1.0E-79 BE394211.1	-		9.0E-80 AA725848.1	9.0E-80 BE798603.1	11433924 NT	11433924 NT	B.0E-80 U94387.1	11422647 NT	11422647 NT	MT 8005921 NT	FX 1285009	7.0E-80 AF127882.1	6.0E-80 AI422197.1		6831094 NT	6631094 NT	6.0E-80 AB032981.1	6.0E-80 AB032981.1	11421462 NT	6.0E-80 AJ404468.1	11436736 NT	7682393 NT		11526464 NT
	Most Similar (Top) Hit BLAST E Value	1.0E-79	1.05-79	1.0E-79	1.0E-79	9.0E-80	9.0E-80	9:0E-80	9.0E-80	9.0E-80	8.05-80	8 OF 80	8.0E-80	8.0E-80	8.0E-80	7.0E-80	6.0E-80	6.0E-80	6.0E-80	6.0E-80	6.0E-80	6.0E-80	6.0E-80	6.0E-80	6.0E-80	6.0E-80	6.0E-80	6.0E-80
	Expression Signal	0.51	0.51	67.0	2.64	6.25	6.25	1.02	8.28	8.28	123	285	2.85	1.14	1.14	0.58	0.7	2.17	1.17	1.17	1.1	1.1	132	3.12	3.84	0.83	0.88	3.06
	ORF SEQ ID NO:	33200	33204	34971	38419	28131	ळ्ळ	36772	38104	38105		34183	١			31242	_	ŀ									32770	Ц
	Exam SEQ ID NO:	18905	<u> </u>					23286	l	l	<u> </u>	1	20806	22698	22698	18397	13956				<u> </u>	L		<u> </u>	L			LJ
	Probe SEQ ID NO:	288	986	8687	194	3161	316	10373	11606	11606	2848	2 6	2007	9757	8757	7168	٤	1650	2307	2307	4314	4314	2839	6194	8366	<b>8</b>	6455	9176

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Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor	Hamo sepiens G protein-coupled receptor 61 (GPR51), mRNA	Hamo sepiens chromosome 21 segment HS21C101	Homo sapiens HSPC148 mRNA, complete cds	Homo sepiens Xq pseudoautosomal region; segment 1/2	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, etch 21	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA	Hamo sepiens Cyt19 mRNA, complete cds	Homo sapiens N-acetylghucosamine-phosphate mutase mRNA, complete cds	Homo sapiens glutathtone S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5	Hamo saplens mRNA for sodium-glucose cotransporter (SQL,T2 gene)	Homo sapiens protessome (prosome, macropain) 26S subunit, non-ATPasse, 3 (PSMD3) mRNA	Homo sapiens serine-firecraine protein kinase (MNBH) mRNA, complete cds	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds	H.saplens nox1 gene (exon 12)	Hamo sepiens chramosame 21 segment HS21C083	Human (3)mbt protein homolog mRNA, complete cds	Homo saptens mRNA for KIAA1434 protein, partial cds	Homo septens H3 histone family, member J (H3FJ) mRNA	Homo sepiens HMT-1 mRNA for beta-1,4 mannosytranstenase, complete cds	Homo sapiens HMT-1 mRNA for beta-1,4 mannosymansterase, complete cus	Homo sepiens chromosome 21 segment HS21C068	Mus musculus keratin complex 2, gene 6g (Kr2-5g), mrthA	HSPD13165 HM3 Hamo sapiens aDNA dans s400045Ft3	Homo sepiens chromosome 21 segment HS21C010	PM0-GN0018-040900-002-E03 GN0018 Homo septens cDNA	QV4-BN0283-040600-241-g10 BN0283 Hamo septens cDNA	oo23e12.xt Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1567054 3' similar to TR:035790 035780 PIG-L.;	yg65s08.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:38060 5	RET4B7 subtracted retina cDNA library Homo sapiens cDNA clone RET4B7	DKFZp434D1323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1323 6	WIN49C10.XT NCT_CGAP_LU19 Hamo septems cDINA done IMAGE_2446760 3
Source		NT	H IN	Ĭ				Ĭ	<u>i 8</u>	Ŧ	IN					H. H	H	H			Ŧ			T_HUMAN		EST_HUMAN P	EST_HUNAN Q	EST HUMAN T	Т	Г	П	EST_HUMAN W
Top Hit Acession No.	11526484 NT	6.0E-80 AL163301.2	6.0E-80 AF161495.1	6.0E-80 AJ271735.1		427366			6.0E-80 AF240786.1	6.0E-80 AB028900.1		4506228 NT	5.0E-80 AF108830.1			5.0E-80 AL163283.2			5.0E-80 4504292 NT			5.0E-80 AL163268.2	8910283		3.0E-80 AL163210.2			3 NE. 90 A (100/6775 1	2.0E-80 R35321.1	_	2.0E-80 AL043116.2	2.0E-80 Al923972.1
Most Similar (Top) Hit BLAST E Vaitue	6.0E-80	6.0E-80	6.0E-80	6.0E-80	6.0E-80 U20211.1	6.0E-90	6.0E-80	6.0E-80	6.0E-80	6.0E-80	6.0E-80/	5.0E-80	5.0E-80	5.0E-80	5.0E-80 X91647.1	5.0E-80	5.0E-80	5.0E-80	5.0E-80	5.0E-80	2.0E-80	5.0E-80	5.0E-80	4.0E-80	3.0E-80	3.0E-80	3.05-80	2 PF 80	2.0E-80	20E-80	2.0E-80	2.0E-80
Expression Signal	3.06	1.56	980	0.47	1.55	2.43	20.37	1.64	2.39	6.41	4.47	2.89	1.49	1.40	96'0	221	1.92	6.37	S.	1.28	1.28	1.53	1.14	15.19	12.8	1.45	3.11	000	47	1.49	5.1	0.69
ORF SEQ ID NO:	35569	35768	36125	36233	36634	37766	38054	38521				28572	26848	26849			28400	28462			29999	30894	16058	36069		30653		0.2407				32684
SEQ ID	22142	22338	22867	22777	23145	24239	24498	24024	25787	25243	25014	13857	13883	13893	14233	14483	15377	15444	15798	17105	17105	18006	21688	22617	L	l_		i				19442
Probe SEQ ID	9178	8373	9714	25.	10220	11289	11558	12051	12304	12506	- 28 8	88	838	88	118	<u>\$</u>	2388	2437	8082	4068	4069	4091	8700	9613	218	4738	4945	2	484	1877	2071	6374

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Marrow
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Expressed
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Fxon
Single

Top Hit Descriptor	undo-do y NO. OSAP 1 do Homo seniens cONA cione IMAGE 2448786 3'		m80d01.s1 NCL CGAP C09 Hamo sepiens CUNA cone IMAGETUROTITA	Homo saplens Colgi transport complex protein (90 kDa) (GTC80), mrRNA	yc86f12.rf Sceres Infent brain 1NIB Homo septens cDNA clone IMAGE:22851 6' stimiler to SP:K1CR_XENLA P08802 KERATIN, TYPE I CYTOSKELETAL ENDO B;	EST378343 MAGE reseguences, WAGH Homo septems cDNA	Homo seniena GGT gane, escn 6	Appear of Second Appear No. 1 Company of No. 1 Appear 18 April 27 F. Similar to TR (5191315	ZZ/UTZT SORRE, ISBUS NHT FIGURE BAPAR CORE INVISE. ZT. ZT. Z. C. SHIBER TO TOOL STORY CORE INVISE. ZT. ZT. ZT. ZT. ZT. ZT. ZT. ZT. ZT. ZT	Homo sapiens chronosome 21 segment HS21C103	Homo sapiens chromosome 21 unknown mPNA	rm01f12.x5 NCI_CGAP_Co9 Hamo saptens cDNA clane IMAGE:1076495 3' stmilar to cantains OFR.t1 OFR	repetitive element;	2838g07.rd Scares fetal liver spleen 1NFLS Homo expiens cDNA clone IMAGE:204972 & shrifter to contains	Alu repetitive element;	601274305F1 NIH_MGC_20 Hamo sepiens cDNA clans IMAGE:3615433 5	Human pro-alphat type II collegen (COL2A1) gene excres 1-54, complete cds	Homo sapiens malate dehydrogenase 2, NAD (mitochondria) (MDH2), nuclear gene encoding mitochondrial	protein, mRNA	Homo sapiens mRNA for lipophilin B	wq25c05x1 NCL_CGAP_Kid11 Hamo sepiens cDNA clane IMAGE:2472296 3'	wq25c05x1 NCI_CGAP_Kld11 Homo sepiens cDNA clone IMAGE:2472296 3'	Homo sepiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA	Homo sapiens protein tyrostne phosphatase, receptor type, A (PTPRA), mRNA	Homo sepiens protein tyrosine phosphetase, receptor type, A (PTPRA), mRNA	Hamo sepiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds	Homo sapiens mRNA for KIAA0145 protein, pertial cds	Homo saplens similar to ret myomegalin (LOC84182), mRNA	Homo sapiens similar to rat myomegalin (LOC64182), mRNA	Homo saptens myostn, heavy potypeptide 2, sketetal muscle, adult (MYH2), mRNA	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA	601310531F1 NIH_MGC_44 Homo sepiens cDNA clone IMAGE:3832070 5	2291c08.x5 Scares_fetai_lung_NbHL19W Homo sapiens cDNA cione IMAGE:289918 3
Top Hit · Detabase · Source	TOTAL LINEAN	٦	EST_HUMAN		EST HIMAN	Т	Т		EST_HUMAN	¥	F		EST_HUMAN		EST_HUMAN	EST_HUMAN	NT			IN	EST HUMAN	EST HUMAN				LN.	N.							EST_HUMAN
Top Hit Acession No.			2.0E-80 AA582952.1	11421930 NT					2.0E-80 AA393362.1	1.0E-80 AL163303.2	ļ		1.0E-80 AI732656.1		199620.1	1.0E-80 BE386815.1			6174640 NT	1.0E-80 AJ2241721			ध्यया	11421211 NT	11421231 NT	1.0E-80 AF245219.1	1.0E-80 AF245219.1		11641276 NT	11641276 NT	TN 6525288	11417901 NT	8.0E-81 BE394525.1	7.0E-81 AI822115.1
Most Similar (Top) Hit BLAST E	100	70E-207	2.0E-80/	2.0E-80	2 OF BO T75245 1	200	205.00	700-307	20E-80	1.0E-30/	1.0E-80/		1.0E-80		1.0E-80 N99620.1	1.0E-80	1.0E-80 L10347.1		1.0E-80	1.0E-80	1.0E-80	1.0E-80/	1.0E-80	1.0E-80	1.0E-80	1.0E-80	1.0E-80	1.0E-80	1.05-80	1.0E-80	1.0E-80	1.0E-80	8.0E-81	7.0E-81
Epression Signal	1	0.08	1.01	1.51	2	5 8	7 5	JATO	8.05	2.11	195		2.82		0.78	3.62	624		1.3	1.09	26	26	1.17	0.92	0.92	1.26	1.28	1.12	1.72	1.72	1.67	227	9.7	2.97
ORF SEQ ID NO:			33530	33335	1			3003	37697		26806				30762		32375		32880					35437			L							
SEQ ED			20200	20032	<u> </u>		l	23052	24169	1	L		14992		17874	1_	<u> </u>	1	19704	L			<u>.</u>	<u>L</u>		L	<u> </u>	丄				L	L	Ш
Probe SEQ ID NO:		6374	<i>11</i> 69	8802		3	8014 1	19728	11216	3,00	S C	3	1974		4867	5400	6083		9848	7414	7824	7874	8573	8048	8048	9840	8840	10791	11013	11013	11443	12578	11488	7464

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Table 4
Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	601111970F1 NIH_MGC_16 Hamo septens aDNA done IMAGE:3352840 5	601111970F1 NIH_MGC_16 Hamo sapiens cDNA clane IMAGE:3352840 5	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), miKNA	Hamo septens chromosome 1p33-p34 beta-1,4-gatactosyltransferase mFNA, complete cas	EST69129 Fetal lung II Homo sapiens cONA 5' end	602153666F1 NIH_MGC_83 Hamo sapiens cDNA clone IMAGE:4294601 5	602153666F1 NIH_MGC_83 Hamo septens CDNA clone IMAGE: 4284601 5	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345460 5	Hamo septens mRNA for KIAA0454 protein, partial cds	Hamo saplens mRNA for KIAA0454 protein, partial cas	Human transforming growth factor-beta (tgr-beta) mi-dNA, complete cos	Human transforming growth factor-beta (tgf-beta) miRNA, complete cds	(Hamo sepiens hypothetical protein (FLJ11045), mRNA	W60612.X1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:085560 Q85500		Infeedozia NCL CGAP Co14 Homo sepiens dinna dane IMA(de:3035607 3' semien to 5 W : CUP-o_BOVIN Pesezo COATOMER GAMMA SUBUNIT ;	Homo septens mRNA for KIAA1345 protein, partial cds	ws90h03.x1 NCI_CGAP_Co3 Homo saplens cDNA clone IMAGE:2505269 3' similer to TR:043815 O43815 STRIATIN.;	Homo saplens rab3 interacting protein variant 2 mRNA, partial cds	Hamo sapiens rab3 interacting protein varient 2 mRNA, pertial cds	Homo sepiens hypothetical protein FLJ20220 (FLZ0220), mRNA	Homo espiens ceiclum channel, voltage-dependent, L. type, sipha 2/delta subunit (CACNA2) mRNA	[Hamo sapiens ets variant gane 1 (ETV1), mRNA	Human mRNA for amyloid A4(751) protein	Human cone photoreceptor cGMP-phosphodiesterase alpha subunit gene, exons 2 and 3	Human cone photoreceptor cGMP-phosphodiesterase alpha subunit gene, exons 2 and 3	Hamo sapiens mRNA for Death-essociated protein kinase 2, complete cas	Homo capiens ligase I, DNA, ATP-dependent (LIG1), mRNA	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAU8), mirdva	Homo sapiens acy-Coenzyme A denyarogenase taminy, member 6 (ACAUS), mrava
,	Top Hit Detabase Source	EST_HUMAN	EST_HUMAN	TN	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	M	NT	NT.	NT	NT		EST HUMAN	EST_HUMAN	Į.	EST HUMAN	F	NT	NT	¥	NT	TN.	M	M	M	M	M	토
, 	Top Hit Acession No.	6.0E-81 BE256829.1	6.0E-81 BE256829.1	4501848 NT	O1848	8.0E-81 AF038880.1	8.0E-81 AA360017.1	8.0E-81 BF879022.1	6.0E-81 BF679022.1	5.0E-81 BE268042.1	5.0E-81 AB007923.1	AB007923.1	5.0E-81 M60316.1	5.0E-81 M80316.1	9506834 NT		4.0E-81 AI521435.1	4.0E-81 AW779612.1	4 OF-81 AR037788.1	4 0F-81 AW004608.1	4.0E-81 AF283306.1	AF283306.1	4.0E-81 8923209 NT	TN 8883 NT	11420544 NT	4.0E-81 X06989.1	U20197.1	4.0E-81 U20197.1	AB018001.1	11425281 NT	11439065 NT	11439065
	Most Similar (Top) Hit BLAST E Vatue	6.0E-81	8.0E-81	6.0E-81	6.0E-81	ROE-81/	a0E-811 /	6.0E-81	6.0E-81	5.0E-81	5.0E-81	5.05-81	5.0E-91	5.0E-81	5.0E-81		4.0E-81	4.0E-81	4 OF-81	4.05-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81
	Expression Signal	4.98	4.98	1.8	1.65	0.58	1.17	2.68	2.68	2.27	1.57	1.57	0.81	18.0	1.84		121	.1.36	440	08 0	8:	- 85	=	0.83	0.680	8	3.34	3.34	3.82	1.82	0.67	0.67
	ORF SEQ ID NO:	30331	30332	31329	31330	34168	36004		31769	28265	35148	35147	36396		L		26700	27865													36950	36961
	Ean SEQ ID NO:	17441	17441	18480	18480	20782	22554	25364	26364	15240	27723	21723	22833	22833	24789		13785	14866	1004		L	17218		ı	1	1_	1	<u> </u>	L	上	23453	Ш
Γ	SEO ID	4414	14	9383	5355	18	2838	707	12707	8222	8755	828	10008	1000	11908		ğ	1830	2400	2844	4187	4187	419	7492	7629	8830	8890	8890	9581	10461	10531	10531

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Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor Source	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA	Homo saplens vesicle trafficiang protein sec22b (SEC22B) mRNA	Homo eapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo septens beta-ureidopropionese (LOC51733), mRNA	Homo sapiens beta-ureidopropionase (LOCS1733), mRNA	Homo sapiens transcobelantin II; macrocytio anemia (TCN2), mRNA	Homo saptens NF2 gene	Homo saplens NF2 gene	Homo sepiens cullin 4A (CUL4A) mRNA, complete ods	Homo sapiens pleiotrophin (heparin binding girowth factor 8, neuritie growth-promoding factor 1) (PTN) mRNA	Homo sepiens pleiotrophh (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA	601474072F1 NIH_MGC_88 Homo saplens cDNA clone IMAGE:3877121 5	601474072F1 NIH_MGC_68 Hamo sapiens cDNA clane IMAGE:3877121 5'	hg85c01.x1 NCL_CGAP_Kid11 Hamo septems cDNA clane IMAGE:2852384 3'	Homo sepiens hypothetical protein (LOC56586), mRNA	hg85c01x1 NCI_CGAP_Kd11 Homo sepiens cDNA done INAGE:2852384 3'	zk45h09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:485825 5' similar to PIR:S52437 S52437 CDP-diacylglycerol synthese - fruit fly ;	tz45c04.y1 NCI_CCAP_Bm52 Homo sepiens cDNA clone IMAGE 22291528 5	Human accritate hydretase (ACO2) gene, excn 3	Homo saplens polymerase (DNA directed), gamma (POLG), mRNA	Homo sapiens polymetase (DNA directed), gamma (POLG), mRNA	2/85d08.rf Science, NhHMPu_S1 Homo sepiens cDNA clone IMAGE:682475 6' similar to SW:PRI2_HUMAN DAGGAS DNA DELIMACE SS KD SI IRI INTF	Homo septens erm-repeat protein NPRAP/heurojungin (CTNND2) mRNA, pertial ods	Homo sapiens arm-repeat protein NPRAP/heurolungin (CTNND2) mRNA, partiel cds	602137864F1 NIH_MGC_83 Homo septems cDNA clane IMAGE:4274635 5	Homo sepiens phosphodiesterese 1C, calmodulin-dependent (70kD) (PDE1C), mRNA	Homo sepiens phosphodiesterese 1C, calmodulin-dependent (70kD) (PDE1C), mRNA	Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
Top Hit Defatorse Source								H.		H.			EST_HUMAN 8	EST_HUMAN 6	T_HUMAN		T_HUMAN	T_HUMAN	EST_HUMAN t	NT			Z WALKILL TOO	Т		T HUMAN			NT 2)
Top Hit Acesston No.	4759085 NT	4759085 NT	11417862 NT	11417862 NT	11417871 NT	11417871 NT	11417974 NT	3.0E-81 Y18000.1	•	3.0E-81 AF077188.1	4506280 NT	4506280 NT	20E-81 BE784636.1	2.0E-81 BE784636.1	2.0E-81 AW611542.1	2.0E-81 8923839 NT	AW6115421	1.0E-81 AA040370.1	1.0E-81 BE047996.1	1.0E-81 U87928.1	11432988 NT	11432966 NT	A 00 04 A 00 000 4			-	11420965 NT	11420965 NT	1.0E-81 AJ133289.1
Most Shullar (Top) Hit BLAST E Vatue	4.0E-81	4.05-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	3.0E-81	3.0E-81	3.05-81	3.0E-81	3.0E-81	20E-81	2.0E-81	2.05-81	20E-81	20E-81	1.0E-81	1.0E-81	1.0E-81	1.05-81	1.0E-81	70 20 7	19. 19.	1 0F-81	1.0E-81	1.0E-81	1.0E-81	1.0E-84
Expression Signal	3.39	3.30	3.45	3.45	1.71	1.71	3.69	10.2	10.2	1.65	6.19	6.19	2.48	2.48	0.88	9.0	2.55	3.12	9.34	3.31	3.6	3.6	8	337	337	1.56	0.56	0.56	1.28
ORF SEQ ID NO:	38010	38011	31438	31439	31753	31754	31729		27267	28412	28980	18687	28828	28829	28736	34670	28735	30463	30583	38611	31409	31410	-	32000	32010				
SEQ ID NO:	24460	24460	25853	25853	25389	25389	26472	14307	14307	15388	16062	16062	16904	15904	16828	21260	16828	17568	17696	18326	18530	18530		18834	18831	18342	19756	19756	1 1
SEO IO NO:	11519	11519	1220	12200	12737	12737	12878	1272	1272	2380	3004	3004	284	284	3787	8280	13032	4543	4675	8083	5427	5427		6737	2	883	888	6836	6907

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Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor	Hamo sepiens polymerase (DNA directed), gamma (POLG), mRNA	601645051F1 NIH_MGC_56 Hamo saplens cDNA clane IMAGE:3930228 5	601645051F1 NIH_MGC_56 Hamo septens cDNA clane IMAGE:3830228 5	601343180F1 NIH_MGC_63 Hamo septems aDNA clane IMAGE:3685483 5	ec14d06.s1 Strategene HeLa cell s3 837216 Homo saplens cDNA clone IMAGE:856427 3' stmilar to SW;YB36 YEAST P38126 HYPOTHETICAL 60.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC	REGION.;	001577339F1 NIH_MGC_9 Hamo septens cONA clone IMAGE:3838280 6	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5	CARS-NN0069-140400-147-e12 NN0069 Hamo saplens CUNA	MR0-CT0008-250599-019 CT0008 Homo sepiens cDNA	MR0-CT0008-250599-019 CT0008 Homo saplens cDNA	RC3-LM0048-290200-011-e08 UM0046 Homo sapiens cDNA	RC3-UM0046-290200-011-e06 UM0046 Homo sapiens cDNA	601867714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5	Home sapiens phorbolin (similar to apolipoprotein B mKNA editing protein) (LU/42C18.2), mrnvA	Hamo sapiens HSPC288 mRNA, partial cds	Homo sapiens HSPC288 mRNA, pertial ods	Human CRFB4 gene, partial cds	Human CRFB4 gene, partial cds	Human CRFB4 gene, partial cds	Homo sapiens mRNA for KIAA1327 protein, partial cds	Hamo sapiens glutaffilione perceidasse 5 (epididymal endrogen-related protein) (GPX5), transcript variant 2,	MENA	Homo sapiens gluternate receptor, ionotropic, kanate 1 (GKIR1) mKIVA	Homo sapiens hypothetical protein FL/20461 (FL/20461), mRNA	601458531F1 NIH_MGC_66 Homo sepiens cDNA clone IMAGE:3862086 5	AU144050 HEMBA1 Homo sepiens cDNA clone HEMBA10007523'	as68e04.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:968342.3*	Homo sepiens alpha-tubulin isoform 1 mRNA, complete ods	QV2.HT0540-120900-362-408 HT0540 Homo sapiens cDNA	QV2-HT0540-120900-362-f08 HT0540 Hamo sepiens cDNA	Humen von Willebrand factor gene, exon 9
Top Hit Defaberse Source	Į.	EST HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	M	NT	M	N	N	NT	M		¥	N	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	¥	EST_HUMAN	EST_HUMAN	Ā
Top Hit Acesslon No.	11432966	1.0E-81 BE958278.1	1,0E-81 BE958278.1	1.0E-81 BE564367.1		1.0E-81 AA630784.1	1.0E-81 BE744545.1	1.0E-81 BE744546.1	1.0E-81 AW897550.1	1.0E-81 AW844986.1	1.0E-81 AW844988.1	1.0E-81 AW798167.1	1.0E-81 AW798167.1	1.0E-81 BF204253.1	11418138 NT	8.0E-82 AF161408.1	8.0E-82 AF161408.1	J08988.1	J08988.1	8.0E-82 U08988.1	8.0E-82 AB037748.1		6715801 NT	4504116 NT	8923432 NT	7.0E-82 BF035327.1	7.0E-82 AU144050.1	7.0E-82 AA663747.1	4.0E-82 AF081484.1	4.0E-82 BF351691.1	4.0E-82 BF351691.1	4.0E-82 M25833.1
Most Smiler (Top) Hit BLAST E	105.84	1.0E-81	1.05-81	1.0E-81		1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	8.0E-82	8.05-82	8.0E-82 U08988.1	8.0E-82 U08988.1	8.0E-82	8.0E-82		8.0E-82	8.0E-82	8.0E-82	7.0E-82	7.0E-82	7.0E-82	4.0E-82	4.0E-82		
Expression Signal	7.53	7.65	7.66	4.63		-8:	3.01	3.01	1.7	2.9	2.9	6.55	6.55	2.11	4.59	26.0	2.07	2.7	14.95	1.44	1.36		1.7	0.62	0.75	253	1.8	1.75	25.07	0.83	0.89	0.50
ORF SEQ ID NO:	34382	38637	38538	38731		38878	36880	3888	37296	37805	·					L		L	L				27674	30040			28789					
SEO ID	20088	2000	1		·l	23385	23387	23387	23794	24369		1	<u> </u>	<u></u>	1_	13133		13359	1_	1_	14520		14698	17148	L	1_	L			┸	1	Ш
Probe SEQ ID NO:	9740	43484	2	1028		10463	10465	10465	10874	11425	11425	11429	11420	11861	12414	13	107	283	845	888	1487		1668	4114	4272	1444	1111	12053	丄	5574	5574	5851

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Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	wp75e09.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR:075276 O75276 PVD1;	Homo expiens presentiin-1 gene, exans 1 and 2	Homo sapiens amyloid beta (A4) precursor protein (protesse nextn-ll, Alzheimer disesse) (APP), mRNA	RC2-BND/20-010400-013-f02 BN0120 Homo sepiens cDNA	Homo sepiens transforming growth factor beta-activated kinase-binding protein 1 (1AB1), miXNA	Homo seplens amyloid beta (A4) precursor protein (protesse nextr-II, Alzheimer disesse) (APP), mRNA	ai23e05.s1 Scares_testis_NHT Homo sapiens cDNA clone 1343648 3	RC6-PT0001-190100-021-B02 PT0001 Homo saplens cDNA	Homo sapiens chromosome 21 segment HS210085	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA	Homo sapiens adenylate cyclase activating polypaptide 1 (pituitary) receptor type I (ADCYAP1R1) mRNA	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (N IRK2) mrtNA	Homo sapiens ankyrin-like with transmembrane domains 1 (ANK I M1), mixwy	Homo sapiens contactin 6 (CNTN6), mRNA	Home sapiens contactin 6 (CNTN6), mRNA	Homo sapiens mRNA for KIAA1077 protein, pertial cots	Homo sapiens mRNA for KIAA1077 protein, pertial cds	Homo sapiens contactin 6 (CNTN6), mRNA	Homo sepiens contactin 6 (CNTN6), mRNA	Homo saplens mRNA for KIAA0999 protein, pertial cas	Hamo sepiens mRNA for KLAA0899 protein, perties cas	DKFZp434M117_r1 434 (synonym: htes3) Homo sapiens cDNA crone DKr-zp434M117 5	Homo saplens chromosome Z1 segment HSZ1C001	Homo sepiens DNA for amyloid precursor protein, complete cds	Human integral membrane serine protesse Seprase mRNA, complete cos	Homo septens glutamate receptor, tonotropic, kainate 1 (GRIK1) mRNA	Homo sapiens mRNA for KIAA1096 protein, partial cds	Homo sapiens mRNA for KIAA1096 protein, partial cds	Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, effemetively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5 5	Ostaberse Source	EST_HUMAN	F	7	EST_HUMAN	Į,	¥	EST_HUMAN	EST_HUMAN	N	EST_HUMAN	MT	F	M	片	F	IN	K	N N	NT	¥	ᅜ	EST_HUMAN	NT	IN	¥	NT	NT	NT	¥
,	Top Hit Acession No.	-	4.0E-82 AF029701.2	4502166 NT	3.0E-82 BE005705.1	6174702 NT	502168	T.	1.1	2	3.0E-82 BE813232.1	4501822 NT	5453811 NT	11425206 NT	11432889 NT	11432889 NT		3.0E-82 AB029000.1	11432889 NT	2889		.1	.1	2.0E-82 AL163201.2	2.0E-82 D87675.1	2.0E-82 U76833.1	4504116 NT	2.0E-82 AB028019.1	2.0E-82 AB029019.1	2.0E-82 AF045555.1
Most Similar		4.0E-82 AB37300.	4.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.05-82	3.05-82	3.0E-82	3.0E-82	2.0E-82	2.0E-82	2.0E-82	2.0E-82	2.0E-82	2.0E-82	2.0E-82	2.0E-82	2.0E-82	2.0E-82
	Expression Signal	7.32	3.69	16.34	2.78	10.4	6.11	53.62	1.01	2.61	1.95	12	2.31	2.7	0.77	0.77	3.98	3.88	1.6	1.8	1.98	1.96	2.13	92.0	1.07	0.65	1.07	1,09	1.09	321
	ORF SEQ ID NO:	38498		28304	28701		28882		27363	27469				34877	35292	35280					28579	26580	27707							
	SEO D SO :	24801	25337	18873	13766	13847	13927	14108	14392	14485	14041	15043	16339	21460	21888	21868	23108	23108	24978	24978	l	13666	14724	L	L	L	L	L	1	1 1
	SEQ 10 NO:	12025	12857	122	ğ	82	871	1062	1357	1462	1917	202	3285	8462	8902	8902	10183	10183	12108	12108	286	889	1694	289	3860	4052	4281	4588	4588	4904

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Single Exon Probes Expressed in Bone Marrow

ngie Exon Probes Expressed in Borre Martow	Top Hit Descriptor	Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF5) mRNA	Hamo septens tunar necrosis factor receptor superfamily, member 5 (TNFKSF5) mixAA	Homo sapiens mRNA for KIAA0727 protein, partiel cds	Homo sapiens FAM4A1 splice variant a (FAM4A1) missiva, complete dos	Imizig05.x1 Soares_NFL_T_GBC_S1 Hamo septens aDNA dane IMAGE:Z15/2/23	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA	Homo sepiens nucleotide binding protein 1 (E. coti Mirrib like) (NUBP1), mixnA	Homo sapiens stit (Drosophila) homotog 3 (SLI 13), mrthA	Homo sapiens microrchidia (mouse) namadog (MURC), microR	Homo sepiens microcchidie (mouse) namaleg (MUNC), micron	Human endogenous retrovirus-K, LTR U5 and gag gene	Human endogenous retrovirus-K, LTR U5 and gag gane	Homo sapiens feucy/cystiny aminopeptidase (LNPEP), mKNA	Homo saplens laucylicystiny aminopeptidase (LNPt.P.), mrtnA	Hamo sapiens CAGF9 mRNA, partial cds	Homo sepiens CAGF9 mRNA, partial cds	zb31d10.s1 Soares, paradityroid, furnor_NMPA Homo septiens dUNA drone Invalce: 300.dus s	ZOTBOBLI Scares fetal liver spleen 1NFLS S1 Homo explans cDNA done IMAGE: 426008 5	Homo sapiens SRY (sex determining region Y)-box 10 (SUX10), miraya	Homo sapiens melanoma differentiation associated protein-b (MLNa), mixNA	601510858F1 NIH JMGC 71 Hamo sapiens CANA ciane IMAGE:38172207 3	RC4-B10310-110300-019-110 B10310 Home sapiens curviv	Homo sapiens mittha for KlaActood protein, partial cos	Homo sapiens mittha for Kina 1417 protein, perual cus	Homo eaplens mitthe for NAAUGOZ protein, parter cus	UHHBW1-acaf-03-0-U.st NG_CGAP_Stay Hatto sapiens durch date inmediated s	Homo saplens chromosome 21 segment HSZ1CAV8	602/50403F1 NIH_MGC_81 Hamo sepiens cUNA cians IMPGC.4291301 3	601117160F1 NIH_MGC_16 Hamo sepiens dONA cione IMAGE:3337734 5	601273346F1 NIH_MGC_Z0 Hamo sapiens CUNA ciare IMAGE:3014342 5	za48f12.s.1 Soares fetal liver spleen 1NFLS Hamo saplers CDNA clane IMAGE 285323 3	QV4LT0016-271299-068-h11 L10016 Homo septens GJNA	not 2not st NCI_CGAP_Phet Homo sepiens cONA done iMAGE:1100497 3' smilet to conterns Autrepeditive element,
xon Probes E	Top Hit Defeabase Source				П	T_HUMAN						N-	NT			. IN	NT		T_HUMAN			П	HCMAN	M	FN	L L	EST_HUMAN	۲	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
Single	Top Hit Acesston No.	4507580 NT	4507580 NT	1	1	2.0E-82 AH76428.1	8823130 NT	11431845 NT	11321570 NT	7657340 NT	7657340	708032.1	708032.1	11417191 NT	11417191 NT	J80736.1	J80736.1	<b>194950.1</b>	2.0E-82 AA011278.1	11418097 NT	11545921 NT	1.0E-82 BE885106.1	1.0E-82 BE084388.1	1.0E-82 AB011110.2	1.0E-82 AB037838.1	-		2	9.0E-83 BF672220.1	9.0E-83 BE253347.1	8.0E-83 BE383973.1	8.0E-83 N66951.1	7.0E-83 AW385529.1	7.0E-83 AA584655.1
	Most Smiler (Top) Hit BLAST E	20E-82	20E-82	2.0E-82/	20E-82/	2.0E-82/	20E-82	20E-82	2.0E-82	20E-82	2.0E-82	2.0E-82 Y08032.1	2.0E-82 Y08032.1	20E-82	20E-82	2.0E-82 U80736.1	2.0E-82 U80738.1	2.0E-82 N94950.1	2.05-82	2.0E-82	1.05-82	1.0E-82	1.0E-82	1.0E-82	1.0E-82	1.0E-82	1.0E-82	1.0E-82	9.0E-83	8.0E-83	8.0E-83		7.0E-83	
	Expression Signal	1.53	1.53	3.46	4.89	0.88	0.89	0.48	1.94	0.47	0.47	1.86	1.06	3.85	3.95	2.31	2.31	192	4.39	1.53	127	1.09	2.11	1.07	1.09	0.58	1.24	1.87	4.87	0.62	1.55	4.08	66'0	1.82
ļ	ORF SEQ ID NO:	31002	31003	31583	32610		34440	34973	35038	35402	35403	36884	36885		38088	38140					26574		27286		36689	36403		37681			27417			
	Exam SEQ ID NO:	18127	18127	18643	18371	ı	l	21557	21616	21983	21983	23390	23390	24538	24638	24575	24575	25062	25403	25598	13661	14251	14325	14326	22260	22838	Ŀ	24057	L	L	14446		14394	
	Probe SEQ ID NO:	5117	5117	25 25 25 25 25	83	350	8104	8280	88	208	9917	-12488 88	10468	11680	1160	11638	11638	12221	12760	13064	露	1213	1280	1281	9294	1001	10606	11097	9085	10637	1412	169	1359	2876

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Probe SEQ ID NO: NO: 1802 3084 3083 3575 6167 10035 10177 45 10177 11859 3652 3652 3652 3652 3652 3652 3652 3652	8		AW673088.  AW673088.  AW673088.  AW70467.  AM70467.  AM70467.  AM70467.  AM486105.  AA486105.  AL133207.  AL133207.  AH133207.	Top Hit   Top Hit   Top Hit   Top Hit   Top Top Top Top Top Top Top Top Top Top	Top Hit Describion  Top Hit Describion  Top Hit Describion  ToST407.x1 NCL_CGAP_P28 Homo septens cDNA done IMAGE-3847893 % similar to TRC997316 Q97316  DL207H1.1:  Homo septens KIAA0100 gens product (KIAA0100), mRNA  Homo septens KIAA0100 gens product (KIAA0100), mRNA  Homo septens KIAA0100 gens product (KIAA0100), mRNA  Homo septens KIAA0110 gens product (KIAA0100), mRNA  Homo septens Claycoproduct in CPCAP HOMO septens cDNA done IMAGE-2833825 % similar to SW-7PEB JAAC11 HYPOTHETICAL PROTEIN H10034.;  GVA-ST0224-181 169-037-405 ST0224 Homo septens cDNA done IMAGE-283080 %  Homo septens Promoscopens Claycoproduct (REA0100), mRNA  Homo septens bunor necrosis factor (Igenof) superfamily, member 18 (TNFSF18) mRNA  Homo septens hypoductical protein FL110370 (FL110370), mRNA  Homo septens products  Homo septens products  Homo septens mot products  Homo septens mot products  Homo septens mot products  Homo septens products  Homo septens products  Homo septens products  Homo septens grand manual (16500) (MYOM2), mRNA  Homo septens products  Homo septens grand manual (16500) (MYOM2), mRNA  Homo septens grand manual (16500) (MYOM2), mRNA  Homo septens grand products  Homo septens grand manual (16500) (MYOM2), mRNA  Homo septens grand products  Homo sep
6245 3525	31124	2.28	6.0E-83 4505802 NT 4.0E-83 AF224689.1 NT 4.0E-83 BE888078.1 ES	NT NT EST_HUMAN	Homo sapiens phosphatidylinosital 3-kinase, cafalytic, gamma polypeptide (PIK3CG) mKNA Homo sapiens mannosidase, beta A, hysosomal (MANBA) gene, and ubiquifin-conjugating enzyme E2D 3 (UBEZDS) genes, complete ods 601511580F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913195 5
866	Ш	6.39	3.0E-83 AA368311.1	EST_HUMAN	EST79642 Placenta I Homo saplens cDNA similar to similar to endogenous retrovirus ERV9

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Single Exon Probes Expressed in Bone Marrow

Most Similer  Expression (Top) Hit Top Hit Acession Detabase Signal BLAST E No. Source	1.82 3.0E-83 AA632854.1 EST_HUMAN repetitive element;	3.0E-83 AI217223.1 EST_HUMAN	2.0E-83 AA983492.1 EST_HUMAN	1.68 2.0E-83 AA993492.1 EST HUMAN	3.01 2.0E-83 N66951.1 EST_HUMAN	1.36 2.0E-83 BE828694.1 EST_HUMAN	2.14 2.0E-83 11430834 NT	2.0E-83 AL163202.2 NT	AF202879.1 NT	6.03 2.0E-83 7706398 NT	30591 6.03 2.0E-83 7706398 NT Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mixWA	0.94 2.0E-83 U08679.1 NT	1.09 2.0E-83 11024711 NT	11024711 NT	0.54 2.0E-83 11428081 NT	1 EST_HUMAN	5.47 2.0E-83 AF129533.1 INT	0.52 2.0E-83 BF105097.1   EST_HUMAN			1.46 2.0E-83 U66707.1 NT	1 NT	2.5 2.0E-83 AF011920.1 NT	36342 0.46 2.0E-83 5453881 NT Homo saptens phospharylases kinase, gamma 1 (muscle) (PHK41) minnA	0.46 2.0E-83 6463881 NT	0.43 2.0E-83 BF128748.1 EST_HUMAN	2.53 2.0E-83 M22094.1 NT	2.63 2.0E-83 M22094.1 NT	1.2 2.0E-83 AU117859.1 EST_HUMAN	0.74 2.0E-83 AW505600.1 EST_HUMAN	37681 3.48 2.0E-83 11438448 NT   Homo Sapiens KIAA0985 protein (KIAA0955), mixna
<u> </u>			27834	77875	27963	28843				1													L		l						
in SEQID	2788 15780	L	1	<u> </u>	L		1	3788 16829	4363 17390		L	1		5547 18844			7669 20628	L	L				11	9952 22879	<u> </u>	1_	L				L
Probe SEQ (D NO:	1 8	3   8			-   9	188	8	8	A.		4	8	18	33	8	g	1	<u></u>	80	ώ	88	8	<b>1</b> 8	Į.	8	ļģ	Ę	T <sub>e</sub>	<u> </u>  2	٤	Ξ

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Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	DKI-Zp547J135_r1 547 (synanym: htbr1) Hamo sepiens cDNA clane DKF-Zp547J135 5	DKFZp547J135_r1 547 (synanym: hfbr1) Hamo sapiens cDNA clane DKFZp547J135 67	Homo sapiens gene for AF-8, complete cds	Hamo sapiens hydraxyacył-Coenzyme A dehydrogenase/3-ketoacył-Coenzyme A tholasa/encył-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA	Homo sepiens hydroxyecyl-Coenzyme A dehydrogenase/3-ketoecyl-Coenzyme A thiolass/enoyl-Coenzyme A hydratiase (trifunctional protein), beta subunit (HADHB) mRNA	Homo sepiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds	Homo sepiens lipopolyseccheride-binding protein (LBP) mRNA, complete ods	601507370F1 NIH_MGC_71 Hamo sapiens cDNA clans IMAGE:3908754 5	Hamo sepiens cell recognition malecule Caspr2 (KIAA0868), mRNA	Rettus norvegicus brain specific cortectin-binding protein CBP90 mRNA, partial cds	H.seplens gene for mitochondrial dodecencyl-CoA delta-Isomerase, exon 3	ov89b08x1 Sogres_testis_NHT Hamo septens cDNA done IMAGE:1645431 3' etmilar to gb:IMS4241 QM PROTEIN (HUMAN);	801676023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958853 5	RC2-FN0119-200600-011-g05 FN0119 Homo septens cDNA	RC2-FN0119-200600-011-g05 FN0119 Homo septens cDNA	ee88a03.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'	DKFZp434H0322_11 434 (synonym: htes3) Homo sapiens cDNA clane DKFZp434H0322 6"	847g03.s1 Sogres_NFL_T_GBC_S1 Hamo sapiens cDNA clone IMAGE:1460500 3' similar to gic.M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);	Homo sepiens acetyl LDL receptor; SREC—scavenger receptor expressed by endothelial oetis (SREC), mRNA	Homo sapiens acetyl LDL receptor; SREC-scavenger receptor expressed by endothelial cells (SREC), mRNA	PM0-LT0019-190600-004-F02 LT0019 Homo sepiens cDNA	Hamo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds	PM4-FT0054-160600-004-e10 FT0054 Homo saplens cDNA	EST86084 Testis I Hamo sapiens aDNA 6 end	Homo sapiens chromosome 3 subfetomeric region	2439e07.r1 Strategene hNT neuron (#837233) Homo septens cDNA clone INAGE:632100 6' similer to TR:G483915 G483915 RETROTRANSPOSABLE L1 ELEMENT LREZ FROM CHROMOSOME 10.;
	Top Hit Detraberse Source		EST_HUMAN [	TN IN				IN IN	EST_HUMAN (		IN.	NT TN	EST HUMAN	П	EST_HUMAN	EST_HUMAN I	EST_HUMAN	EST_HUMAN	EST HUMAN			T HUMAN	E	т		NT	EST_HUMAN
	Top Hit Acesslon No.	20E-83 AL134452.1	2.0E-83 AL 134452.1	2.0E-83 AB011399.1	4504328 NT	4504328 NT	1.0E-83 AF105087.1	Ļ	1	7682349 NT	1.0E-83 AF063768.1		1.0E-83 AI027614.1	7.0E-84 BE901209.1	6.0E-84 BE838864.1	6.0E-84 BE838864.1	6.0E-84 AA776574.1	6.0E-84 AL042863.2	G.0E-84 AA897339.1	11426718 NT	11428718 NT	8 0F-84 BE810371.1	_	۳.	_	_	5.0E-84 AA167678.1
	Most Similar (Top) Hit BLAST E Value	20E-83/	20E-83/	2.0E-83 /	1.0E-83	1.05-83	1.0E-83/	1.0E-83/	1.0E-83	1.0E-83	1.0E-83	1.0E-83 Z25822.1	1.05-83/	7.0E-84	6.0E-84	6.0E-84	8.0E-84/	8.0E-84	8.0E-84	6.0E-84	26.70 R	8.0F-84	8.0E-84/	6.0E-84	5.0E-84	6.0E-84	5.0E-84
	Expression Signal	18.	1.84	4.91	92.1	88	0.93	0.83	1.16	0.65	3.33	2.31	8	3.98	4.11	4.11	5.78	1.9	68	9	9	335	0.80	205	0.81	1.54	. 0.49
ŀ	ORF SED ID NO:	37749			27414		27481	27462	28681	229173	29830			29758	27284		ŀ		31682								32634
	SEO ID	24224	24224	25429	14443	14443	14486	14488	15662	18253	16922	17302	19907	16850	14333	14333	15414	18328	<u> </u>			L	20808	21377	1_		
	Probe SEQ ID NO:	11272	11272	12802	1410	1410	148	455	2885	3188	3882	4273	7589	3810	1208	1298	2407	834	9899	67.43	57.43	744	E P	808	715	3027	6227

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Top Hit Descriptor	Hamo sepiens regulatory factor X, 3 (Influences HLA class II expression) (RFX3), mRNA	Homo sepiens mRNA for KIAA1131 protein, partial cds	Homo sapiens mRNA for KIAA1131 protein, partial cds	wa78c04.x1 Scares_NR_T_GBC_S1 Homo sepiens cDNA clone MAGE:2302088 3' similar to . SW:NRDC_HUMAN 043847 NARDILYSIN PRECURSOR;	Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA	Hamo septems myosin light chein kinese Isafam 2 (MLCK) mRNA, complete cds	Hamo sapiens multidrug resistance protein (MRP), excn 13	Hamo sepiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA	Homo sepiens protein tyrosine phosphatase, receptor type, G (PTPKG), mKNA	Hamo sapiens histone deacetylase 3 (HDAC3) gens, complete ods	Hamo sepiens KIAA0783 gene product (KIAA0783), mRNA	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA	Homo sepiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA	Homo sapiens mRNA for KIAA1130 protein, partial cds	Homo sapiens Bach1 protein homolog mRNA, pertial cds	Homo sapiens chondroitin suffate proteogrycan 2 (versioan) (CSPG2) mRNA	Homo sepiens perfoertriolar material 1 (PCM1) mRNA	Novel human mRNA containing Zinc finger C2H2 type domains	Homo septens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, commisse exts)	Homo sapiens X-linked juvernile retinoschists precursor protein (XLRS1) mRNA, complete cds	wi20405.x1 Sogres Dieckgrassfe colon NHCD Homo septiens cDNA clone IMAGE:2520585 3" similar to	gh:L05053 60S RIBOSOMAL PROTEIN L18A (HUMAN);	CA/1-BT0795-190600-272-b08 BT0785 Homo sepiens cDNA	CM1-BT0796-160600-272-508 BT0795 Homo septems cDNA	Homo sapiens myelin transcription factor 1-like (MYT1-1) mRNA, complete ods	H.sapiens DNA for endogenous retrovinal like element	UI-H-Bit4-act-a-02-0-UI.st NCI_CCAP_Sub8 Homo sepiens cONA clone IMAGE:3084963 3	UI-H-BI4-ed-a-02-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084963 37	yr56e11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2093243	qm87c09.x1 NC_CGAP_Lu5 Homo saplens cDNA ctone IMAGE:1895/28 3	Homo sapiens chromosome 21 segment HSZ1C004	Homo sapiens chromosome zi segment nazi cut4
Top Hit Database Source		H H	H	EST HUMAN S		TN TA	NT		_					NT TN	NT IN			NT	5			EST_HUMAN		EST_HUMAN (		IN IN	EST_HUMAN I			T HUMAN		Ę
Top Hit Acession No.	11428740 NT	6.0E-84 AB032957.1			4.0E-84 4505928 NT	_	4.0E-84 AF022835.1	11396168 NT	11386168 NT	AF0596	11421326 NT	4557528 NT	4557528 NT	4.0E-84 AB032956.1	3.0E-84 AF028200.1	4758081 NT	3.0E-84 5453855 NT	AL096880.1				3.0E-84 AI983801.1	2.0E-84 BE695397.1	2.0E-84 BE695397.1	2.0E-84 AF036943.1	2.0E-84 X89211.1	2.0E-84 BF511575.1	2.0E-84 BF611575.1	2.0E-84 H63370.1	2.0E-84 AI298674.1	2,0E-84 AL163204.2	2.0E-84 AL163204.2
Most Similar (Top) Hit BLAST E Vatue	5.0E-84	6.0E-84	50E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	3.0E-84	3.0E-84	3.0E-84	3.0E-84	70.00	3.05.84	10.0	3.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2,0E-84	2.0E-84
Expression Signal	208	2.29	229		0.99	2.19	0.53	1.28	1.28	1.80	12.53	6.0	6.0	5.34	1,92	595	124	3.11		01.10		172	5.68	5.68	7.98	1.36	0.88	0.88	0.88	1.62	0.56	0.58
ORF SEQ ID NO:	38334		<u> </u>				31163	31902	31903	32714										2024	1		28153				L	31672				35122
Exan SEQ ID NO:	24753				L	18003			<u> </u>	19467			1_	24215	<u>l</u>		14998	_	1	Sec. 2		24179		L	<u> </u>	1_	1_	I_			21696	ш
Probe SEQ ID NO:	11871	11884	11984	604	4087	4988	5335	5642	5642	6889	9082	9282	8282	11283	316	1157	1877	2024			3/07	11228	2115	2115	2864	2873	28	560	6783	8392	8728	8728

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Top Hit Descriptor	AU120280 HEMBB1 Homo sapiens cDNA clone HEMBB1000339 5	yn49e11.r1 Soeres infant brein 1NIB Homo sepiens ONA clone IMAGE:51383 5' similiar to SP:APOH_RAT P26844 BETA-2-GLYCOPROTEIN I ;	nae30a02.x1 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4080251 3' similar to TR:QBUGS3 QBUGS3 DJ756323.1 ;	nae30a02.x1 Lupski_sympathetic_trunk Homo sapiens cDNA cione IMAGE:4090251 3' similiar to TR:QGUGS3 QQUGS3 DJ756G23.1 ;	Homo sapiens intersectin short isoform (ITSN) mRNA, complete ods	Homo sepiens tyrosine 3-monockygenase/hyptophan 5-monockygenase activation protein, zeta polypepäde (YVVHAZ) mRNA	Hamo sepiens complement companent 5 (C5), mRNA	em85511.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1628885 3"	601308006F1 NIH_MGC_44 Hamo sapiens cDNA clane IMAGE:3828257 5	Homo sapiens pericentrioler material 1 (PCM1), mRNA	mrt2806.s1 NCL_CGAP_SS1 Hamo septens cDNA clone IMAGE:1239106 3'	Homo sapiens 959 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3	DKFZp434N0323_r1 434 (synonym: htse3) Homo sapiens cDNA clone DKFZp434N0323 5	DKFZp434N0323_r1 434 (synonym: https3) Homo sepiens cDNA clone DKFZp434N0323 6	Homo sepiens 959 to config between AML1 and CBR1 on chromosome 21q22, segment 1/3	Homo sapiens speckle-type POZ protein (SPOP), mRNA	utarine water channel=28 kda erytirocyte integral membrene protein homdog (human, utarus, mRNA, 1340 mil	Novel human gane mapping to chomosome 13	Novel human gene mapping to chamosome 13	Novel human gane mapping to chomosome 13	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA	Homo sapiens NGFLA binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA	Homo sepiens NGFI-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA	Homo sepiens Ca2+-binding protein CABP3 (CABP3) gene, exon 6 and partial cds	Homo sepiens ubiquitin specific protesse 13 (isopeptidase T-3) (USP13) mRNA	Homo sapiens ubiquitin specific protesse 13 (isopeptidase T-3) (USP13) mRNA	Novel human gene mapping to chamocane 13	Homo sepiens purmergic receptor P.ZX-tine 1, orpinan receptor (P.ZXVL.1), mixwy
Top Hit Databese Source	EST_HUMAN	EST HUMAN		EST HUMAN	П			EST_HUMAN	EST_HUMAN		EST_HUMAN			EST_HUMAN	NT		1			NT	NT	K	NT	NT	NT	NT	NT	K	Į,
Top Hit Acessian No	20E-84 AU120280.1	122841.1	2.0E-84 BF448000.1			4507962 NT	11427631 NT	1.0E-84 AA984379.1	1.0E-84 BE392137.1	11427197 NT	1.0E-84 AA720851.1	1.0E-84 AJ229041.1	1.0E-84 AL043314.2	1.0E-84 AL043314.2	1.0E-84 AJ229041.1	11434422 NT	276482 4	1.0E-84 AL049784.1	1.0E-84 AL049784.1	1.0E-84 AL049784.1	TN 4685858	11430846 NT	11430846 NT	5031984 NT	1.0E-84 AF224511.1	4507848 NT	4507848 NT	AL049784.1	11417812NT
Most Similar (Top) Hit BLAST E Vetue	20E-84	2.0E-84 H22841.1	2.0E-84	2.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	4 05 94 579489 4	18. 18.	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84		1.0E-84
Expression Signal	68'0	29. 0	3.28	3.28	1.44	15.79	1.18	3.1	2.34	1.27	2.47	3.92	2.66	2.66	2.12	0.86	8	4	4	2.66	4.72	0.63	2.13	291	0.62	2.65	2.65	2.67	2.03
ORF SEQ ID NO:	38108							27282	28106		29717	30360	30639	30640	30360								١.		36533		31286	33626	
SEQ ID	22854		1	.L	13404	1	13783	14331	15087	L	16806	17472	17748	L.	Ł	L		20086		1_		L.			<u> </u>		18337		26126
Probe SEQ ID	200	10080	12445	12445	312	58	2	1288	202	2232	3764	4448	4728	4728	4 <del>0</del> 48	6029	3	2007 4007	7084	7314	7708	7814	7859	8833	10128	10150	10150	12121	12324

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Single Exon Probes Expressed in Durie Mariow	Top Hit Descriptor	Hamo sepiens exantitase 2, mitochandrial (ACO2), mRNA	Homo saplens chromosome 21 segment HS21C009	Hamo sapiens nuclear protein Skip mRNA, complete cds	Homo septems nuclear protein Skip mRNA, complete cds	Human plasminogen gene, excn 7	Human plasminogen gene, extn 7	Homo sepiens DKFZp434P211 protein (DKFZP434P211), mkNA	Homo sepiens chromosome 21 segment H321CO80	Homo sepiens heat shock transcription record iz pirroing protein (nor zon), litroins	Homo sapiens chromosome 21 segment NS21 CV06	Homo sapiens ribosomal protein LZ7 mrkNA, compress cos	Homo sapiens MSTP030 mRNA, complete cds	Homo sapiens DEAD/H (Asp-Gtu-Ala-Asp/Hts) box polypeptide 10 (RNA heitcase) (DDX10), mRNA	Homo sepiens DEAD/H (Asp-Gtu-Ala-Asp/His) box potypeptide 10 (RNA helicase) (DDX10), mRNA	Homo sapiens chromosome 21 segment HS21 CX84	601458646F1 NIH_MGC_68 Homp sapiens cDNA clane IMAGE:3882402 5	601458646F1 NIH_MGC_68 Hamo sapiens CUNA Gare IMAGE_3002402 3	Homo sepiens T-type celotum channel alphaf subunit Alphafl-e isoform (CACNA1I) mRNA, complete cds	602084730F1 NIH MGC 83 Homo sapiens CUNA dane IMACE: 4246007 3	602084730F1 NIH MGC 83 Homo sepiens dunk dana IMM CE. 4246007 3	1/84g01.x1 NC_CGAP_Kid11 Hamo signers guith dure invalorzobobo s	RC1-B10823-120200-011-007 B10023 Hamo septems CLNNA	HSDHEGC03 Stratagene dDNA Ebrary Human heart, cat#838208 Homo seplens dDNA done HEGC03	Homo sapiens protein phosphatase 2A BK gamma subum gene, erom o	ye53g09_r1 Scares fetal liver spieen 1NPLS Hamo sepients duina cane limage: 121 avr 3	Homo sepiens F-box only protein 24 (FBXO24), mRNA	Homo sapiens F-box only protein 24 (F-BXO24), mrthA	Homo sepiers lectinel protine non protein (LFRF), mixar	Homo septens mer proporticogene (nepetucyte grown recommy (mm. ), min.co.	din septents are and septents are also and are also are a
con Probes EX	Top Hit Databese Source		¥	¥	H H	H	H					Ĭ	H			H		EST HUMAN 6				╗	EST HUMAN R	EST_HUMAN H		T HUMAN					
Single	Top Hit Acesslan `No.	11418185 NT	9.0E-86 AL163209.2					T857020 NT	9.0E-85 AL163280.2	5901979 NT	9.0E-85 AL163268.2		7.0E-85 AF113210.1	11438573 NT	114385 <u>73</u> NT	5.0E-85 AL163284.2		5.0E-85 BF035674.1		4.0E-85 BF677910.1	4.0E-85 BF677910.1	4.0E-85 AI628119.1	4.0E-85 BE079263.1	4.0E-85 Z18867.1	3.0E-85 AF096157.1	3.0E-85 T97495.1	11024695 NT	· 11024695 NT	11436001 NT	11422024 NT	
}	Most Similar (Top) Hit BLAST E Vetue	1.0E.84	9.0E-86/	9.0E-85 U51432.1	9.0E-85 U51432.1	9.0E-85 M33282.1	9.0E-85 M33282.1	9.0E-85	9.0E-85	9.0E-85	9.0E-85	7.0E-85 L05094.1	7.0E-85	6.0E-85	6.0E-85	5.0E-85	5.0E-85	5.0E-85	5.0E-85	4.0E-85	4.0E-85	4.0E-85	4.0E-85	4.0E-85	3.0E-85	3.0E-85	3.0E-85	3.0E-85	3.0E-85	3.0E-85	3.0E-85
	Expression Signal	232	18	221	221	1.31	131	295	1.11	1.05	F	13.33	9.76	2.61	2.51	1.67	1.37	1.37	6.19	1.42	1.42	95.0	1.35	1.31	1.02	3.9	1.37	1.37	0.65	0.68	269
	ORF SEQ ID NO:	31825		27069	27070	27586	27587	27695	30188	30821	30855	27132		38200				31561		32576		33456			27301			30843	31485		32560
	Exem SEQ ID NO:	26201	14020	14119	14119	14614	14614	14715	17309	17930	17965	14181			1	1	1	L	<u>.                                    </u>				<u> </u>	25772		1_	1_	<u> </u>			19330
	Probe SEQ ID NO:	12438	200	407	4074	1884	185	1684	4280	4913	4950	1138	11958	11745	11745	240	5526	5528	13030	6271	6271	2013	10937	12875	1302	1785	4935	4935	6476	6204	6257

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SEQ ID NO: NO: 20116 201
SEG ID NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:

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	Top Hit Descriptor	245f03.s1 Soares, fetal Incr. spleen, INFLS, S1 Homo seplens aDNA clane IMAGE:453245 3'	801897003F1 NIH MGC_19 Homo septens CLYNA Clone IMALKE: 412044U 5	601897003F1 NIH_MGC_19 Hamo saplens cDNA clane IMAGE:4128440 5	gi58a07-x1 NGI CGAP_Brn25 Homo septens dDNA clone IMAGE:1860488 31	Home semiens calcineurin binding protein 1 (KIAA0330), mRNA	Library senions colchesim berding protein 1 (KIAA0330), mRNA	TAIN SUBJECT HILL MORE OF THE SECOND STATE OF	001120/1017 INIT MICE OF THE CONTROL	HOTHO SEPTIMENT TO COUNTY PRODUCT NATIONAL (1) CONTROL (1) COUNTY (1) MRNA	Home suprems synchrotree 150, exclaims in the property of the Control MAGE: 1403559 3	BESTUG. 81 SOCIETY DELIGITATION IN THE TRANSPORT OF THE PROPERTY OF THE PROPER	BERCOS, ST. SORTES, DEFERING LIMING JULIA OF TRUIN SEPARATE MAIN MAINTENANCE AND AND AND AND AND AND AND AND AND AND	Homo sapiens fumor encochetta maner / precursor ( 15/41 ), missor	Homo sapiens tumor endothetial marker / predured (   EMI ), micros	Homo septiens Text (furmen I -cen reuteanns wrus type I) parturing process 1 ext. (furmen I	Homo sapiens galactocerebrosidase (GALC) gene, exp. 13	Homo septiens RAN binding protein / (RANDIN), minuty	Homo saplens Diceage syndrome oracla region gare o (Locato), minum	Homo sapiens conglutaratia dehydrogenessa (iipoamide) (USUTI) miraw	601072594F1 NIH MGC 12 Hamo sapiens duny draie invider Processory	601176885F1 NIH MGC 17 Homo sapiens Curk Garo Invocation 1850 5	601072594F1 NIM MISC. 12 Frontile September CANA change IMAGE: 2871719 3'	ANTENDED LINE CONTACTOR CONTACTOR FILE CONTACTOR FI	AV 7223 TID THUIN SEPTENS CONTROLLED TO THE SEPTENS CONTROLLED INACES 1901 1908 5	COLORGON TWILLIAM TO 74 Home servines CINA close IMAGE 39/1303 6	COLOROSCO I MILL MOST BOTH Home contents CDNA clone IMAGE 22513713'	WIGOLXI INC. CAT. FIZE INITIO OPPORTO CONTROLL	AVENDED GIVE THIS SECTION SECTION CONTRACTOR IN THE IMAGE 3838753 5	60136/23351 NIT MGC_KI TUIN SEPARA CONTRACTOR CONTRACTO	EXIII/ZX JUNAI I-com VI muito separate universi o ser	Hamo septens and inches a september 1 Not	yzi 0808. Ti Sogres muliume scherosis Zivinimar muliu septens como umo minima menuma	Human encoganous reuremes, centificate services	HOMO SEPTEMS MINIMA TO NAVA 12.1 parcel to september 12.1 parcel to sep	ESTS/02/10 MENCE I recorderated, mence in the control of the contr
XOII LIONES	Top Hit Database Source	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN		Z	- 1	EST_HUMAN	5	¥	EST HUMAN	EST HUMAN	¥	M	NT	NT	M	LN LN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	ESI HUMAN	ESI HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	뉟	EST HOMAN	Ę	Į.	EST HUMAN
	Top Hit Acession No.	AA778785.1	4 0F 85 BF3415521		Ī	2006	1141/802 N	17802	9.0E-86 BEZ74217.1	11424140 NT	03224		7.0E-86 AAB60801.1	896686 NT	9966886 NT	11421737	38557.1	5453997 NT	11528307 NT	4505492 NT	4.0E-86 BE547173.1	4.0E-86 BE295843.1	4.0E-86 BE547173.1	3.0E-86 AW340946.1	3.0E-86 AV722329.1	3.0E-86 BE888479.1	3.0E-86 BE888479.1	3.0E-86 AI659240.1	3.0E-86 AV600469.1	3.0E-86 BE410854.1		2.0E-86 AL163203.2	2.0E-86 N58977.1	9635487 NT	2.0E-86 AB033103.1	2.0E-86 AW966142.1
-	Most Similar (Top) Hit BLAST E Value	1.0E-85/	4 OF AS	4 05-85	4 NF B5 /	3 1	1.0E-85	1.0E-85	9.0E-86	8.0E-86	8.0E-86	7.0E-96/	7.0E-96	7.0E-86	7.0E-86	7.0E-86	7.0E-86 1.38557.1	7.0E-86	7.0E-86	6.0E-88	4.0E-86	4.0E-86	4.0E-86	3.0E-86	3.0E-86			3.0E-86								
-	Expression Signal	201	SA C	2,48	2000	767	3.47	3.37	12.78	1.27	1.57	0.83	0.83	0.85	0.85	6.12	4.12	1.49	1.67	320	1.76	10.88	2.44	6.64	1.12	3.26	3.26	5.6	1.66	1.35	1.83	2.72	2.88	2.54		1.47
	ORF SEQ ID NO:	37746	9700	37010	37017	38035	31780	31780		32552	38477	26839	28940	32631	32632	31248	35487		38522		1			31944		36995	36896	37437	38312		26286		27189	28238		
	SEQ ID	24224		74000	74077	24837	25289	25289	14459	19322	24881	13989	13989	L	1	_		1_		L	1	1	1_	18772		23503	23503	23919	24725	Ĺ.		<u> </u>	<u> </u>	15216	L	L
	Probe SEQ ID NO:	44260		2 2	Ž Ž	12064	12328	12583	1426	828	12004	88	888	6530	833	7160	808	1005B	10416	1207	272	6151	11572	5677	8605	10581	10581	11764	11842	12295	8	414	<u>+</u>	22	727	3428

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Top Hit Descriptor	Homo sepiens lysophosphatidic acid acylinansferaso-delta (LPAT-delta) mRNA, complete cds	Homo sapiens lysophosphatidic acid acythansferase-delta (LPAAT-delta) mRNA, compitete cos	hd87g08x1 NCI_CGAP_GC8 Hamo septems cDNA clane IMACE-2916542 3"	Homo sepiens cAMP-specific phosphodiesterese 8A (PDE8A) mRNA, pertial cds	H. sapiens mRNA encoding phospholipase c	H.septens mRNA encoding phospholipase c	Homo sepiens similar to ectonuclectide pyrophosphatase/phosphodiestorase 3 (H. sepiens) (LOC632714), mRNA	Human Chediak-Higashi syndrome protein short Isoform (LYST) mRNA, complete cds	Hamo sapiens chramosome 21 segment HS21C027	Homo sepiens butyrobetaine (gamma), 2-cooptuarate dioxyganase (gamma-butyrobetaine nyoroxyesse) (BBOX), mPtvA	Homo septiens butyrobetaine (gemma), 2-coogluterate dicxygenase (gamma-butyrobetaine hydroxylasse) poe xxx	(BDCX), in VX Homo seniens phospholind scrambiase 1 (PLSCR1), mRNA	1. September 1 (SE1) mRNA	Homo saptens chromosome segregation 1 (year nothing) para (with the control of th	Homo sapients basso-neuk-kod-neuk-r-kod javeen (h. 1755).	Homo saplens basic-heitk-loop-heitk-PAS protein (Mr. A.S.), linuum	Homo sepiens mituNA for KLAA1411 protein, per use cus	Homo sapiens thyroid autoentigen 70k0 (Ku emigen) (52271), missis	Hamp sapiens gene for Ah-6, complete cas	Homo sapiens NADH dehydrogenase (ubiquinane) 1-6-5 protein 1 (73kD) (NADH Fouet Zynie 4 tourcessy) (NDDES1) mRNA	Homo saplens fibutin 5 (FBLN5) mRNA	Human gamma-gudamyi transpeptidasse mRNA, complete ods	Hamo saplens chranosome 21 segment HS210009	Homo sapiens chromosome 21 segment HS21Cx08	Homo sapiens hypothetical protein (LOC51318), mRNA	Homo saplens hypothetical protein (LOC51318), mRNA	Homo saplens chromosome 21 segment HS21C100	Homo sapiens synaptojanin 1 (SYNJ1), mRNA	Homo saplens chromosome 21 segment HS210084	4b77c09.x1 Soares_fetal_heart_NbH119W Homo sepiens cONA clone IMAGE:1706128 3' similar to sw:k1c.j_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL_10;
Top Hit Deschasse Source	¥	¥	T_HUMAN				Ę	Ę	F			Z		¥	F	M	M	M	NT.	5	1	Į.	¥	F	¥	LN.	¥	E	Ę	EST_HUMAN
Top Hit Acession Det	2.0E-98 AF156778.1		_				11419429NT		2.0E-86 AL163227.2	11437135INT		1143/135 IN	10eccent	11422084	11545848 NT	11545846 NT	2.0E-86 AB037832.1	11418180 NT	2.0E-86 AB011399.1	TM REBACEA	TA GARGRAD NT	20492.1	1 0E-86 AL163209.2	1 0E-86 AL 163209.2	T/06/18/	T/06/16/1		4507334 NT	1.0E-86 AL163284.2	9.0E-87 AI150703.1
Most Similar (Top) Hit BLAST E Vatue	2.0E-88.A	2 OF-86 A	20E-88A	2.0E-86	2.0E-86 Z16411.1	2.0E-86 Z16411.1	2.0E-88	20E-861	2.0E-86	205-86		2.05-86	205-80	2.0E-88	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	90 70	201-04-04-04-04-04-04-04-04-04-04-04-04-04-		1 0E-86	1 0E-86	1 OF 86	4 OF 88	1 05-86	1 OF-86	1.0E-86	9.0E-87
Expression Signal	255	258	3.01	333	12	1.53	180	0.77	0.53	24.0		2.44	1.48	2.12	2.88	2.88	1.63	282	6.37	8	8 2	284	2.18	2 18	2 5	5	2 2	1 42	144	1.78
ORF SEQ ID NO:	28711	207/12		30745	32267	32258	38814	34728		95340	<u> </u>		35651	36080	37237	37238	37289	31750		1	2/19/2									
SEO ED	16800	46000	4748	4784K	1965	19057	2000	24342	21828	700	1		22220	22828	23735		L.	1		<u>.                                    </u>		10001	L	1.	┸		l			
SEO ID	8778	320	8 6	200	202	200		272	3 8	8	7	883	888	8873	10814	10814	10869	12732	12901		189	37/08	9507	2000	300	999		4054	583	6430

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	Top Hit Descriptor	Homo saplens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), misuva	O cumpatus mRNA for elongation factor 1 alpha	TARREST OF INC. COAP CARE Home sentens CONA clone IMAGE:3322779 3	Thesens will Coap Code Home saplens cDNA clone IMAGE:3322779 3'	INDUCATION CONTROL AND INTEREST OF THE CONTROL OF T	MKG-VILOSE-VZDOV-VO-FELLINI DOSE TOTIO SEPTEIS COLOR	ILS-HI0619-000/00-196-D10 H10019 name saparas carva	ILSHI 0702-1606W-103-400 FI 1070Z FIAIRO Squesis COLOS	UKFZP434NG23 T1 434 (synonym: mass) nomo septens cuito cuito bui promoces.	UKFZPARANGZ T 424 (synanym: mass) namin septembarang and promise a	CASSINOT.ST Scenes Nintiminal ST Hamp Sequens County Card Invited. 1000 1	Human mRNA from chromosome 15 gene with from controlly to minch 11 4 55 4 1-1- A	Human mRNA from chromosome 15 gane with homology to Minichal Annu	Homo septiens hormonally upregulated neu tumor-essociated ignesse (norus), merusa	Homo espiens mRNA for KJAA1081 protein, partial cds		Homo septens similar to SET translocation (myeloid teukemia-essociated) (H. septens) (LOCSSTUZ), mixiva	EST96094 Testis I Hamo saplens cDNA 5' end	EST96094 Testas I Hamo sapiens curva 5 end	Homo sepiens chromosome 21 segment HSZI 0010	Hano sapiens mKNA for KIAA1414 protein, per tell cas	Homo septems micha for Kirakustoo protein, per usi cas	Homo sapiens myeldd/ymphaid or mbad-lineage laukema (ururatak ("Jroschala) normoey), ua saccano. L., (MLLT4) mRNA	Homo sapiens smell inducible cytokine subtamily A (Cys-Cys), member 10 (SCTATO) minuth	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 16 (SCYA16) mixiva	ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)	Human transcription factor NFATx3 mRNA, complete cds	TCBAP1E4051 Pediatric pre-B cell scute lymphoblastic leukemia Beylor-HGSC project=1 CBA Home saprans con a con a CBAP4051	Homo sapiens KIAA1072 protein (KIAA1072), mRNA	Homo sapiens KiAA1072 protein (KIAA1072), mRNA	Homo sepiens tuberth (TSC2) gene, exon 10	Homo sepiens KIAA09714 protein (KIAAU9714) mrdviv, comprete cos
186	Database	Σ	Ę	Į.	h	ESI HUMAN	ESI HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	Į.	TN	NT .	NT		M	l⊢1	EST_HUMAN	Į.	노	Ę	뒫	NT	뒫	SWISSPROT	노	EST HUMAN	Z	보	NT	토
	Top Hit Acession No.	4757721 NT	4757724	R2245 4	١			7.0E-87 AW890338.1	7.0E-87 BF352778.1	7.0E-87 BE712961.1	7.0E-87 AL043314.2	7.0E-87 AL043314.2	Al081565.1	(03002.1	(03002.1	7667243 NT	6.0E-87 AB029004.1		11432444 NT	5.0E-87 AA382811.1	5.0E-87 AA382811.1	4.0E-87 AL163210.2	4.0E-87 AB037835.1	4.0E-87 AB007925.1	6174674 NT		4759073 NT		4.0E-87 U85429.1	4 0F-87 BF247284.1	11425291 NT	11425291 NT	L48624.1	4.0E-87 AF223470.1
<u> </u>	(Top) Hit T BLAST E Vatue	9.05-87	0.05.87	8 NE 87 YR2245 1	ON LOCAL	7.0E-87	7.0E-87 E	7.0E-87	7.0E-87	7.0E-87	7.0E-87 /	7.05-87	7.0E-87	7.0E-87	7.0E-87 K03002.1	6.0E-87	6.0E-87		6.0E-87	5.0E-87	5.0E-87	4.0E-87	4.0E-87	4.0E-87	4.0E-87	4.0E-87	4.0E-87		4.0E-87	4 0F-87				
<b>├</b>	Expression Signal	1,7	2	2 8	07.30	3.11	3.11	1.01	2.50	99:0	3.41	3.41	0.48	10.09	10.09	0.78	18.		6.13	1.86	2	98.0	15.32	1.40	1.57	880	98'0							
	ORFSEQ ID NO:	34001	5000	3000			28337	32864	34015	34535	36837	36838		37708						27157				28084		L								
	S C C C	20830		STORY.	13307	16316	15316	19602	21499	21132	23353	23363	25703	24190	24180	L	1_	L	24041	L	L_	L	<u>L</u> _		<u> </u>		L	L			$\perp$	L.		22545
	SEQ ED	ž		8	84	2304	2304	88	8831	6086	10431	10431	10834	11237	11237	35.00	1929		11079	1162	12585	198	1178	2045	3478	5307	202	6534	7/8	8 8	3 6	2002	8050	9583

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Table 4
Single Exon Probes Expressed In Bone Marrow

	Top Hit Descriptor	Human von Willebrand factor pseudogene oorresponding to exone 23 through 34	Homo sapiens calcineum binding protein 1 (KIAA0330), mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens purinergio receptor P2X-like 1, orphen receptor (P2RXL1), mRNA	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA	QV0-BN0148-050600-254-e03 BN0148 Homo saplens cDNA	AU116885 HEMBA1 Hamo sapiens dDNA dane HEMBA1000807 6	CMO-TNICO38-150800-552-h08 TNO038 Hamo saplens cDNA	RC6-HT0580-200300-031-G04 HT0580 Homo sapiens cDNA	601569041F1 NIH_MGC_21 Homo septens oDNA clone IMAGE:3843730 5	601569041F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3848730 5	601341383F1 NIH_MGC_63 Homo septems cDNA clane IMAGE:3683348 6	y/21e07.11 Sources fetal liver spleen 1NRLS Hamo expians cDNA clane IMAGE:243396 5	AV654143 GLC Hamo septens cDNA clane GLCDSG043"	601176032F1 NIH_MGC_17 Homo septens cDNA clone IMAGE:3531511 5	Homo septens hect domain and RLD 2 (HERC2), mRNA	w21e07.rt Soeres fetal liver splean 1NRLS Homo saplens cDNA clone IMAGE:243396 6	y/21e07.r1 Scares fetal liver spleen 1NFLS Homo septems cDNA clone IMAGE:243398 5	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)	601278315F1 NIH_MGC_39 Homo sapiens dDNA clone IMAGE:3610539 5	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA	Humen mRNA for T-cell cyclophilin	Homo sapiens neuredn III (NRXN3) mRNA	Rettus narvegicus taste buid receptor protein TB 641 (TB 641) gene, compitate cds	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8	Hamo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8	Home septens corticotropin-releasing factor type 1 receptor gene, each 8	Homo sapiens conticotropin-releasing factor type 1 receptor gene, exon 8	Homo sepiens IQ motif containing GTPese activating protein 1 (IQGAP1) mRNA	Homo saplens protein kinase C, beta 1 (PRKCB1), mRNA	Homo sapiens IQ motif containing GTP ase activating protein 1 (IQGAP1) mRNA	Homo saplens solute cerrier family 22 (organic cation transporter), member 1-like (SLC22A11.), mRNA	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
	Top Hit Database Source	NT	NT.	μ	L	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	NI	FN	NT	N	NT	IN	본	Į.	Ë	¥	אַנ	IN	Σ
Signify of the state of the sta	Top Hit Acession No.	A60676.1	11417862 NT	11417862 NT	11417812 NT	4885420 NT	2.0E-87 BF327920.1	2.0E-87 AU116935.1	2.0E-87 BF376311.1	2.0E-87 BE175478.1	2.0E-87 BE734190.1	2.0E-87 BE734190.1	2.0E-87 BE567193.1	448128.1	2.0E-87 AV854143.1	2.0E-87 BE294432.1	11433046 NT		448128.1	G2851.1	2.0E-87 BE531136.1	7705683 NT	700052.1	4758827 NT	J50949.1	1.0E-87 AF073371.1	1.0E-87 AP073371.1	1.0E-87 AF039517.1	1.0E-87 AF039517.1	TN 98786 NT	11431590 NT	4506786 NT	4505528 NT	1.0E-87 AF214562.1
	Most Smiler (Top) Hit BLAST E Value	4.0E-87 M60676.1	4.0E-87	4.0E-87	4.0E-87	20E-87	2.0E-87	20E-87	2.0E-87	2.0E-87	2.0E-87	2.0E-87	2.0E-87	2.0E-87 N48128.1	2.0E-87	2.0E-87	2.0E-87	2.0E-87 N48128.1	2.0E-87 N48128.1	2.0E-87 X52851.1	2.0E-87	1.0E-87	1.0E-87 Y00052.1	1.0E-87	1.0E-87 U50949.1	1.0E-87	1.0E-87	1.0E-87	1.0E-87	1.0E-87	1.0E-87	1.0E-87	1.0E-87	1.0E-87
	Expression Signal	5.12	1.47	1.47	3.11	£.73	0.79	6.0	1.64	99.0	8.67	8.67	3.73	1.12	0.84	1.31	18.0	37.21	36.03	13.21	5.58	3.71	4.15	2.03	1.88	192,	<u>2</u> .	0.84	0.84	1.03	1.17	. 0.85	0.64	11.12
	ORF SEQ ID NO:	37894	31428	31429		28796		29745	30856	30800	32020			33205		33700	33757	34008	34284	L	L		29677	29700			32663		L		l			34837
	SEQ ID NO:	24443	25839	25839	25444	15779	16017	16838	17966	18013	18838	18838	19625	19910	20172	20349	1	$\mathbf{I}_{-}$		21708	23070	15818	16766	L	18162	L	L	L	20353			1_	L	
	Probe SEQ ID NO:	11600	12878	12678	12825	2787	2859	3798	4851	4998	5744	5744	8460	6857	86 848	7378	7438	7688	188	8738	10144	1186	3723	3746	5152	6352	6352	7383	7383	2380	7828	7783	8908	8453

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	Top Hit Descriptor	Homo sapiens mRNA for alpha2,3-stalytransferase ST3Cal VI, complete eds	Homo septens mRNA for alpha2,3-stafytransferase ST3Gal VI, complete cds	RC8-BN0278-050700-012-E02 BN0278 Homo sapiens cDNA	RC8-BN0278-050700-012-E02 BN0278 Homo sepiens cDNA	Human L-plastin mRNA, 5' end	Homo septens hect domain and RLD 2 (HERC2), mRNA	Homo sapiens suitotransferase-related protein (SULTX3), mRNA	Homo sepiens double stranded RNA activated protein kinase (PKR) gene, excn 12	Homo sepiens mRNA for KIAA1369 protein, pertiel cds	Homo sapiens mRNA for KIAA1399 protein, pertial cds	Hamo sapiens DKFZP586P1522 protein (DKFZP588P1522), mitOVA	Homo sepiens chromosome 21 segment MS210009	H.sapiens ECE-1 gane (exem 9)	H.sapiens ECE-1 gene (exxn 9)	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cts)	Home sanisms X. Inked anhidratific echadermal dysolesia protein gene (EDA), exan 2 and flanking repeat	regions	Homo sepiens KIAA0083 gene product (KIAA0083), mRNA	K9719F Human fetal heart, Lambda ZAP Express Homo sepiens cDNA clone K9719 6' similar to ZINC FINGER PROTEIN HZF1	Homo sapiens intersectin short Isoform (ITSN) mRNA, complete cds	Homo sapiens intersectin short Isoform (ITSN) mRNA, complete cds	Homo septens intersectin short isoform (ITSN) miRNA, complete cds	wdeshoevd NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE:2336799 3' similar to contains Atu	repositive matricularities etailistit micrat. Micrata repositive etailisti.	WINDS ILLUSTRATION OF THE PROPERTY OF THE PROP	Homo sepiers drightosome 21 sepimen nozi cuo:	602164958F1 NIH MGC 83 Hamp sapiens Curva dane IMAGE:42507755	Homo sepiens KIAA0068 gene product (KIAA0063), mRNA	PMH-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA	PMA-TN0028-050900-004-f10 TN0028 Homo saptens CUNA	602/49/62F1 NIH MGC_81 Home sapiens conviced involutional to the converse	Homo sapiens transforming grown racial, bearn narea, when the e.g
	Top Hit Detabese Source	F	¥	EST_HUMAN	HUMAN		NT			M	NT	NT	LN.	TN	¥	ļ ţ		호	Z	EST HUMAN	Į.	¥	Ę		EST HUMAN	EST_HUMAN	토	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST HUMAN	¥
200	Top Hit Acession No.	1.0E-87 AB022918.1			Ţ		729867	7857832 NT	9.0E-88 AF167465.1	9.0E-88 AB037820.1	9.0E-88 AB037820.1	7881701 NT	9.0E-88 AL 163209.2				S.UE-66 ADUZOGSO.1	6.0E-88 AP003628.1	T881887	E OF OR MEDICAL	AF114488.1	5.0E-88 AF114488.1	6.0E-88 AF114488.1		5.0E-88 AI693217.1	5.0E-88 H10932.1	5.0E-88 AL163284.2	5.0E-88 BF680206.1	7661887	4.0E-88 BF091229.1	4.0E-88 BF091229.1	BF670714	11416585 NT
	Most Similar (Top) Hit BLAST E Value	1.0E-87	1.0E-87	1.0E-87	1.0E-87	1.0E-87 M34426.1	1.0E-87	1.0E-87	9.0E-88	9.0E-88	9.0E-88	9.0E-88	9.0E-88	9.0E-88 X91929.1	9.0E-88 XD1929.1	100	8.0E-00/	6.0E-88	5.0E-88	90 110 4	5.0E-88	5.05-88	6.0E-88		5.0E-88	5.0Ё-88		88-30'S	5.0E-88		4.0E-88	4.0E-88	4.0E-88
	Expression	26'0	260	8.68	899	3.11	£.	1.48	8.48	2.58	2.56	1.14	98.0	3.27	327			3.88	1.13	2 4 4 5	2	77.0	77.0		2.76	3.32	244	0.57	1.73		1.49		1.35
	ORF SEQ ID NO:	35855							27102						30208		30831	35771	Ì	L	280007					33481	34639	1		27338			33775
	E con SEQ ID	22728	1.		270AB	23881	L				14386	15147	16685		L	1	18051	22340	ł	L	1304		L	丄			21230	L	L		1_		ш
	Probe SEQ ID NO:	88	888	8 8	800	10739	11084	12875	168	1351	1351	2130	3842	4298	4208		2038	0275	4845		2047	208	300	3	3400	6936	828 F	8896	12435	1332	1332	5185	7454

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Table 4
Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA	Homo sepiens hypothetical protein FLI21634 (FLI21634), mRNA	Homo sepiens zinc finger protein 259 (ZNF259) mRNA	2848/12.5/ Sogres fetal liver spicen 1NHLS Homo septens CLINA Gone IMM-CE 25002.5	Homo sepiens a disintegrin and metalicproteinase comen 23 (ADAM23) minner	Homo saplens a distribgrin and metallicproteinase domain 23 (ADAM23) minuth	Homo sapiens hypothetical protein FL/20/220 (FL/20/220), mrkna	Homo sepiens valosin-containing protein (VCP), mkNA	Homo saplens polycythemia rubra vera 1; cell surface receptor (PRV1), mrXNA	Homo sapiens v-ral simian laukemia viral oncogene homolog A (ras related) (rALA), mrvvA	Homo sepiens interleukin 13 (IL13), mRNA	Homo sapiens activator of S phase kinase (ASK), mRNA	Homo sepiens activator of S phase khase (ASK), mithA	Homo sapiens putetive anion transporter 1 mRNA, complete cos	Homo sapiens retinoblastoma-binding protein 2 (RBBI-2), mrtNA	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA	Homo sepiens molybdenum cofactor blosynthesis protein A and molybdenum cotactor biosynunesis protein C mRNA, complete cds	Homo sapiens wets awan erythroblastosis whs E26 oncogene related (ERG), mRNA	Homo sapiens mRNA for RALDH2-T, complete cds	Homo sapiens mRNA for RALDH2-T, complete cds	Homo sepiens acyl-Coenzyme A dehydrogenesse family, member 8 (ACAUS), mrvva	Homo sapiens cubilin (htthrsic factor-cobalamin receptor) (Cubin) mixina	Homo sapiens transcobalamin II; macrocytic anamia (TCNZ), mytyk	Homo sapiens Calsentiin, presentiin-binding protein, E.F. hand transcription racid (CCEN), minner	Homo sepiens SNARE profeth kinase SNAK mRNA, complete cos	Homo sepiens SNARE protein kinase SNAK mRNA, complete cds	Homo sepiens dynein, exchanal, light polypeptide 4 (DWAL4), mitNA	UI-H-BIT-BEB-4-04-0-UI-BIT NCI CGAP SUBSITION SEPTIMENT CAMP THE INVALCE 27 107 30 3	ULHBIGGBB-04-0-U.SI NG CGAP DUBS TOTTO SEPTENS CONTINUED INTOCACT TOTALS	Homo septers KIAAJA17 miKNA, cumplete cus	HOMB SEPERS NIPAWATT MINNAY, CUITAGE CAS
Top Hit Database Source					EST HUMAN Z													<u> </u>		Į.	NT IN					H NI			7	EST_HUMAN	T	E
Top Hit Acession No.	7661947 NT	7661947 NT	11545800 NT	4508020 NT		4501912 NT	4501012 NT	4429300 NT	11428587 NT	TN 8888888	11420697 NT	11417370 NT	11418210 NT	11419210 NT	AF279265.1	11436400 NT	11421728 NT	3.0E-88 AF034374.1	526262	3.0E-88 ABO15228.1		11439065 NT	4557502 NT	11417974 NT	7305198 NT	2.0E-88 AF246219.1		88		-2	-	
Most Shnikar (Top) Hit BLAST E Value	4.0E-88	4.0E-88	3.0E-88	3.0E-88	3.0E-88 N66951.1	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.05-88/	3.0E-88	3.0E-88/	3.0E-88	3.0E-88	3.0E-88	3.0E-88	2.0E-88	2.0E-88	2.0E-88	2.0E-88	1.0E-88	1.0E-88	1.0E-88	1.0E-88
Expression Signal ·	3.12	3.12	0.85	1.78	2.51	80.0	86.0	3.64	245	4.05	3.62	0.95	0.77	72.0	15.04	6.35	10.99	82	214	0.74	0.74	0.89	3.65	7.12	61.67	1.66	4.07	1.86	5.17	6.17	23.82	23.82
ORF SEQ ID NO:	38282	38283	28731		28944	30175	30176		31350	31830	32063	32583	32877	32878	33302	34114								L	27033		L		L	32301		33142
SEQ ID NO:	24701	24701	13794	14858	16016	17298	17298	17529	18477	18761	18881	18357	25862	25662	20002	20741			1	2223	23213	1_		L	ľ	1	1		L	19099	. !	19856
Probe SEQ ID NO:	11818	11848	82	88	888	4289	4200	4504	8372	9899	08/6	8285	8533	6553	7267	7788	8283	0630	2380	9000	10288	10316	12088	12421	1037	1628	1765	4455	6016	6018	6802	6802

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Table 4
Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	wq70a12.x1 NCI_CGAP_GC8 Homo saptens cDNA clone IMAGE:2476606 3'	eas54e11.s1 NCI_CGAP_GCB1 Hamp sepiens aDNA clone IMAGE:8247323' strates to Wir:DU2/22	CE00851;	Homo saplens Recq helicase o (KECCI) gene, ausmano spino promove, verpress conferma	2987c02.rf Strategene HeLa cell as 83/216 Hanto septens culvis calle inschillor. Strategene HeLa cell as 83/216 Hanto Septens culvis calle in control of the septens culvis called the septens culvis called the septens culvis called the septens culvis called the septens culvis called the septens cal	DKFZp434N0323_r1 434 (synanym: htes3) Hamo sepiens cDNA clane DKFZp434N0323 6	0691g03.s1 NCI_CGAP_GC3 Hamo saplens cDNA clone IMAGE:1612766 3' similar to gb:M16342	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);	Hamo sapiens and mosalife at segment to a recommendation and the rec	Homo septens transgetin z ( I Actual), minaya	601142408F1 NIH MGC 14 Horns Equate curve times to the horse down as consider	Homo sapiens similar to sema domain, immunoglobulin domain (19), short besto domein, sou coo., (semaphortn) 3A (H. sapiens) (LOC83232), mFNA	Home sapiens hormonally upregulated neu tumor-essociated kinase (HUNK), mirror	Home expiens homonally upregulated neu timor-descolated in these (notify, illustro	Homo saplens complement component 8, beta polypeptide (C8B) mKNA	DKFZp434E248_r1 434 (synonym: hbs3) Homo sapiens cUNA cione UNFZp434E240 o	H.saplens CLN3 gene, complete CDS	H. sapiens CLN3 gene, complete CDS	Homo sepiens plestin 3 (T isoform) (PLS3), mYNA	Homo sapiens plastin 3 (1 isotom) (*1.23.), mrvva	Homo sapiens acun relativa protein 2.5 continues, outside in 17 mm.	HOMO SERBERS CLANAS AND A LOCAL (VIA A A 23) MRNA	Home segments Nutrackets   American (Nutrackets)   Indiana   American   Ame	Human co-tunestating through the control of the con	H.Sapielis Weet Italgane	H.Sapiens West nu gare	HOME SECRETS INTO NATIONAL PRINCIPLY FOR THE COLOR	Homo septems mixing to numerous process, process, process, consistent (NUMT) mixing	Homo sapiens time membrans proudit, (times DODA homolog (DRDA) mRNA	Homo septens semineral rough misser in Themase (100 7)	Homo sandans unqualificanjugala e sizinio 22. 3 (UBEZI.3) mRNA	Tions orders and the control of the
1	Top Hit Detebase Source	EST HUMAN		EST_HUMAN	NT	EST HUMAN	EST HUMAN		EST_HUMAN	Ę	¥	EST_HUMAN	Į,	NT	NT	ĮN.	EST_HUMAN	¥	NT	۲	¥	늇	Z	Z	ĮN.	5	¥	뉟	노	Ę	¥	Į.	N
	Top Hit Acession No.			1.0E-88 AA486981.1	1.0E-88 AF135183.1					1.0E-88 AL163246.2	1142H238 NT	8.0E-89 BE311557.1	11421514 NT	TNS7213	7857213 NT	4557390 NT	7.0E-89 AL045748.1	(99832.1	09832.1	7549808 NT	7549808 NT	11420754 NT	11417118 NT	11417118 NT	102923.1	XB2048.1	X62048.1	7.0E-89 AB020630.1	7.0E-89 AB020830.1	5803114 NT	4506124 NT	4507788 NT	4507788JNI
-     	Most Similar (Top) Hit T BLAST E Vetue	1.0E-88 AI969034.1		1.0E-88	1.0E-88 A	4 OF 88 AA190368	4 05 88 4	200	1.0E-88	1.0E-88	9.0E-89	8.0E-89 B	8.05-89	7.0E-89	7.0E-80	7.0E-89	7.0E-89/	7 0F-80 X99832 1	7.0E-89 X99832.1	7.0E-89	7.0E-89	7.0E-89	7.0E-89	7.0E-89	7.0E-89 J02923.1	•	7.0E-89 X62048.1	7.0E-89	7.0E-89	6.0Ε-89	6.0E-89		6.0E-89
	Expression Signal	8		3.9	0.47	8	3 2	277	3.86	49	3.66	1.74	7	7	7	2 95						1.42	0.57	29.0	3,88	125	1.25	1.11	1.11	1.23	1.17		0.89
	ORF SEQ ID NO:	A 20 B 4 A	E S	33741		Ì		3652/	37449	l	37774													34590	35212						7 28261		7 28465
	Eken SEQ ID NO:	00000	ALC: N	20359	21445		_1	22805	23928	_	24248	L	l		1	J.			19905		1_		L		L	L	L	┖	_				15447
	Probe SEQ ID NO:	1	RZE)	S	8478		<b>188</b>	8888	11773	12840	4,28	27.45	2 2	7110	3 8	3 5	818	QQ I	3000 3000 3000 3000 3000 3000 3000 300	6477	6477	7741	2	25	8823	10897	10897	10913	40043	1025	2223	2440	244X

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	Top Hit Descriptor	Homo sepiens mRNA for KIAA0406 protein, partial cds	Homo sapiens mRNA for KIAA0408 protein, partial cds	TCBAPZE0383 Pedlatric pre-B cell acute lymphoblastic laulernia Baylor-HGSC project≓1 CBA Homo sapiens cDNA cone TCBAP0383	TCRAPYERSS Perfeate ma-B cell acuta lumbablessic leutemia Baylor-HGSC project=TCBA Homo septems	CDNA clone TCBAP0383	QV3-NT0022-080800-219-g03 NT0022 Homo septens dDNA	EST388200 MAGE resequences, MAGN Homo sapiens dONA	ch17b08.x1 Soares_NR_T_GBC_S1 Homo septems CUNA crone IMAGE:1844615 3	yw88e11.r1 Soares_placenta_8tc9weeks_2NbHP8tc9W Homo sepiens cDNA clone IMAGE:258148 5' similar to SW.PI4K_HUMAN P42358 PHOSPHATIDYLINOSITOL 4-KINASE ALPHA;	Homo sapiens PXR2b protein (PXR2b), mRNA	Homo sapiens PXR2b protein (PXR2b), mRNA	Homo sapiens PXR2b protein (PXR2b), mRNA	Homo sapiens PXR2b protein (PXR2b), mRNA	Homo sepiens mRNA for KJAA1342 protein, partial cds	998608.xf Soares_NFL_T_GBC_S1 Homo capiens cDNA clone IMAGE:1843022 3' striitar to gb:J04131 GAMMA-CLUTAMM_TRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Atu repetitive element;	ah mens et Soares testis NHT Harto sepiens cDNA clane 13.20988 3'	ATTACK ST. Science Aredia NHT Homo septems CDNA clone 1320988 3"	United sealons transformenses related function traffet (TRF4-2) mRNA, partial cds	U amina LICK gans for tempine lineas (PTK) entres 10-11	Lambase LCK care for tunshe kinesa (PTK) erors 10-11	Long ambase shromeone 24 comment HS2/C203	Tulio dipata au universito de la cognicia del la cognicia del la cognicia de la cognicia de la cognicia del la cognicia de la cognicia del la	HOURD SEPTEMBEN SEAL IN SECTION OF THE CONTROL OF T	601006680F1 NIT MOST TO FIGURE SQUAY COLIS INVOICEMENTS	Homo sapiens gane for LECTZ, complete cos	Human N-ethylmalemide-sensitive itacid mixivi, parua cos	Homo sapiana chromosome 21 segment HSZI CURS	Human G [24 (G   24) mrdVA, perual cas	Homo sepiens solute cerrier family 24 (sodium/potessitum/calcium exchanger), member 2 (SLC24A2), mRNA
	Top Hit Detabase Source	NT	Z	EST HUMAN		EST_HUMAN		EST_HUMAN	EST_HUMAN	EST HUMAN		F	F	7	K	ECT WIMAN	EET LI IMAN	EST TOWNS	ESI_TOMMIN	2	Z	Į.	i N	2	EST_HUMAN	¥	NT	۲	Ę	¥
	Top Hit Accession No.	6.0E-89 AB007888.2				5.0E-89 BE244323.1	_	Ť.			7706670	TX06870 NT	TN06670 NT	2.0E-89 7708670 NT						-			2		4	1	2.0E-89 U03985.1	2.0E-89 AL163285.2	2.0E-89 U81004.1	11428801 NT
-	Most Straiter (Top) Hit BLAST E Value	8.0E-89/	6.0E-89/	200 30 3	300	5.05-89	4.0E-80	3.0E-89	3.0E-89	3.05-89 N57357.1	20E-89	2 0E-89	2.0E-89	2.0€-89	2.0E-89	S S S	2.05-09	2.05-68	2.0E-89	2.0E-89	2.05-89	20E-89	2.0E-89	20E-89	2.0E-89	2.0E-89	2.0E-89	2.0E-89	2.0E-89	2.0E-89
	Expression Signal	8,	404	4,0	14:0	3.41	0.84	1:1	125	1.79	890	8	0.64	0.64	880	,	5-1	0.00	0.65	1.41	4.88	4.98	0.83	1.1			1.69	0.67	4.07	2.9
	ORF SEQ. ID NO:	30673	30574	388	OSSASS	30008	1	Ĺ	33683	37838	28416	28417	26416	26417	28520									30437		31600			34263	34646
	SEO ID No:	17688	17888	1	ואנפר	18121		1		2444	13481	43484	13484	13481	42602	<u> </u>	┙							17549	18519	18655		L	20874	21235
	Probe SEQ ID NO:	4667	4687		בנם		78.42	2888	73.47	44454	1	13	8	88	704		2882	3565	3565	4169	4180	4180	4376	4524	5416	6658	5886	6335	7831	8266

Page 408 of 546 Table 4 Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor		Homo sepiens pertial mRNA for PEX5 related protein	Homo eaplens mRNA for KIAA1333 protein, perual cus	Homo sepiens CaBP5 (CABP5) gene, exon 5	Homo sapiens CaBP5 (CABP5) gene, exon 5	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA	Homo septens cell adhesion motecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA	Human MAGE-7 entigen (MAGE-1) pseutoogens, contineus cus	hreiddes y NG, Coap Math Haine sapers ally date introcess of single with the same of the coapers of the same of the coapers of	hreidoext NCI_CGAP_Kid11 Homo septens CLNA done IMACE:3134691 3 BITTING DI INCOMITO COMITO SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN;	Homo sapiens chromosome 21 segment HS210046	Hano sapiens chramosome 21 segment HSZ10346	Hamo sapiens chramosome 27 segment 1321 0040	HOMO SEDIENTS CRITICISMINE Z. SEGUINAL NOZI WAYS INTRACES 304583 3"	7630B08X1 NCJ CGAP LLZ4 Framo septems contraction living 14A CF-3294583 3	/esonext NC CASA Luza routh espesie com consumerations	RC1-H 10386-12/400-022-000 ft 10380 ft full S S1 Homo saniers CDNA clone IMAGE:461442 3'	Aparticus Sources Jean Harry School Line Control of Homo Septems CDNA Clone IMAGE:4614423	Apost 10.51 Course John Thomas alribatE submit (CACNA1E) gene econs 7-49, and partial ods, alternatively	paigs	#63d08.s1 Soares_bestis_NHT Homo sapiens c.DNA crone 13/0003 3	601655837R1 NIH JMGC 68 Homo sapiens culvA date IMAGE 305002# 3	601655837R1 NIH_MGC_00 HOMO SEDIENS CLAYA GADE INMACE, 202000 3' similar to	ye8e04.s1 Soares fetal liver spieen 1NHLS Homo squeris curin cario livrocal 12.500 c	yr86604.s1 Sogres fetal liver spicen 1NFLS Homo septens cDNA clone involved 1212190 3 summa to SP-C1TC_HUMAN P11586 C-1-TETRAHYDROPOLATE SYNTHASE, CYTOPLASMIC;	602071208F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214257 5	H.saplans ECE-1 gene (exon 6)	H.saplens ECE-1 gene (exon b)
	Top Hit Databese	Source	H	¥	F	± E			Ę	EST_HUMAN S	EST_HUMAN S	NT.			П	Т	Т	П	Т	ESI HOMAN				EST_HUMAN	EST_HUMAN	EST HUMAN			Į.
28.10	Top Hit Acession	d Ž	2.0E-89 AJ245503.1				11434411 NT	433673		1.0E-89 BF198052.1	1.0E-89 BF198052.1	9.0E-60 AL163246.2	9.0E-90 AL163248.2	8.0E-60 AL163246.2	8.0E-90 AL163248.2	8.0E-90 BE570581.1	8.0E-90 BE670561.1	8.0E-90 BE177830.1	8.0E-90 AA705222.1	8.0E-90 AA705222.1	7.0E-90 AF223391.1	7.0E-90 AA782977.1		7.0E-90 BE962525.2	7.0E-90 H68849.1	7.0E-90 H68849.1	7 0F-90 BF526089.1		6.0E-90 X91926.1
	5	BLAST E.	205-89	20E-89	2.0E-89 /	2.0E-89	20E-89	2.0E-89	2.0E-89 U10692.1	1.0E-89	1.0E-89	9.0E-90	9.0E-90	8.0E-60	8.0E-90	8.0E-90	8.0E-90	8.0E-90	8.0E-90	8.0E-90	7.0E-90	7.0E-90	7.0E-90	7.0E-90	7.05-90				Ш
	- <del>5</del>	Signal	140,0	0.67	1.11	1.11	2.63	3.64	1.63	5.65	5.85	1.77	1.11	1.93	2.43	4.85	4.85	0.78	1.68	8.	3.74	2.07	1.82	1.82	2.08	2.08	200		
		Ö Q	35149	36065	36572	36573	38243	38363	38407	38372	38373	34957	34958					35298	37848	37849			35712						29050
ļ	E CE	ÿ	27727	22812	28082	23094	24688	24777	1		1	21537	21537	1:			15864		24321	24321	13804	┸	丄	L.			L	l.	Ш
	Probe	_	8780	809	42.60	<b>₹</b>	11791	11896	12026	419R	11903	25.5	8998	1064	1085	1333	1333	9068	11374	11374	222	8787	8317	8317	40.405			3084	3081

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Table 4
Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA	Homo septens hypothetical protein PLJ10388 (PLJ10388), mRNA	Homo sapiens HsCCN1 mRNA, partial ods	Homo sapiens HsGCN1 mRNA, partial cds	Homo sapiens inceltol 1,4,5-triphosphate receptor, type 3 (11PM3) mitth	Homo septens inosital 1,4,5-triphosphate receptor, type 3 (TIPR3) mRNA	Homo sapiens TCLB gene, exon 1-10b	Human gamma-aminobutyric acid transaminase mrtnA, partial cos	opsecos.x1 Scares_NRT_GBC_S1 Homo sepiens cDNA done IMAGE:1843022 3' similar to gb:J04131 GAMMA-CLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Au repetitive element;	oge8c08.x1 Scares_NR_T_GBC_S1 Hamo septens cDNA dane IMAGE:1843022 3' similar to gb.:04131 GAMMA-GLUTAMM-TRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Abu repetitive element;	Homo sapiens intersectin long isotiom (TSN) mRNA, complete cds	Homo sapiens pregnancy-zone protein (PZP) mRNA	Homo sapiens chromosome 21 segment HS21C001	H.sapiens mRNA encoding phospholipese c	Homo sapiens EVI5 homolog mRNA, complete cos	Homo sapiens ELKS mRNA, complete cds	H.saplans mRNA ercoding phosphotpase c	Homo sapiens Carbonio antiyarasa-ratared protein 10 (LOCcoscy), mirawy	Homo saplens Carbonic anhydrase-related protein 10 (LOCoced-4), mixwy	Homo sapiens englopesan 4 (NNC4) milky, par all all all all all all all all all a	Homo sapiens angiopoletin 4 (ANG4) mrdN4, partial cus	Homo sapiens adenylate cyclese 9 (ALYCY9) mitwA	Homo saplans hypothetical protein FLJ13222 (FLJ13222), mrvvA	Homo sapiens similar to ectonucleotide pyrophosphalasse/phosphodiesterase 3 (n. sapans) (LOCO3214), mRNA	Homo sepiens calcium-binding transporter mRNA, partial cds	Homo sapiens KIAA0433 protein (KIAA0433), mRNA	Homo septens KIAA0433 protein (KIAA0433), mRNA	Homo sepiens ATPass, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
AUN 110000	Top Hit Detabase Source			NT					H H	EST_HUMAN G	est_HUMAN_G	NT IN		<u> </u>	NT														
	Top Hit Acession	TN 8622298	8622388			4604794 NT	4504794 NT	AB035344.1		5.0E-90 AI222095.1	6.0E-90 Al222095.1	5.0E-80 AF114487.1	506354	5.0E-90 AL163201.2		5.1	7.1	5.0E-90 Z16411.1	8910365 NT	3865		5.0E-90 AF113708.1	4557258 NT	11345483 NT	TN 9429429	5.0E-90 AF123303.1	11417118 NT	11417118NT	11483721 NT
-	Most Similar (Top) Hit BLAST E Vetue	8.0E-00	6.0E-90	6.0E-90 U77700.1	6.0E-90 U77700.1	6.0E-90	6.0E-90	5.0E-90/	5.0E-90 U80226.1	5.0E-90 /	6.0E-90	5.0E-80	5.0E-90	6.0E-90	5.0E-90 Z16411.1	5.0E-90	6.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.05-90	6.0E-80	5.0E-90	5.0E-90	5.0E-90
	Expression Signer	9.77	9.77	3.07	3.07	3.16	3.16	25.81	1.84	1.33	1.33	2.8	132	0.7	2.08	Ю.0	48.	222	0.73	0.73	2.09	2.09	8.82	4.98	1 43	0.74	0.53	0.53	5.86
	ORF SEQ ID NO:	30164	30165	32383	32394	35081	35062		27182	27860	27861	28582	30487	30508	31939		32052	31939	33242		33741	33742	34138	35028	26493				37236
	SEQ ID	17283	17283	19176	19176	L		L		14863	14863		17593		L	_	L.				20390	_	20762	21604	<u> </u>		L	1_	
	Probe SEQ ID NO:	4254	4254	6097	2609	2298	8670	8	1197	1838	1836	2562	4674	4508	5672	0699	5777	2880	689	8894	7423	7423	7813	8636	,	10644	10,	10777	10813

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Table 4
Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor	Homo sepiens KIAA0317 gene product (KIAA0317), mRNA	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA	Homo sepiens gene for AF-8, complete cds	ar78h05.x1 Barstead earta HPLRB6 Homo septens cDNA clone IMAGE:2128761 3'	Homo seniens chromosome 21 unknown mRNA	Hans expense characters 21 inferent mRNA	Allo septeds ducinosmos a materimismos and the party mRNA	Homo septens myosin prosprietese, target subutitit 1 (m) 1 1/1, ill septens myosin prosprietese, target subutitit 1 (m) 1 1/1, ill septens myosin prosprieteses	H. sapiens gene encoding discolain receptur tyrosine kinase, ekun 10	Hamo septens DNA for amylatia precursor protecting companies outs	Homo sapiens mRNA for KIAA1244 protein, partial cos	Human profromone converting enzyme (NECz) gene, extri 8	HUML12582 Human fetal lung Homo sapiens CUNA b	UIHHBW1-4my-b-04-0-UI.81 NCI_CGAP_Sub7 Homo sapiens curve carre investigations of	I.H.BW1-anyb-04-0-U.st NCI_CGAP_Sub/ Homo september annu constituyor_coccos o	601335244F1 NIH MGC 39 Hamo sepiens aDNA dama IMANGE 3069147 3	601087378F1 NIH_MGC_10 Homo sapiens clina cione ima dell'associatione	Home septens high-mobility group (notified at tomoscone) protein 17 (1 mos 17), III von	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mitural	qc54c02.x1 Soares_placanta_8tc9weeks_2NbHP8tc9W Homo sapkens culv.A crore IMA cc. 17 13+10 3	similar to SW:OLF3_MOUSE PZ3Z75 OLFACIORY RECEPTOR ONS.;	Homo septens mRNA for KIAAUZ89 gene, parasi cos	Homo sepiens GRB2-related actapion protein (GRAP) intruva	Homo sapiens RaP2 merecung protein 8 (rC-178), mr.vA	Homo septens ReP2 Interacting protein 8 (KPIPS), mixty.	be49d05;33 NIH_MGC_10 Hamo sapiens cDNA done IMAGE:2039881 9 SIMBET to Inc. of ozone of ozone HYPOTHETICAL 35.5 KD PROTEIN.;	Homo sepiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sepiens) (LOC83484), mRNA		Homo sepiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sepiens) (LOC63484), mRNA	AU118985 HEMBA1 Hamo segiens cunk dana nickiba 100-7 83 5	AU118985 HEMBAT From Septems Guyer with Triangle (NYTA) mRNA	נונום פוליות ופ ווויספור וופסג ליהול ליהול ליהול המספר וויספור ליונים ליהול לי
Top Hit Delabase Source				T HI IMAN							TN	7	EST HUMAN				HUMAN				L HUMAN					EST HUMAN				Τľ	5.1 EST HUMAN	7
Top Hit Acession No.	7862051 NT	7682084	5 0F-00 AB011399.1	Ī			4.0E-90 AF231920.1	4505316			1.1				3.0E-90 BF516168.1	.1	2.0E-80 BE537913.1	5031748	5031748 NT		2.0E-90 AI138213.1	2.0E-00 AB008827.1	6729855 NT	11525901 NT	11525901 NT	2 0F-90 AW672888.1	11427320 NT		11427320 NT	2.0E-90 AU118985.1	AU11898	
Most Shmiler (Top) Hit BLAST E Value	5.0E-90	A 0E 00	505-00	700 20 2	3.05-80/	4.05-60/	4.0E-90	4.0E-90	4.0E-90 X99033.1	4.0E-80 D87675.1	4.0E-90/	4.0E-90 M95967.1	4.0E-80 D31124.1	3.0E-BO	3.0E-90	3.0E-80	2.0E-90	2.0E-90	2.0E-90		2.0E-90	2.0E-00	2.0E-90	2.0E-90	2.0E-90	2.05-90	2 OF BO		2.0E-80	2.0E-90	20E-90	2.0E-90
Expression Signal	0.67	280	0.0	8	8.4	282	282	4.74	8.84	6.15	2.4	98.1	1.75	1.72	1.72	67.58	5.41	48.4	48.4		2.03	1.17	822	0.57	0.57	47	8 8		823	1.27		5.5
ORF SEQ ID NO:	37294		3/282			28323	26324	27084								ļ			27174		29801				32148			20000	36551			37475
SEQ ID	23704		5/87	3	25496	13396	13396	14132	14728	17707	17852	17873	25003	21155	21155	24830	13315	44248	14218		16898		L			L	1	22073	23075			Ш
Probe SEQ ID NO:	10874		108/1	7/07	12920	302	305	<del>1088</del>	1688	4688	4835	4856	12134	8185	8185	11851	215	143	1177		3850	4714	4947	5870	5870	6.00	8/95	101	10149	10319	10319	11798

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Table 4
Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor	Homo espiens amyloid beta (A4) precursor protein (protesse nechnii, Abtheimer disease) (APP), mRNA	Hamo sapiens chramosome 21 unknown mRVA	Homo sepiens chromosome 21 unignown mRNA	Homo sapiene mRNA for 1-box trenscription record (15AZ) gene, perusa	Homo sepiens mRNA for T-box transcription factor (TBXZ0 gene), partual	Homo sapiens ALR-tive protein mitthe, partial cos	Homo sapiens ALX-titre protein mixth, partier cas	Homo sapiens Kruppel the factor 7 (uniquitods) (KLT7), mixty.	Homo saplens protein phosphatase 2A bK gamma subumit gene, excri 3	Home capiens protein prosphatese 2A BK garmna subumit gene, exten 3	801158563F2 NIH MGC 53 Home explens curve cone liment would be a second to be a second by a second beautiful to be a second by a second beautiful to be a second by a second beautiful to be a secon	Homo sapiens similar to SALL1 (sei (Urosquille Pilos (LOCO) 107), Illinoso	Home sapiens chromesome 8 open resum marte 2 (Court 2), minutes	Homo sapiens mikina tor kilaadus protein, par usi cas	Homo saplens miRNA for KIAAUSUS protein, parter cas	Homo sepiens soluble interfeutan 1 reception encessory protein (1L.17047) gara, cuun c, accurative courses and complete cds, alternatively spliced	Homo sapians mRNA for KIAA1399 protein, partial cds	Homo sapiens mRNA for KIAA1399 protein, partial cds	Homo sepiens mRNA for KIAA0633 protein, partial cds	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA	Human refine-derived POU-domain factor-1 mKNA, complete cas	Homo sapiens gutamate receptor, tonocropec, N-merny U-esperate A (GrunzA) IIIn Ven	Homo sepiens solute center family 1 (high efinity esperate) guarrene transparter j, menuoe o (SLO INV), mRNA	Homo sapiens brefeldin A-thibited guarrine nucleotide-exchange protein 2 (BKS2), mKVA	Hamo sepiens SNCA isafarm (SNCA) gene, complete cds, alternatively spliced	Homo sapiens CGI-15 protein (LOC51006), mRNA	Homo sapiens CGI-15 protein (LOC51008), mRNA	H.sapiens dDNA for CREB protein	H. saplens cDNA for CREB protein	yg44d11,2 Soares infant brain Thilb Homo sapiens CONA Cours Information of the Course Information of the Lower Course of the Cou	AUMONOSSOI LIVER NEPOSE COLITINE SEPERIS COLOS CONTROLOS COLOS COLOS COLOS CONTROLOS COL
 Top Hit Defebese Source	•									П	T HUMAN				5	<del></del>							•						П		EST_HUMAN
Top Hit Acession No.	4502166 NT	1.0E-60 AF231920.1		1.0E-90 AJ237589.1			1.0E-90 AF264750.1	X07828	1	1	1.0E-60 BE379884.1	11420514 NT	05720		1.0E-80 AB020710.1	1 DE -80 AF167340.1	ļ		<b>-</b>	11426910 NT	1.0E-90 U91834.1	8006002 NT	11426768 NT	11422086 NT	1,0E-80 AF163864.1	11422109 NT	11422109 NT	1.0E-90 X55545.1	1.0E-90 X55546.1	1.0E-60 R25686.1	8.0E-91 D12234.1
Most Similar (Top) Hit BLAST E Veitue	1.0E-80	1.0E-90 /	1.0E-90 /	1.0E-90/	1.0E-B0	1.0E-90/	1.0E-90[/	1.0E-90	1.05-60/	1.0E-90/	1.0E-80	1.0E-90	1.0E-80	1.0E-90/	1.0E-80 /	1.05-90	4 05 00	100	1.05-90	1.05-90	1.0E-90	1.0E-90	1.05-60	1.05-80	1.0E-90	1.0E-90		١	1.0E-90		
Expression Signed	388	1.13	204	255	2,65	17.02	17.02	2.23	2.39	289	1.78	2.77	7.85	0.72	0.72	4.47		17	1.78	0.99	0.67	9.0	263	3.96	1.08						6.09
ORF SEQ ID NO:	28300	28389	28383	26889	26890	26728	28729		27310	27311		27938		29810		79808		34444					<u> </u>			39075					30140
SEQ ID NO:	18372	15812	15812	13768	13758	13792	13792	14156	14345	14345	14708	14942	15926	16904	16904	277.00		182//	1.	L	1_	L	<u> </u>				L		1_	L	17253
Probe SEO ID NO:	1	37.6	375	88	88	Ę	200	1112	1309	1300	1678	1918	2888	3865	3865	877	3	3270	02/0 67/58	5036	7278	7626	7084	2 2	BYYO		8278	10990	10990	11021	4224

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Table 4
Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	Homo sapiens makonin, ring finger protein, 1 (MKRN1), mRNA	CM-BT043-090289-075 BT043 Homo septens cDNA	±300-04.s1 Scares_feta_iner_splean_1NFLS_S1 Hamo sepiens cDNA clone IMAGE:448015 3	AU143539 Y79AA1 Hamo sapiens cDNA dane Y78AA1002087 6	AU143539 Y79AA1 Hamo sapiens cDNA done Y79AA1002087 6	au49f09.x1 Schneider fetal brain 00004 Homo sepiens cDNA clone IMAGE-2518121 3' straiter to SW:ASPG_FLAME Q47898 N4{BETA-N-ACETYLGLUCOSAMINYL}-L-ASPARAGINASE PRECURSOR ;	601901624F1 NIH_MGC_19 Hamo septens dDNA clane IMAGE:4130833 5	AV649878 GLC Hamo sapiens cDNA dane GLCBYF08 3'	AV649878 GLC Hamo septens cDNA clane GLCBYF08 3'	qe70f11.x1 Soares_fetal_kmg_NbH1.19W Homo sepiens cDNA clone IMAGE:1744365 3' simiter to contains MIR.b2 MIR MIR repetitive element;	Homo sapiens lysophosphatidic acid acytransferase-delta (LPAAT-delta) mRNA, complete cds	Homo saplens lysophosphaldic acid acyltransferase delta (LPAAT-delta) mRNA, complete cds	Home saplens chromosome 21 segment HS21C084	EST01579 Hippocampus, Strategene (cat. #836205) Homo sepiens cDNA clone HHCMC80 smilar to Retrovinus-related gag potyprotein	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC80 similar to	Retrovirus-related gag polyprotein	Homo sapiens solute carrier family 4, ention exchanger, member 3 (SLC-4-53), metrox	Homo sapiens southe carrier family 4, ention exchanger, member 3 (SLC-443), mrtnA	Homo sapiens chromosome 21 segment HS21 CU83	Homo sapiens mRNA for KJAA1278 protein, pertiel cos	Hamo sepiens mRNA for KIAA1278 protein, pertial cas	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cas	Human Ku (p70/p80) subunit mRNA, complete ods	Homo seplens chromosome 21 segment HS210085	Homo saplens chromosome 21 segment HS210085	Homo sapiens epididymal secretory protein (19.5kD) (HE1), mRNA	Homo sepiens cyclin-dependent kinase 6 (CDK6) mRNA	Homo sepiens gennne-eminobutyric ecid (GABA) B receptor, 1 (GABBR1), trenscript vertent 2, mRNA
-	· Top Litt Detatherse Source		EST_HUMAN C	EST_HUMAN Z	EST_HUMAN A	EST_HUMAN 4	EST_HUMAN S	EST_HUMAN 6			EST HUMÁN		Ę	F	EST HUMAN	Г	T HUMAN						NT	NT		攴			
-	Top Hit Acession	11419234 NT	7.0E-91 AISO4151.1			6.0E-81 AU143539.1	6.0E-01 AI870805.1	5.0E-01 BF314682.1			6.0E-91 AI193506.1	_			777894.1			11430193 NT	30183	3.0E-91 AL163283.2	3.0E-91 AB033104.1	3.0E-81 AB033104.1	3.0E-91 AF084530.1	3.0E-91 M30938.1	3.0E-01 AL163285.2	3.0E-91 AL.163285.2	11434984 NT	4502740 NT	11497811 NT
	Most Shriller (Top) Hit BLAST E Velue	7.0E-91	7.0E-91	5.0E-91 A	SOE-ON A	6.0E-91	6.06-91	5.0E-91	5.0E-91	5.0E-01	5.0E-97	4.0E-91	4.0E-91	4.0E-91/	4 DE-64 M77894.1		4.0E-61 M77994.1	3.0E-91	3.0E-91	3.0E-91	3.05-91	3.05-91	3.0E-01	3.0E-91	3.0E-91	3.05-01	3.05-91	3.05-91	3.0E-91
-	Expression Signal	4.36	0.67	1.71	1.05	1.05	67:1	1.85	1.28	1.28	228	1.41	1.4	3.24	÷		1.55	5.97	283	1.76	3.84	3.84	147	4.36	13	13	1.43	2.97	3.34
	ORF SEQ ID NO:	35039	37083	29459	30454	30455	33108	١				29192					31858	27630		28323	29445	29446				١.			33071
	Exan SEQ ID NO:	21617	23585	16534	17567	17567	19825	21515	22070	22073	25470	18270	16270	24228	25,50	20102	25159	14654	14684	16401	16522	16522		l		ı	l_		I I
	Probe SEQ ID NO:	88	10863	3488	4544	454	02.29	2547	9113	913	42802	3216	3215	11276	1,30		12377	153	1621	3350	3478	3476	3802	4624	5018	5018	2//3	6437	6735

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Single Exon Probes Expressed in Bone Marrow

Igle Extra Pubescent in Doire immore	Top Hit Descriptor	Homo sepiens gamma-aminobutyntc acid (GABA) B receptor, 1 (GABBR1), transcript wariant 2, mRNA	Human L-type catchum channel beta-1 subunit (CACNLB1) gene, exons 10 and 11	Human L-type catcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11	Homo sapiens ankyrh-like with transmembrane domains 1 (ANK I M.1), mruna	Human mRNA for very low density lipoprotein receptor, complete cos	Homo sapiens mRNA for KLAA0584 protein, perus cas	Homo sepiens EHM2 mRNA, complete cos	Homo sepiens mRNA for KIAA1080 protein, per us	Homo sapiens mRNA for KUAA1080 protein, parties cas	Homo sapiens gutathtone S-transferase theta 2 (GSTT2) and gutatricine S-transferase unear 1 (GSTT1) corress. complete cds	Homo sapiens beta-ureldoproplonase (BUP1) gene, excn 6	Loren comione hote implementates (RI IP4) cena entre esta 6	Trans square bear district of the second HSP CD8.	NOTING SEPTEMBER SHIPLING A SOFT SEPTEMBER SOFT FOR THE PROPERTY OF STATEMENT OF ST	UHHBIS486-0-0-0-0-31 NG COOK JOHO HAID SAPARS COOK COOK TO COO	Homo septents inflormed a record of the reco	602022088F1 NCI CCAP BIN6/ Hamo septens curva crane IMA/CE-4157804 57	SCALZZOBBIT NG CGAP BITO, FIGURE SQUARE CONT. CALL TANGENING 2/81 DID) cone error 10	Human micleus-emboded immodicational automyco deriya ogenese a (man 14) yene, man 19	Homo septems Nikoszu gene, exam 10	Homo septens NNG-ZJ gene, exem 10	Human Na+,K+ A I Pasa aptra-cupumit mixtox, paruar cus	Homo sapiens hypometical protein FLLANCOV (FLLANCOV), IIII VIV.	Homo sapiers NALP1 mKNA, complete cas	Homo sapiens partial 1M4Sr2 gene to recreasparin process, even o	Homo sapiens pertial TMASF2 gene for tetrasperan protein, excrib	Homo sepiens mRNA for KIAA1512 protein, pertial cos	Homo sapiens mRNA for KIAA1512 protein, pental cos	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange provein 2 (51934), mirava	268. Human retina cDNA randomly primed substantly income septems curviv.	601273513F1 NIH MGC ZU HOMO septens curve done investigation of	Homo septens discyglycator kinesse, garrina (solo.) (Dono), minos	TOTIO SELECTS LIEU DE JOSEPH PRINCES BONNING (SOC.)
XOII LIORS	Top Hit Database Source	¥	TN	TN					LN L	¥	F4			Z		HUMAN	. I	EST HUMAN	EST_HUMAN	¥	Ę	Ę	Į,	攴	E	Ę	된	NT	NT	N	EST_HUMAN	EST HUMAN	Z.	Ž.
	Top Hit Aceeston	1497811			1 9801589 NT		1	2	1	3.0E-61 AB029003.1	Ţ		ŀ		1	1.0E-91 AW449748.1	11434402 NT	1.0E-91 BF348182.1	1.0E-91 BF348182.1	1.0E-91 M20463.1	9.0E-82 A,001689.1	9.0E-92 AJ001689.1	J03007.1	11427149 NT	9.0E-92 AF310105.1	9.0E-92 A.250568.1	9.0E-92 AJ250568.1	9.0E-92 AB040945.1	9.0E-62 AB040945.1	11422086 NT	8.0E-82 W28367.1	8.0E-62 BE386363.1	11434722 NT	11434722 NI
	Most Similar (Top) Hit BLAST E Veitue	3.0E-91	3.0E-91 U86959.1	3.0E-91	3.0E-91	3.0E-81 D16484.1	3.0€-91 /	3.0E-91/	3.0E-81	3.0E-01/	200	3.00	3.05-81	3.0E-91	1.0E-01/	1.0E-91	1.0E-91	1.0E-91	1.0E-91	1.0E-91	9.0E-82	9.0E-92	9.0E-92 J03007.1	9.0E-92	9.0E-92	9.0E-92	9.0E-92	9.0E-92	9.0E-92	9.0E-92				8.0E-92
	Expression Signal	38.	4.07	4.07	0.44	2.51	9.0	2.53	23	2.3	,	1.48	00.0	3.88	239	7.11	67.0	1.9	4.9	0.59	6.04	6.04	294	2.18	3.86	0.47	0.47		1.73	.1.69	3.76			1.08
	ORF SEQ ID NO:	33072	34228	34227	34659	36517	36036		38026	38027					28078	27262	31498	33464	33465	34498	27246	27247	31578	31953	32828	34569					Ĺ	28308		Z7864
	SEQ ID NO:	1979H	20843	20843	21247	22080	22587	24188	24477	24477		25314	18335	18335	13170	14286	18587	ı		21089	L	L.		ŀ	L	L	L	1		L		l	14865	14865
	Probe SEC ID NO:	6735	8	000	828	9	88	11235	11536	11536		12820	12850	12950	8	1250	5487	7020	70207	8161	1248	1246	9239	888	6596	8190	8490	8747	8747	0829	82	285	1838	1838

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	Top Hit Descriptor	au83H08.x1 Schneider fetal brain 00004 Homo saplens cDNA clone IMAGE:2782911 3' similer to TR:060302 060302 KIAA0555 PROTEIN ; contains element MER22 repetitive element;	Homo sepiens mRNA for KIAA1600 protein, partial cots	Homo sapiens FYVE domain-containing dual specificity protein prospinatase FTVE-Cor 2 IIII vivi, variance ods.	Homo saptens MCP-4 gene	Homo septens DNA polymerase zeta catalytic subunit vertent 1 (REV3L) mRNA, complete cds	Homo sapiens double FYVE-containing protein 1 mRNA, complete cds	Homo saplens AJM-1 protein (LOC61161), mRNA	Human lens membrane protein (mp19) gene, excn 11	Human lens membrane protein (mp19) gene, exch 11	Homo saplens transcription termination racid, RNA polymerase II (1172), minuty	Homo sapiens mRNA for KIAA0611 protein, partial cds	Homo sepiens mRNA for MENL protein	Homo serpiens nuclear mitagen- and stress-activated protein lunese-1 (MSK1) mRNA, complete cds	Homo sapiens dihydrolipoamide S-succhyfransferase (E2 component of 2-oop-grunnane complient (ULS I)	mRWA	Homo septens Livia, with cassa i region, 1.1 stressura represipe	Homo sepiens mRNA for KIAAU/36 protein, peruse cos	Homo sepiens mixiva ra Nakau roo protein, pel tell complete cars.	HOME SEPTEMS STATEMENT OF THE WAY WITH THE STATEMENT OF THE STATEMENT OF THE WAY WAY THE STATEMENT OF THE WAY WAY THE STATEMENT OF THE WAY WAY THE STATEMENT OF THE WAY WAY THE STATEMENT OF THE WAY WAY THE STATEMENT OF THE WAY WAY THE STATEMENT OF THE WAY WAY THE WAY WAY WAY WAY WAY WAY WAY WAY WAY WAY	Homo septens o-coar C.C. (minute) in Cocar C. (minute) in Cocar (ACTR2), mRNA	Trans Espera is Ann's (south control to your) from the (ACTR2) mRNA	Hamp separas ANT 2 (acut Helated Information Legisland Stormanson mRNA, complete ods	HOTO SEPRETS CYSTETION I SPORT VALUE IN IN IN IN IN IN IN IN IN IN IN IN IN	Homo septens NRAS-retained gare (U.S. 1985), Hithary	Homo sapiens DNA, MITC crass I region, 7.1 stressular industry.	Homo sapiens T-cell ymphoma invesion and meastasis 1 (11/4/11) innvex	Homo sapiens T-cell lymphoma trivision and measures 1 (11/4/11) intriviry	N-CAME145 kds neural cel sansson maecule (inmet, sine) cel ma cel	N-CAM=145 kda neural cell adhesion molecule (numan, smail cell lung carios cell luns cours, illings, and a	
	Top Hit Defetbese Source	EST_HUMAN	NT						NT				Ŋ	¥		토	攴	첫	Ę	Į.	Ę	ĮŲ.	Ę	¥	Ę	Į,	NT	Ę	M	ļ	Z
	Top Hit Acession No.	8.0E-82 AW157571.1			ONE OF A MANAGO 4			11416981 NT			1426569	8.0E-92 ABO14511.1		8.0E-92 AF074393.1		4503340 NT	7.0E-02 AB031007.1	7.0E-92 AB018301.1	7.0E-92 AB018301.1	7.0E-02 AF007822.1	4502384 NT	5031570 NT	5031570	AF167706.1	6005738 NT	7.0E-02 AB031007.1	4607600 NT	4507500 NT	7.0E-92 S71824.1		7.0E-82 S71824.1
	Most Similar (Top) Hit BLAST E Value	8.0E-92 A	8.0E-02	2	8.0E-82.4	A OF-92 A	8.0E-92 A	8.0E-92	8.0E-92 L04193.1	8.0E-92 L04193.1	8.0E-92	8.0E-92	8.0E-82 Y13829.1	8.05-92/		8.0E-62	7.0E-92	7.0E-92	7.0E-92	7.0E-02			7.0E-02				7.0E-92	7.0E-92			
	Expression Signal	0.7	180	3	TRO .	ar.c	1.16	0.56	3.52	3.52	99.0	2.48	1.86	334		1.72	1.60	0.89	0.89	1.22	1.14	3.62	3.62	1.27		1.31			1.4		1.44
	ORF SEQ ID NO:	31028	31478		31635	33031	34491		35155							38233	28046		26263			28230	28231	28591	28743	Ĺ			30528		30520
1	εΩ.	4846	858		18872	19754	2 2 2	7397	7735	24735	7836	22382	23308	24444		24664	13147	15836	15836	13660	14320	15212	15212	15571	15729	15/55	18314	18314	17638		17638
	Econ SEQ ID NO:	•				_[`		8428	┸	8768	08		10388	44486	_	11688	L	82	822	88	1285	2197	2197	2573	2735	2788	+=	188	128	+	4617

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Too Hit Describior		Hamo septens thyroid stimulating harmone receptor (TSHR), mRNA	Homo sapiens male specific lethal-3 (Drosophila)-like 1 (MSL3L1), mrtnA	Homo sapiens mRNA for KJAA1093 protein, partial cds	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	y80e08.r1 Soares placenta Nb2HP Homo septens cDNA clone IMAGE:145574 5	y80e08.r1 Scares placenta Nb2HP Homo septiens cDNA clone IMAGE:145574 5	Homo sapiens ribosomai protein, large, P1 (RPLP1) mRNA	HTM1-288F HTM1 Homo sapiens cDNA	tgo1b02x1 NCI_CGAP_CLL1 Homo expiens cDNA clone IMAGE:2107467 3' stritier to SW:P1NF_FLOWAN Over-5 PROTTEIN_TYROSINE PHOSPHATASE D1 :contains Alu repetitive element;contains element	MER17 repetitive element;	tgo1502.x1 NCI_CGAP_CLL1 Homo sepiens cDNA clone IMAGE:2107467 3' stmilar to SW:PTNF_HUMAN	Q16825 PROTEIN-TYROSINE PHOSPHATASE D1; combains Alu repetitive element, contains element	MER17 repolitive element;	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000/38 5	<b>EST188414 HCC cell line (materiasts to liver in mouse) 11 Homo signeris CLINA 3 end sinning to Historia</b>	protein L29	Homo septens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and parcal cas, anamauvery	peojids	801281867F1 NIH MGC 44 Homo sapiens curva dans image coupos o	Homo sapiens ribosomial protein Litua (Mr.L.10A), mitura	ULH-BIO-BRITA-US-ULIST NOT COMP SUB- I TUTIN SQUARE COM SUB- BRITA- COMP 13	HEBBOARTHURST NOT COMP SUBTINGUES COMP COMP TO THE SECOND RESERVED T	6014606271F1 NIM MGC TO THATO SEPTENS CLITA CALIFO INVICE SECTION OF SEPTENS CLITA CALIFORNIA CONTRACTOR CONTR	Homo sapiens chromosome zi umrown mixwa	Homo sapiens T-cell Improma invasion and measuress 1 (114M1), introva	Homo sapiens hypothetical protein FLJ1089/ (FLJ1089/), mravy	Homo sepiens hypothetical protein FLJ10897 (FLJ10897), mrana	Homo septiens mRNA for KIAA1287 protein, pertual cos	Homo sapiens PTH-responsive osteosarcoma B1 protein (B1) minnivin, complete cus	Homo sapiens mRNA for KIAA0611 protein, partial cos	WOODGOOSTA NCT CCAP TYZO FIGURE SEPRENS CONTA CLUTE LIMANOLIZA 14010 5	WCGCCBCA NCI CCAAP TIZO Traino septemble VIZIVA CAMB INFOCESSION CONTRACTOR C	HOTTO SEPRETS CHICALITICS AT SOCIETY TO STOCK TO
100 Hit				¥		T_HUMAN	HUMAN		T HUMAN	ÞC	EST HUMAN M		<u>'</u>	EST_HUMAN M	EST_HUMAN A		EST_HUMAN   PA	<u> </u>		T_HUMAN		┪	┑	T HUMAN							П	Т	T HUMAN	L
Top Hit Acessian	ď.	11434900 NT	E803103 NT	20E-82 AB029016.1	6912457 NT			1506668	1.0E-62 BE439625.1		4 0F.02 Al380358 4			1.0E-92 AI380356.1	9.0E-83 AU121681.1		9.0E-93 AA316723.1		9.0E-83 AF223391.1	BE388571.	11418526 NT	8.0E-83 AW014042.1	8.0E-63 AW014042.1	8.0E-83 BF036384.1	7.0E-83 AF231919.1		114	11450204 NT	6.0E-83 AB033083.1	8.0E-83 AF085771.1	5.0E-63 AB014511.1	5.0E-83 AI674184.1	5.0E-83 AI674184.1	5.0E-83 AL 163201.2
Most Similar (Top) Hit	BLAST E Vedue	20E-82	2.0E-92	20E-92	20E-82	1.0E-02	1.0E-92	1.0E-92	1.0E-82		1 OF D2			1.0E-92	9.0E-83		9.0E-93			8 <del>0</del> -∃0:6	8 <del>0</del> -30'6							6.0E-83						
Expression	Signal	4.68	4.54	3.75	2.05	1,71	1.1	34.86	0.77		6/2	2		3.43	277		11.43		44.1	1.44	35.01	0.52	0.52	3.82	9.15	1.58		0.59			3.77	4.78		1.02
ORF SEO		37594	37864	31773							25077			35928						28584		32913	32014	33079									27409	
Eben	SEO SO SO	24072	24335	25370	4 EARS	2002	14802	45404	21558		2			22482		L	15077		15652	1	24838	19645	19645	19789	<u> </u>	l .	1_		L.				14439	14504
Probe	SEQ NO NO NO	41412	11380	47748	12002	1905	1867	200	8590		0,10	808		0510	204		2058		2655	3628	11959	6585	6585	6744	246	3094	9609	9609	8838	7101	1381	1406	1406	1471

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Single Exon Probes Expressed in Bone Marrow

igle Extended Extended in Control management	Top Hit Descriptor	Human skeletal muscle 1,3 kb mRNA for tropomyosin	Human somatic cytochrome c (HCt) processed pseudogene, complete cds	Homo sepiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, atternatively spliced end replication factor C subunit 2 (RFC2) gene, complete cds	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cde and efformatively spliced product	Homo sapiens discs, large (Drocophila) homolog 2 (chapsyn-110) (DLG2) mRNA	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA	Homo sapiens secretory paffrway component Sec31B-1 mRNA, alternatively spliced, complete ods	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA	Homo sepiens WSB1 protein (WSB1) mRNA, complete cds	Homo sapiens nucleobindin 2 (NUCB2), mRNA	Homo sapiens gamme-glubamyfransferase 1 (GGT1), mRNA	Homo sapiens gamme-glutamytransferase 1 (GGT1), mRNA	2x50e09.s1 Sceres_testis_NHT Homo sapiens cDNA clone IMAGE:786688 3' struiter to SW:CLPA_KA I P37397 CALPONIN, ACIDIC ISOFORM;	Homo saplens Interferon gamma receptor 1 (IFNGR1) mRNA	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo sapiens pescedillo (zebrafish) homolog 1, containing BRCT domain (PES1), miRNA	Hemo saplens hypothetical protein FL/20/31 (FL/20/31), mrt/NA	Homo sapiens dystrophin (DMD) gene, deletion breatpoints 1-3 in intron 6	Homo sepiens TNF-Inducible protein CG12-1 (CG12-1), miXNA	Homo sepiens fumor entigen SLP-8p (HCC8), mKNA	Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA	Homo seplens tumor entigen SLP-8p (HCC8), mRNA	y694c12.r1 Strategene liver (#637224) Homo sapiens cDNA clone IMAGE:78838 5' similær to similær to SP-A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SNE-ZBP - HUMAN ,	AV882051 GKC Hamo septems cDNA dane GKCDRF07 5	602246554F1 NIH_MGC_62 Homo septems cDNA clone IMAGE:4332008 5	602246554F1 NIH_MGC_62 Homo sepiens aDNA dane IMAGE:43332386 5	Homo sapiens tensin mKNA, complete cas
T SOUL LIOY	Top Hit Databese Source	NT	NT	¥	LN.			NT	NT	NT	NT	NT	NT	EST HUMAN	4557879 NT	K	NT	M	토	NT	¥	Ŋ	NT	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	¥
aligne.	Top Hit Acession No.			2		5.0E-83 4557526 NT	455752B NT	6.0E-63 AF274863.1	5032156 NT	5.0E-63 AF068313.2	11439599 NT	11417877 NT	11417877 NT	AA459833.1	4557879	TN 657879 NT	7657454 NT	7657454 NT	8923658 NT	4.0E-83 AF047677.1	7858972 NT	7705396 NT	4504654 NT	7705396 NT	146864.1	4.0E-83 AV692051.1	3.0E-63 BF690630.1	3.0E-63 BF690630.1	3.0E-93 AF225896.1
	Most Shulfar (Top) Hit BLAST E Velue	5.0E-83 X04201.1	6.0E-63 M22878.1	5.0E-907	5 OF 03 1	5.0E-93	5.0E-83	5.0E-83	5.0E-83	5.0E-83	6.0E-83	5.0E-83	6.0E-83	4.0E-83/		4.0E-93	4.0E-83	4.0E-83	4.0E-83	4.0E-93	4.0E-93	4.0E-93	4.0E-83	4.0E-93	4.0E-83   146864.1	4.0E-93	3.0E-83	3.0E-83	3.0E-93
ľ	Expression Signal	3.94	6.0	122	8	0.58	0.56	2.06	1.33	1.59	2.48	2.55	1.32	7.06	1.25	125	138	1.38	1.62	4.21	1.08	0.94	201	58'0	4.28	13.22	9.21	9.21	1.23
t	ORF SEQ ID NO:	29228	32175		24342		35344			36836	37661				26450				27183		28638	29546		28546					
	SEQ ID	16302	18984	10304	7000	2000	21918	22808	23091	23352	24131	25622	25822	13204	13518	13518	13832	13832	14227	15015	15613	16625		1_		L	1_	L	17292
	Probe SEQ ID NO:	3247	2897	6230	Ş	/80K3	8962	88	10168	9530	11174	12827	13088	8	445	445	132	E	1187	1894	2015	3580	4078	8503	5727	11468	3865	3665	4263

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	Top Hit Descriptor	In 29g03.x1 NCI_CGAP_Brn25 Homo expierts a DNA dame IMAGE:21690763'	In 29g03 x1 NCI_CGAP_BIN 25 Hamb septems d.D.N.A. digite IMAGE 27 0597/6 3	Hamo saptens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA	wbozato5.x1 NCI_CGAP_GC8 Homo septens cDNA clone IMAGE2304489 31	Chlarocebus aethiops mRNA for ribosomal protein S4X, complete cds	Chlorocebus esthicps mRNA for ribosomal protein S4X, complete cds	Homo sapiens chromosome 21 segment HSZ1ON85	Homo sapiens chromosome 21 segment HS21 (XIS)	Human Cikeassociated RS cyclophilin CARS-Cyp mRNA, complete cds	601117586F1 NIH_MGC_16 Hamo sapiens dJINA ciche IMAGE:3336ZZJ 3	EST376458 MAGE resequences, MAGH Homo sapiens cDNA	Homo sapiens deafness, autosomal dominant 6 (DFNAs), mRNA	QV3-HT0513-290300-128-h04 HT0513 Homo saplens cDNA	Homo sepiens hypothetical protein (LOCS1318), mRNA	HSU74313 Human chromosome 14 Homo sapiens CUNA clone 1-86	UI-HF-BNO-aks-g-09-0-UI.1 NIH MGC 50 Hamo sapiens CDNA done IMACE:3076322 5	228c10.s1 Scares, pregnant uterus, NbHPU Homo sapiens cLNA cione iMAGE: 303346 3	Homo saplens CYP17 gene, 5 end	601458531F1 NIH MGC_66 Hamp septems aDNA date IMAGE:3862085 5	Homo sapiens CTR1 pseudogene	Homo saplens CTR1 pseudogene	Homo sapiens hypothetical protein (U.4328-19.01.1), miruna	oy84608.x1 NCI_CCAP_CLT1 Hamo septens curva date invace: 167.2505 5 siniler to invace. Tale curva curva zinc Finger PROTEIN.;	Homo sapiens DNA for emyloid precursor protein, complete cds	Homo sapiens hypothetical protein FL/20291 (FL/20291), mRNA	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA	Homo septems long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete ods	Homo sapiens MHC class 1 region	601177686F1 NIH _MGC_17 Homo sapiens cDNA clone IMAGE:3532465 5	601177686F1 NIH MGC_17 Hamo sapiens cDNA clane IMAGE:35322655 5	Homo sapiens DNA for amyord preductor protein, compares cos
B	Top Hit Database Source	П	EST_HUMAN	<u> </u>	EST_HUMAN	NT	NT	NT.	M	NT	EST HUMAN	EST HUMAN	NT	EST_HUMAN	NT	EST HUMAN	EST HUMAN	EST HUMAN	N-I	EST HUMAN	Z.	N	보	EST_HUMAN	TN	뉟	N.	ᅜ	Ŋ	EST HUMAN	EST HUMAN	Z
	Top Hit Acession No.		3.0E-63 AI663863.1	11428182 NT	3.0E-63 AI824829.1	2.0E-83 AB015610.1		2.0E-63 AL163285.2			2.0E-63 BE252382.1		8153	2.0E-63 BF351459.1	11430039 NT	174313.1	2.0E-63 AW 502002.1	2.0E-63 AA126735.1	A1825.1	2.0E-63 BF035327.1	1.0E-83 AF238997.1	1.0E-83 AF238997.1	7657016 NT	1.0E-83 AI146755.1	387675.1	8923270 NT	B923270 NT	1.0E-03 AF231981.1	1.0E-93 AP055066.1	1.0E-83 BE297369.1	1.0E-83 BE297369.1	1.0E-93 D87675.1
	Most Similar (Top) Hit BLAST E Vatue	3.0E-B3 AI553853.1	3.0E-93 A	3.0E-83	3.0E-83 A	20E-83 A	20E-83 A	2.0E-93	20E-83	2.0E-63 U40783.1	20E-83	2.0E-93/	2.0E-83	20E-83	2.0E-83	2.0E-83 U74313.1	2.0E-63/	2.0E-93/	2.0E-93 LA1825.1	2.0E-83	1.0E-93/	1.0E-93	1.0E-83	1.05-63	1.0E-63 D87675.1	1.05-83	1.05-93	1.05-03	1.0E-83	1.05-93	1.0E-93	1.0E-93
	Expression Signal	0.56	0.56	1.65	3.04	8.05	8.05	12.88	B.81	1.15	2.03	5.04	0.78	0.63	1.08	0.7	1.06	3.14	269	3.40	1,82	1.82	16.6	5.09	4.11	8.85	8.85				2.05	2.18
	ORF SEQ ID NO:	32161	32162		37637	28219	26220	26340		28173					31993	32008					26143		28510						L			
	SEQ ID NO:	18970	18970			13283	13288	13415	13415	15157	15497	L	L		L	L	L	L	L	L	L		13690	L	L	L	上	1		L.		$\sqcup$
	Probe SEO ID NO:	1889	5881	67.15	14152	192	192	38	324	248	\$	250	6602	282	5720	456	248	12520	12801	12853	\$	18	518	\$	878	1241	1241	2344	2471	2833	2883	2945

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Table 4
Single Exon Probes Expressed in Bone Marrow

igle Exoli Plobas Expressed in Colles interior	Top Hit Descriptor	Homo sapiens long chain polyunçaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds	Homo sapiens chronosome 21 segment HS210084	Hamo septens glucocarticoid receptor (GRL) gene, intran D, exan 5, end intran E.	Homo sepiens ghicocordicald receptor (GRL) gene, intran 0, excn 5, and intran E.	Hamo sepiens candidate taste receptor T2R14 gene, complete ods	Hamo sapiens neurofibramin 1 (neurofibramatasis, van Recklinghausen diséase, Watson assesse) (NF1) mRNA	Hamo sapiens KIAA0672 gene product (KIAA0672), mRNA	Homo saplens protein kinase C, bata 1 (PRKCB1), mRNA	Human mRNA for NF1 N-Isoform-excn11, complete cds	Homo sapiens mRNA for KIAA1411 protein, pertial cds	H. sepiens mRNA for MEMD protein	Homo sapiens protein kinase inhibitor gamma (PKIG) mrtNA, comprese cos	Homo sepiens mRNA for KIAA1011 protein, partial cots	Homo saplens mRNA for KIAA1011 protein, pertial cds	Homo sapiens mRNA for KIAA1485 protein, partial cos	Homo sapiens Trio isoform mRNA, complete cds	Human PreA4 gene for Alzheimer's discess A4 amyddu proesin procus ou (ewul e)	Human PreA4 gane for Azheimer's disease A4 amyond process precultar (caust s)	Novel human gane mapping to chomosome 13, sumiar to rat rybowy	Homo sapiens rysnodine receptor 3 (RYK3), mkNA	Homo sepiens GGT1 gane, excn 1	Homo saplans gutadrione Stransferase thera 2 (UST 1.2), mixtvA	Homo sapiens chromosome 21 segment HSZI UVV8	Homo sapiens transcription enhancer racid-o innova, compress cos	Homo sepiens mRNA for KIAA0612 protein, perteil cos	Homo sepiens mRNA for KUAA0812 protein, partial cots	2087g08.sr1 Soares fetal heart NortH19W Homo sapiens culture comes in the contraction of	ot83405.s1 Scares total fetus NbZHF8 9w Homo sapaens curve come invace: 1023309 3	602042163F1 NCL CGAP_Bm67 Homo septens CLINA Come IMACUE: 41 CML23 5	Homo sapiens adenyase kinase Z (ANZ), mruwa	Homo septents adenytate runase 2 (ANZ), minnyta	OSCIONA.81 SOCIETA INTERIOR INTERIOR INTERIOR CONTRACTO
COIL FIGURES CA	Top Hit Databese Source	T.	H		NT TN					TN TN	T L		N.	NT	M							NT.					N			T HUMAN			EST HUMAN
Single	Top Hit Acession No.	1.0E-68 AF231981.1				3.1	4557782	7862241 NT	11431590		2.1		2.1	1	1.0E-83 AB023228.1	1.0E-63 AB040918.1	1.0E-83 AF091395.1			1.0E-03 ALD49801.1	11433646 NT	1.0E-83 A.1230125.1	17858	8.0E-04 AL183209.2	1	1	1	5.0E-04 AA722434.1	5.0E-84 Al015800.1	5.0E-84 BF529115.1	11423982 NT	11428962 NT	5.0E-94 T89398.1
	Most Similar (Top) Hit BLAST E Valtue	1.05-88	1.0E-83	1.0E-83 U78509.1	1.0E-83 U78509.1	1.0E-03/	1.0E-88	1.0E-83	1.0E-83	1.0E-83 D42072.1	1.0E-83	1.0E-83 Y10183.1	1.0E-83/	1.0E-83	1.0E-83	1.0E-83	1.0E-83	1.0E-63 X13474.1	1.0E-83 X13474.1	1.0E-03	1.0E-83	1.05-83	1.0E-83	8.0E-04	6.0E-94	5.0E-94	5.0E-94	5.0E-04	5.0E-94	5.0E-94	5.0E-94	5.0E-94	5.0E-94
	Expression Signal	6,	86,	1.88	8.	1.02	10.68	0.91	208	3.07	1.97	1.12	1.28	0.47	0.47	1.85	49.1	4.08	4.08	0.71	83.0	211	3.14	1.25	2.15	323	3.23	3.06	1.34	0.82	2.81	2.81	6.07
	ORF SEQ ID NO:		30373	31907	31908	32/35	32308	32633	33507	33785	34987	35274	35387	35776	35778	34533	34637	38833		36482	36924				29937						37795	37798	31318
	Esan SEQ ID NO:	16284	17488	l	ı	ı	10/05	19392	20182	20428	L	1_		L	L	I.	1_		L		L		1_	1_	L	L	L	L		L.		24268	25965
	Probe SEQ ID NO:	888	184	SE AS	8846	05820	6003	832	9999	7462	Bess	8888	8008	8378	8378	7080	8811	88	8048	1008	10.00	17763	12847	10858	3988	544	5441	6168	7206	9868	11318	11318	12497

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32501 0.65 1.0E-84 AE000269.1 NT	19670         32948           20031         37948           23937         37458           13784         28544           14783         27768           14783         27788           14783         27788           14856         32678           18856         32678           21024         34423           21000         35327           21900         35327           22877         38340           24379         38346           24379         38346           24384         38460           23036         38516           19162         22073           16162         22074           17414         30259	3.32 3.0E-94 0.09 3.0E-94 4.81 3.0E-94 1.03 3.0E-94 4.87 3.0E-94 2.17 3.0E-94 0.08 2.0E-94 2.24 1.0E-94 1.18 1.0E-94	4657558   11496288   11496288   1152628   4826863   4826863   4826863   4826863   4757821   4757821   4757821   4757821   4810393.1   4810	TT HUMAN TT HUMAN TT HUMAN ST HUMAN ST HUMAN	Homo sepiens cysteine-tich repeat-containing protein S52 precursor, mRNA, complete cds Homo sepiens E1A binding protein p300 (EP300) mRNA Homo sepiens E1A binding protein p300 (EP300) mRNA Homo sepiens are finger protein 277 (ZNE277), mRNA Homo sepiens are finger protein 277 (ZNE277), mRNA Homo sepiens are are finger protein 277 (ZNE277), mRNA Homo sepiens are are active finger protein 277 (ZNE277), mRNA Homo sepiens are are active fine active (NRCAM) mRNA Homo sepiens protocedien apha 13 (PCDH-elpha13) mRNA, complete cds Homo sepiens glycogenin-til mRNA, complete cds Homo sepiens glycogenin-til mRNA, complete cds Homo sepiens active faresport of synaptic vesicles (ATSV) mRNA Homo sepiens active faresport of synaptic vesicles (ATSV) mRNA Homo sepiens active faresport of synaptic vesicles active in NACE-2331813 3' wi3dh11x1 NCI_CGAP_Co16 Homo sepiens cDNA done IMACE-2331813 3' 601175762F1 NIH_MCC_16 Homo sepiens cDNA done IMACE-3352699 5' 601111696F1 NIH_MCC_16 Homo sepiens cDNA done IMACE-3352599 5' 601111696F1 NIH_MCC_16 Homo sepiens cDNA done IMACE-3352599 5' Homo sepiens hypothetical protein (FL20746), mRNA
NALL TOTAL ACCRETATION OF THE PROPERTY OF THE			AE000269.1	TUMAN	Escherichia coli K-12 MG1655 section 159 of 400 of the complete genome INKE7-434(27314 rt 434 (synonym: thes3) Homo septens cDNA clone DKF2p434G0314 5
0.81 1.0E-84 AL040518.1 EST_HUMAN				Т	DKF2p4343314 T1 434 (smanym: mess) mains equals con one con construction of the constr
49474 39779 0.77 1.0E-94 H08270.1 EST_HUMAN				7	y87(02.11 Sogres infant brain 1NIB Home sapients contactive infance, wood o

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IN EACH FIAMES LAPICES AND INCIDENT AND INCI	Top Hit Descriptor	AV725992 HTC Hamo saplens cDNA clane HTCBEF05 6	Homo sapiens chromosome 21 segment HS210004	Hamo septens chromosome 21 segment HS21C004	Homo saptens patred box gene 5 (B-cell lineage specific activator protein) (PAX5), mXNA	601468748F1 NIH MGC 67 Hamo sepiens CINA ciane IMAGE:3872089 3	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, attenuatively spliced forms, complete cds	ep22e02.x1 Schiller algodendrogiama Hamo saptens CDNA dane IMACE:1956122.5 SIMBET TO INCACASA Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR.;	Homo saplens KIAA0164 gene product (KIAA0164), mittNA	60117676251 NIH_MGC_17 Hamo sepiens CONA clane IMAGE:3331U36 3	601175762F1 NIH MGC 17 Hamo sapiens d'UNA dane IMAGE:3031U38 5	Homo sapiens TNF-aigha stimulated ABC protein (ABCRO) mKNA, complete cos	Homo sepiens KIAA0255 gene product (KIAA0255), mrtnA	Homo sapiena KIAA0255 gene product (KIAA0255), mKNA	M.musculus glyT1 gene (exons 1c and 2)	M.musculus gtyT1 gene (exons 1c and 2)	Haino sepiens progressive ankylosis-like protein (ANK) mRNA, complete cas	we08604.x1 NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE_2340606 3' similer to go; nueces TUBUIJN ALPHA-1 CHAIN (HUMAN);	we08e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00568	TUBULIN ALPHA-1 CHAIN (HUMAN);	Homo sapiens KIAAD183 gane product (KIAAD183), mKNA	Homo sapiens protessome (prosome, mecropein) 200 subunit, nor-A i rese, 11 (FowD 11), illenia.	Homo sapiens probessome (prosome, meropein) 200 submit, indrettiness, 11 (13ML) 1.5 illinoss	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cos	Homo sepiens KIAA0255 gene product (KIAA0255), mRNA	Homo sepiens KIAA0255 gene product (KIAA0255), mRNA	Homo septens profine dehydrogenese (proline addese) (PRODH) mRNA	Homo sapiens mRNA for KIAA1395 protein, partial cds	Homo sepiens early growth response 2 (Krok-20 (Drosophila) homotog) (EGPC), miruw	Homo sepiens HCF-binding transcription factor Zhangret (ZF), mixter	Zu84bOt, s1 Soares_testis_NH   Homo sapiens CLIVA Ciche IMAICE: (14046 3 Sui mai in Cultatin El El El El El El
AUI LIUM	Top Hit Defabese Source	EST_HUMAN	Į.			EST_HUMAN	NT	T_HUMAN			EST_HUMAN	F				NT	NT.	EST HUMAN	Ī	T HUMAN					NT	NT	NT	M	N	Į.	EST_HUMAN
Olligia	Top Hit Acessian No.	1.0E-04 AV725992.1			11428710 NT	1.0E-94 BE780478.1		1.0E-84 AI272244.1	11418871 NT	1.0E-84 BE285714.1	1.0E-94 BE295714.1	1	7682027	7662027 NT	X82569.1	082569.1	9.0E-85 AFZ74753.1	8.0E-95 AI700998.1		8.0E-85 AI700898.1	11418376 NT	11426529 NT	11426529 NT	8.0E-95 AF032897.1	11420944 NT	11420944 NT	6174644 NT	8.0E-85 AB037816.1	9845523 NT	10884024 NT	8.0E-85 AA629058.1
	Most Similar (Top) Hit BLAST E Value	1.0E-04/	1.0E-04/	1.0E.04	1.0E-04	1.0E-94	1.0E-84 U85590.1	1.0E-84	1.0E-94	1.0E-94	1.05-94	9.0E-95	9.0E-95	9.0E-95	9.0E-95	9.0E-95 XB2569.1	9.0E-95	8.0E-95		8.0E-95	8.0E-95	8.0E-95	8.0E-95	8.0E-95	8.0E-95	8.0E-95	8.0E-95	8.0E-85	8.0E-95	8.0E-95	8.0E-95
	Expression Signal	0.56	0.56	0.56	2.57	1.83	2.77	191	3.39	1.43	131	13	1.19	1.19	1.38	1,38	1.61	- 182		1.82	0.83	1.55	1.65	202	1.97	1.97	267	3.08	0.8	221	29.02
	ORF SEQ ID NO:	33000	34833	34834	36067	36547	37881	38151	38520	26182	28182	77480	28740	20141	31489	31490	34077	30482		30483			33774		L				37008		
	Earl SEQ ID NO:	19725	2440	21419	22815	23072	24349	24683	24923	13253	13263	14506	16225	16226	18579	١.		47/KON		17690	L	L	20418	L	L	L		L	<u> </u>	<u> </u>	
	Probe SEQ ID NO:	8888	8450	8	8	10146	11405	11646	12050	12615	12887	1473	3170	3170	54.78	5470	8595	4587		4567	7138	7452	7452	8539	9720	9770	10207	10238	10595	11813	12820

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ngle Exon Probes Expressed in borne mailow	Top Hit Descriptor	Homo sapiens DNA for amyloid precursor protein, complete cds	Hamo sapiens DNA for amyloid precursor protein, complete ods	Homo septens Ly-6-Illes protein (CD59) mRNA, complete cds	Home saniens chromosome 21 segment HS21C048	Limon homodon mutain (PHOX1) mRNA, 3' end	Turing Society Home cariens cDNA	NIMI I I I I I I I I I I I I I I I I I I	ES 1302/04 MAGE resequences MAGA Homo seciens CDNA	ESTSOCIONIMA CONTRACTOR FROM 14 Home seniens CDNA	CONTROL I TOURD BANKA Home semients CDNA clone IMAGE:4214147 5	GLZU/1140F I NOL COMPLETION CHECK 1 (NOCK1) mRNA	Homo sapiens deulcated of cyto-vineses i (Cook) with the company of the company o	ES13/0191 MACE resequences, which runing equations of the	EST370191 MAGE resequences, which in advans ocien	Home sapiens KIAA0763 gane product (navva) vok mista	Hamo saplens KJAA0763 gerte product (NJAH9763), III NATA THE STATE AND THE LAW SECTION AND ALMS INA CET A070451 5	601845Z1Z-1 NIN, INC. 30 TIGHT BEFORE CAN CONTINUE CONTIN	Home sapiens KAAUzes gans proude (KAYAUze) IIINNA	Homo sapiens KIAA0255 gene product (NJAA0259), mirory (TIMP3)	Homo sapiens ussue in modulus of medius of company of the property of medius of company of the property of the	601312161F1 NIH MCC_44 Hamo septens cDNA dans IMAGE:3636862 5	Homo sapians G protein-coupled receptor 19 (GPR19) mixiva	Homo sapiens G protein-coupled receptor 19 (G-R19) mixNA	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase meta 1 (GSTT1)	genes, complete cds	Homo sepiens glycine cleavage system protein H (anumaneury can led ) (CCC) )	Homo sepiens Usurpin-gamma mitthey, completes cus	Homo septens unconventional myostin-15 (LOC3-1198), mrsvA	Hamo sepiens unconventional myosin-15 (LOC61168), mrava	Homo sapiens mRNA for KIAA1386 protein, partial cds	dm01c02.x1 Soeres_Nit-HMPu_S1 Homo septens cDNA clone IMA(2E:1880549 3 strings to vr 1.12307.**	CE03705;	Homo sapiens hypothetical protein (HSSZZB1A), minute	Hamo sapiens NIAAU107 gare product (NIAAV107), III CO.	
con Probes E	Top Hit Detabesse Source	¥			;   <u><u></u></u>	2	2	ESI HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	Ę	EST HUMAN	EST HUMAN	¥	5	EST HUMAN	Z	¥	Ę	EST_HUMAN	Z	N		Ŋ	N	N	IN	Ę	Į,		.1 EST HUMAN	NT	N.	
Single	Top Hit Acession No.				٩	2		_		-			303354	.1	<del>-</del> -	7682289 NT	32280	3.0E-85 BF213446.1	7662027	7662027 NT	4507512 NT	BE303873.1	5453665 NT	5453665 NT		20E-95 AF240786.1	4758423 NT	AF015452.1	2.0E-85 7705900 NT	TN 0065077	2.0E-95 AB037807.1		20E-95 AI290284.1			
	Most Similar (Top) Hit BLAST E Value	7 0F OS D87875.1	7 NE OF D07875 4	7 OF OF MOSTOR 4	7.UE-SO W	7.0E-85 AL163248.	7.0E-95 M95929.1	4.0E-95 BE439625.	4.0E-85 AW950634	4.0E-85 AW950634	4.0E-85 BF371302.	3.0E-85 BF526041.	3.0E- <del>0</del> 5	3.0E-95 AW958121	3.0E-85 AW958121	3.05-05	3.0E-05	3.0E-95	2.0E-95	2.0E-95	2 05.05		20E-95	20E-95		20E-95	20E-95	2.0E-05	Ì	ì					20E-95	
}	Expression Signal	8 60	3	90.0	8.4	1.26	-	0.82	1.93	1.93	1.79	1.61	0.54	F	-	1.75	1.75	0.69	2.18	2.18	2 43					3.35					0.83		1.09		292	
	ORF SEQ ID NO:	1	9000	28288	30307		30876	35985	38487	38488	38534	31550								,			28457	L		28500					20587		29718		7 30967	
	Exem SEQ ID NO:	1000	1/83/	1	]	17460	18100	22534	24890	24890		18817	<u> </u>	١.	l.	1_		_	L	上		44083	1	277	1	45477		1_	Ŀ	L		1	16805	1		
	Probe SEQ ID NO:		2/2	232	4394	4443	90809	8572	12013	12013	12085	6617	5757	7503	7603	97.10	9740	40404	1651	1651		SCSL S		3 5	3	2476	25.25		3577		\co	3	3783	4388	5077	

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Table 4
Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	Homo sapiens CGI 48 protein (LOC51099), mRNA	Hame sepiens CGI-48 protein (LOC51086), mRNA	Homo sepiens angiotenstri I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA	Homo septens engiotenstri I converting enzyme (peptid/4-dipeptidase A) 2 (ACE2), mtRNA	Homo septens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA	Human muscle type phosphofnucbkfnase (PFK-M) gene, exch 7	Homo sapiens transcription factor 2, hepatic, LF-E3; variant naparic nuclear rackr (1 Or.2), minum	Homo septiens transcription factor 2, hepatic; LT-83; variant hepatic nuclear tector (1 LT 2), minutes	Homo sapians ciliary dynain heavy chain 9 (DNA-19) mittina, compage cos	Homo sapiens huntingtin (Huntingtion disease) (HU), mrtiva	Homo sapiens ribophorin II (RPN2), mRNA	Homo saplens KIAA1085 protein (KIAA1085), mrtvA	Home saplens bone morphogenetic protein receptor, type IA (BMPRTA) mixtry.	Homo septens KIAA0763 gene product (KIAA0763), miXNA	Homo sepiens KIAA0763 gene product (KIAA0763), mKNA	Homo sapiens gutrathione S-transferase freta 2 (GSTT2) and gutathione S-transferase theta 1 (GST 11)	genes, complete cds	Homo sepiens edenylosubodnens lyess (ALOSL), minuva	223h04.r1 Soeres overy tumor NibHOT Homo septens cLNVA clone IMAGE:714007 9 Similler to TR:G1067084 G1067084 F55H2.6;	4/3/h04 rd Scares overy fumor NIDHOT Homo sapiens CDNA clone IMAGE:714007 5' similar to	TR:G1067084 G1067084 F55H2.6;	RC8-FN0019-290600-011-G11 FN0019 Homo saplens cDNA	RC8-FN0019-200600-011-G11 FN0019 Homo septens CUNA	601437232F1 NIH_MGC_72 Hans sapiens cDNA dane IMAGE:3822423 5	601497608F1 NIH_MGC_70 Hamo sapiens cDNA dane IMAGE:3889761 5	601497608F1 NIH_MGC_70 Hamo septens cDNA clane IMAGE:3899761 5	PMO-LT0019-080300-002-d09 LT0019 Homo sepiens cDNA	Homo septens chromosome 21 unknown mRNA	Homo saplens chromosome 21 segment HS21C001	Human glycoraddahyda-3-phosphata dahydrogenasa psaudogena 3'end	Homo sapiens statytuansferase 6 (N-acetytlacosaminide alpha 2,3-statytuansferase) (SIAT6), mRNA
	Top Hit Detaberse Source						NT								Ŋ	¥		٤	M	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	EST HUMAN	EST_HUMAN	¥	¥	¥	TN
	Top Hit Acession No.	7706784 NT	TN5784 NT	11225608 NT	11225608 NT	11525883 NT	2.0E-85 M59724.1	11427182 NT	11427182 NT	AF257737.1	11435773 NT	11421785 NT	11434330 NT	4757853 NT	7662289 NT	7662289		2.0E-85 AF240788.1	11418164 NT	0E 08 04.284851 1		1.0E-96 AA284651.1	1.0E-85 BF370000.1	1.0E-95 BF370000.1	9.0E-96 BE897259.1	B.0E-96 BE907607.1	8.0E-96 BE907607.1	8.0E-86 AW836047.1		8.0E-98 AL 163201.2	6.0E-96 MZ6873.1	11422842 NT
	Most Similar (Top) Hit BLAST E Value	2.0E-95	205-95	2.0E-96	20E-85	2.0E-95	2.0E-85	2.0E-95	2.0E-05	2.0E-96	2.0E-95	2.0E-05	2.0E-95	2.0E-95	2.0E-95	2.0E-95		20E-95	2.0E-95	10 TO TO		1.0E-96	1.05-95	1.0E-95	90E-96	8.0E-96	8.0E-98	8.0E-98	7.0E-96	6.0E-96		
	Expression Signal	4.36	436	122	122	0.67	3.71	<u>ا</u>	1.9	2.39	137	2.51	0.54	1.72	2.35	235		269	5.81	1 7	!!	724			1.58	1.36	1.36	2.28	1.06			
-	ORF SEQ ID NO:	31598	34500	32055	32056	32701	32571	32923	L						38484			31782	31718		2 1800	31963							200002		29465	$\perp$
	SEQ ID	18654	4 BBEA	18874	18874	18017	18338	19852	19652	19778	20152	22462	23669	l_	L	24888		25291	25546	<u>l</u> .	19/91	18791	L	L		L	1					
	Probe SEQ ID NO:	5557	153	200	2829	7,687	385	6692	6582	67.22	88	9498	10747	11078	1201	\$		12687	12984		888	5608	77.57	77.57	8588	443	500	A SERO	2000	2000	340%	5722

Page 424 of 546 Table 4 Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA	Homo satilians KIAA0763 gene product (KIAA0763), mRNA	Leave contain march heave ratherentide 2. skeletal muscle, adult (MYH2), mRNA	Truit equal injection in the control of the control	From Septem III Very 10 Nove 11 Proving Proving 10 Prov	IGHIO SEGNETO INVALOR INVALOR IN THE PROPERTY OF THE PROPERTY	Homo sapiens miKNA for KIAATT72 promer, pare war was	(emo saplens phosphodesterese ov. Cuw. specific, I.O., apriz. (1 pres. ).	Hamo sapiens transferit receptor potential continue of the con	H. Sapitats Live in the transfer of the control of	Homo sapiens ALYANA processing 2 and 3	Jamo sapatas noon jaraan (noon) yarah carah tarah	Homo sapiens dNT-2 gene for mitochondrial 5/(3)-decoyribonucleotidase (dNT-2 gene), exons 1-5	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA	Homo sepiens A kinase (PRKA) enchor protein 1 (AKAP1), mRNA	Homo saciens mRNA for KIAA0960 protein, partial cds	Homo seniores mRNA for 14-3-3gamma, complete cds	Human tune IV collectenese (Cl. G4B) gens, exon 5	Limen two IV collegeness (CLG4B) gene, excn 5	The section of the se	France September 10 years of the september 10 Home September 20 NA clone IMAGE 212327 6	yormics character and an and and an anti-	Trains equals and control of segment HS210048	Figure Sayana and Sayana 110-002 HT0230 Homo saplens cDNA	CVA CNIM 20.29 DODA 27-612 GNO120 Homo septens cDNA	CVA CAMA 20. 250500 427-b12 GAVO120 Homo septiens cDNA	AVREGAGE CKC Homo seniens cDNA clone CKCFMD07 5	2910555 Fertine NIH MGC 7 Homo septems cDNA done INAGE:2818351 5	Limma and committee the KINERVAN, gag, pol and any gands	Personal MACE resembarss MAGC Homo saplens cDNA	ESTS 230 IZT MACE recommences MAGC Homo septions cDNA	ES 1.50 1.61 mouth feature game according	Filtration inspection of the contract of the c	Human carlens transfert recents potential channel 5 (TRPC5), mRNA	I falls organis
	Top Hit Database Source												¥	. 4					Ž	Z	Ž	Į.	EST HUMAN	Į	LN.	TOTAL TOTAL	EST HOMEN	TOWNER TO LOS	EST HUMAN	ESI HUMAN	Z	EST HUMAN	EST_HUMAN	LX.	E .	N.
alfillo Talfillo	Top Hit Acession No.	18822891	Total Control	N 807700/	682383					6912735 NT			5.0E-98 AF149773.1	E NE 00 A 1977557 1	24399	TA 000/4474	2 1 1 CONTRACTOR	5.0E-96 AB0231//.1	5.0E-96 AB024334.1	M68347.1	M88347.1	7881973 NT	3.0E-96 H88656.1	4503098 NT	2.0E-96 AL163248.2	2.0E-96 BE1480/4.1	2.0E-96 BF369731.1	2.0E-96 BF369731.1	2.0E-08 AV689461.1	20E-86 AW249440.1	Y18890.1		1.0E-86 AW955054.1	1.0E-96 M75967.1	M75967.	N[65/2/39
	Most Similar (Top) Hit BLAST E	80 20 8	COL	6.0E-96	8.0E-96	5.0E-96 A	5.0E-08 A	5.0E-86 A	5.0E-98	5.0E-98	5.0E-86 XB0812.1	5.0E-96	6.0E-98	2000	3.00	9.00	000	5.0E-96	5.0E-96	6.0E-96 M88347.1	5.0E-96 M68347.1	5.0E-96	3.0€-98	2.05-96	20E-96	2.0E-98	20E-96	20E-96	20E-08	20E-88	1.0E-88	1.0E-88	1.0E-98	1.0E-96		1.0E-96
	Expression Signed		8C7	2.59	2.78	3.08	3.47	3.47	12	0.74	0.83	0.93	1.15		2 2	407	4.02	0.78	0.7	B.11	6.11	1.51	7.1	4.65	1.12	1.39	0.58	0.58	6.83	3.08	2.47	235	235	1.04		1.15
	ORF SEQ 1		38535	38336	38390	26336	28855	26856		29013		31113	33148		8228	33496	33497	33576	34081	34825	34826	L			28750		34017				20063	27809				31234
	SEO EN		24754	24754	24789	13412	1580	8	L		Į.	1	L	L _	_1			20241	20711	21412	21412	J		L	ı	17808	20654	1	78222		13738	14825	<u></u>	L	1_	8 18390
	Probe SEQ ID NO:		11872	11872	11918	333	843	3 2	3 8	8	9	5233	6807		88	98	6949	7219	7758	8453	8443	12078	4219	415	748	4780	288	88	8837	12285	672	1796	, 186	2237	Ñ	7158

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Table 4
Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	Homo septiens guarane nucleotide eachange factor for Rap1 (KIAA0277), mRNA	Homo saplens HSPC144 protein (HSPC144), mRNA	Hamo saplens HSPC144 protein (HSPC144), mRNA	Homo sepiens similar to ectonuclectide pyrophosphatase/phosphodesterase 3 (H. sepiens) (LOCoSZ14), mRNA	Hamo sepiens secretary patitway component Sec31B-1 mRNA, atternatively spilced, complete ods	Homo sapiens mRNA for KIAA1280 protein, partial cds	Homo sapiens mRNA for KIAA1280 protein, partial cds	Hamo sepiens neuronal cell achesion molecule (NIKCAM) mikiNA	Homo sepiens neuronal cell achieston molecule (NKCAM) miron	601863712F1 NIH_MGC_67 Hamo sapiens CLYNA Care IMAGE: 4001202 3	SHT0117-011099-004-D07 HT0117 Home sapiens GLAVA	601440317F1 NIH MKGC 72 Homo saparis guaya cigas immuci. 3923133 3	801440317F1 NIH MISC 72 HOMB SEPTEMS CLINA CALIB INVICE COZZUSOS	EST22672 Adipose tissue, write II Homo sapiens curva o end	ES 122672 Adipose tresue, write II riomo septems curva o enu	Human mRNA for appha-actinin	DKFZp434NGZ3_r1 454 (synonym: mess) Hamo separas curva curio dra transcent	2407e12.s1 Sceres_NYHMPu_S1 Hamo septens d.XXA dane IMAGE:/6/755 5 SITTENE TO IT.C.15X41.25 G1304125 PAIS4 MRNA;	RC0-BT0812-250800-032-409 BT0812 Homo septens cDNA	MR0-HT0241-150500-010-b02 HT0241 Homo septems cDNA	MR0-HT0241-150500-010-b02 HT0241 Homo septems cDNA	CAID-BN0108-170300-283-608 BN0108 Homo septems curva	Homo septens PAD-H18 mrt/N for pepadyserguine certainse type it, culture cus	Homo sapiens PAD-H19 mRNA for peptidykarginine deminese type II, Complete cus	Homo sepiens brefeldin A-Inhibited guanthe nucleotide-exchange protein 2 (BNSZ), Innua.	Homo saplens apolipoprotein H (beta-2-gl)coprotein I) (APOH) mirana	Human N-methyk-D-aspartate receptor modulatory suburit 2A (INNKZA) mrvnA, compress cos	Human N-methyl-D espartate receptor modulatory subunit 2A (mink2A) minvey, cumpress cue	Homo septens mydva tot Genvac epina-c, o-staytuanskense i, kurg kum.	rights sapara interest to cancer appear, o casping and accept the sapara in the ATD december (1 (23) francethy variant alpha mRNA	אמנוס פאסמוצ ווקצפס וווי דורה, רזי באימיויייייייייייייייייייייייייייייייייי
	Top Hitt Destrosses Source										T_HUMAN	HUMAN	٦	П		T HUMAN		EST_HUMAN	EST HUMAN			EST HUMAN	EST_HUMAN	¥	저	אַל	M	Z	F	Ę	Į.	Ł
	Top Hit Acession No.	6912455 NT	7861803	7861803 NT	11419428 NT	1.0E-96 AF274883.1	1.0E-88 AB033118.1	1.0E-98 AB033116.1	4826863 NT	4826863 NT	8.0E-97 BF245240.1	6.0E-07 BE141849.1	6.0E-97 BEB98012.1	6.0E-97 BE898012.1	6.0E-67 AA320332.1	6.0E-97 AA320332.1	6.0E-97 X15804.1	6.0E-07 AL043314.2	5 DE-87 AA418026.1	6.0E-97 BF154912.1	5.0E-97 BE148597.1	5.0E-97 BE148597.1	4.0E-07 BE004436.1	4.0E-97 AB030176.1	4.0E-97 AB030176.1	3		4.0E-97 U09002.1	4.0E-97 U09002.1	4.0E-97 Y11339.2	4.0E-97 Y11339.2	7710125INT
	Most Similar (Top) Hit BLAST E Value	1.0E-08	1.0E-96	1.0E-98	1.05-98	1.05.98	1.0E-98	1.0E-98	1.0E-98	1.0E-98	8.0E-97	6.0E-97	6.0E-97	6.0E-97	6.0E-67	6.0E-97	6.0E-97	6.0E-97	5.05-97	6.0E-97	5.0E-97	5.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97
	Expression	0.55	1.35	1.35	24.61	224	16.0	9.9	1.59	1.59	0.65	3.82	0.85	0.85	0.71	0.71	3.43	227	13.05	2.61	1.75	1.75	2.4	1.87	1.87	0.99	0.86	0.62	0.62	5.9	5.9	1.35
ļ	ORF SEQ ID NO:	33283	34941	34942			36939	36940	31169	31170	28310			36683				34732	<u> </u>									L	L			33573
	SEQ ID	19985	24.673	7.53	23082	2768	23442	23442	18332	18332	16389	l_	L.	L	23879	23879	1.		L		1_	L	<u> </u>		L		L	1	l _	20123		20239
	SEQ ID	200	N S	3	8	8	19520	10520	12272	12272	3338	982	9288	8286	10959	10050	11734	8348	8	100	11873	11873	88	8	8	1925	5645	2998	2956	6997	6997	7217

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ORF SEQ Expression (Top) Hit Top Hit Acession Database ID No. Signal Vatue		34860 0.68 4.0E-97 4557708 NT	35092 1.62 4.0E-97 11421788 NT	35320 0.49 4.0E-97 11431060 NT	35358 0.78 4.0E-97 11423233 NT	36056 1.36 4.0E-97 AB011168.1 NT	36057 1.36 4.0E-97 AB011168.1 NT	37226 0.79 4.0E-97 11431060 NT	37891 2.15 4.0E-97 11863122 NT	37892 2.15 4.0E-97 11863122 NT	7.99 4.0E-97 11418318 NT	26266 1.01		271 3.0E-67 4502168 NT	27446 1.72 3.0E-97 4758813 NT	28470 1.67 3.0E-97 U36255.1 INT	29158 2.22 3.0E-97 K02212.1 NT	5174478 NT	03470 NT	1.0E-97 BE566486.1	1 EST_HUMAN	8.1 EST	R10887.1 EST_HUMAN	37549 3.07 1.0E-97 11427757 NT	7757 NT	AA663781.1 EST_HUMAN	37472 35.59 1.0E-97	37473 35.59 1.0E-97 11426272 NT	26914 1.43 9.0E-98 BE090973.1   EST_HUMAN	27278 2.02 9.0E-98 8393092 NT	
																	,														<u>1</u>
SEQ ID	<u>.</u>	L		<u> </u>	_	<u> </u>	L		<u> </u>		L	L		L_			<u>L</u>		_	L.			L	<u> </u>	L			Ш		1281 1431	6435 1950
Probe SEQ 10 NO:	200	8474	870	8038	8967	196	5093	10803	11498	11498	12467	243	88		1435	2445	3185	3274	4815	1999	978	9789	10122	11062	11062	11639	11796	11796	3	12	ጿ

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	Top Hit Descriptor	Homo capiens leucy-tRNA synthetase, mitochondrial (KIAA0028), mRNA	Homo sapiens A kinase (PRKA) anchor protein (yotiao) 9 (AKAP9), mRNA	Homo sapiens death-essociated protein (DAP), mRNA	Homo sapiens death-associated protein (DAP), mRNA	Human mRNA for emyloid A4(751) protein	Homo sepiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA	Homo sapiens mRNA for KIAA1385 protein, partial cds	Hamo sapiens 17-beta-hydraxysteraid dehydrogenase IV (HSD17B4) gene, exan 8	Homo sepiens SWIGNF related, maths associated, actin dependent regulator of chromatin, substantly a, member 3 (SMARCA3) mRNA	Homo septens SWI/SNF related, metrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCAS) mRNA	Homo sepiens inosital polychosobrate 1-chosobratese (INPP1) gene, complete cds	Homo serieus mRNA for KIAA1006 portein partial cets	Homo sapiens mRNA for KIAA 1005 protein, partial cds	Homo sepiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), mRNA	Homo sepiens pertial MICB gene for MHC class I chain-related protein B, exons 2-3 and joined CDS	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA	Homo sepiens IL2-inducible T-cell kinase (ITK), mRNA	Homo sepiens PMS2L16 mRNA, partial cds	Homo septems PMS2L16 mRNA, pertial cds	Homo sepiens 959 ldo contig between AML1 and CBR1 on chromosome 21q22; segment 1/3	Hamo sepiens 859 lib cartig between AML1 and CBR1 an chranosome 21q22; segment 1/8	Human mitochondrial creatine kinase (CKMT) gene, complete cds	601507503F1 NIH_MGC_71 Hamo saplens cDNA dane IMAGE:3908097 5	AJ403124 3.4 (downregulated in laryrx cardinoma) Homo sapiens cDNA clone 18	Homo sepiens mRNA for KIAA0707 protein, partial cds	7818H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01	Homo sepiens chromosome 12 open reading frame 4 (C12ORF4), mRNA	Homo septems activator of S phase lunase (ASK), mRNA	Homo sepiens activator of S phase kinase (ASK), mRNA	yo17g09.r1 Sogres adult brain N2b5HB557 Homo sapiens cDNA clone IMAGE:178240 5	Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA
	Top Hit Database Source								TN.							토			H	H	H	H] LN	H H		EST_HUMAN A		EST_HUMAN 7				T HUMAN	
	Top Hit Acession No.	7861871 NT	11419408 NT	4758119 NT	4758119 NT	X06989.1	11321580 NT	9.0E-08 AB037786.1	9.0E-88 AF057728.1	4507070 NT	TN OCOCORA	2 2 2	\ \ •		118982	A.125/158.1	31810	5031810 NT	8.0E-98 AB017007.1	.1	1	.1		1	1	3.0E-88 AB014607.1	3.0E-98 AA077498.1	9986846 NT	11419210 NT	1419210		8922096 NT
ľ	Most Similar (Top) Hit BLAST E Vatue	9.0E-98	9.0E-88	90-30'6	90E-98	9.05-98	9.0E-98	/ <del>80-3</del> 0′6	9.0E-88	9.0E-88	80 10 0	9 0F-08 AF141325	O OF OR	9.06	90E-08	8.05-68	8.0E-08	80E-98	8.0E-98	8.0E-88 AB017007.	8.0E-88 AJ228041.	8.0E-88 AJZ29041	8.0E-98 J04469.1	5.0E-98 BE885873.	3.0E-88 AJ403124.	3.0E-98	3.0E-98	3.0E-98	3.0E-98	3.0E-08	3.0E-98 H46698.1	3.0E-98
	Expression	0.55	0.56	5.5	5.5	201	1.44	1.49	0.83	1.16	4	90	200	288	1.76	224	1.49	1.49	273	. 273	0.97	76.0	6.45	274	123	1.19	3.63	0.7	1.63	1.63	3.59	0.65
	ORF SEQ ID NO:	33832	33940		34637	35873	35904	36040		36202	Sec.	37045	27822	37824	37883		27568	27669	27754	27755	29569	29570	29757	32509	28228	28639	   	33418	33422		35486	1
	SEQ ID NO:	20472	20577	21228	21226	22435	22541	22591	22647	22760	22750	23545	3626	24296	24361	13146	14504	14591	14769	14769	. 16862	16852	16849	19276	15203	15814	15751	20107	20110	20110	22070	22595
	Probe SEQ ID NO:	7507	7817	8257	8257	9471	8279	9647	9694	9722	0722	10623	44948	11346	11407	8	1562	1562	1739	1739	3607	3807	3809	620-	2188	2816	2759	7131	7134	7134	9104	8652

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					B		
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signel	Most Similer (Top) Hit BLAST E Vetue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1244	14281		16.34		2.0E-99 AW 274792.1	EST_HUMAN	xp09e08.x1 NCL_OGAP_HN9 Home sepiens cDNA clone IMAGE:2738874 3' similar to gb:M31212 MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN);
3272	1	29248	1.19			NT	Human Ku (p70/p80) subunit mRNA, complete cds
4574	17596	30480	1,95		2.0E-99 AF085703.1	Ŋ	Homo sapiens short chain L-3-hydroxyscyl-CoA dehydrogenese precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7838			29'0			N	Homo sapiens ciliary dyneth heavy chain 9 (DNAH9) mRNA, complete cds
8058					2.0E- <del>89</del> W23507.1	EST_HUMAN	2546d08.r1 Scenes_feta].brng_NbHL19W Homo septens cDNA clone IMAGE:306635 6" similar to gb:M15182 BETA-CLUCURONIDASE PRECURSOR (HUMAN);
8507			0.65		2.0E-89 R78254.1	EST_HUMAN	y81b09.r1 Scares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145025 5
11440	L.	37923	2.56		2.0E-99 AF247467.2	NT	Homo sepiens myosin X (MYO10) mRNA, complete cds
315	L	26333	1.5		1.0E-89 AF114487.1	NT	Homo sepiens intersectin long isoform (ITSN) mRNA, complete cds
378	辶	26393	1.04	1.0E-89	11526150 NT	M	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
1418		27428	1.88		1.0E-89 M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1559	14591	27563	1.52		1.0E-89 AF182523.1	N	Homo sepiens truncated Niemenn-Pick C3 protein (NPC3) mRNA, complete cds
1559	1_		1.52		AF18252	IN	Homo sepiens truncated Niemenn-Pick C3 protein (NPC3) mRNA, complete cds
194	L.		1.18		4503730 NT	M	Homo sapiens FK506-binding protein 6 (384D) (FKBP6) mRNA, and translated products
<u>₹</u>	14968		1.18	1.0E-99	4503730 NT	Z	Homo sepiens FK606-binding protein 6 (3640) (FKBP6) mRNA, and translated products
3101			1.6		1.0E-99 J03171.1	NT	Human interferon-eipha receptor (HulFN-eipha-Rec) mRNA, complete cds
4407	17435		2.26		1.0E-99 AF098018.1	N	Homo sepiens fatty acid amide hydrolesse (FAAH) gene, excn 14
4407	ŀ	30321	228		1.0E-99 AF098018.1	NT.	Homo sepiens fatty acid amide hydrolase (FAAH) gene, excn 14
5836	L		0.59			ᅜ	Homo septems cell recognition molecule Cespr2 (KIA40868), mRNA
8076	20180	33528	1.77		114	된	Horno sapiens glycine receptor, alpha 2 (GLRAZ), mRNA
820	20189		1.77	1.0E-89	11421007 NT	¥	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7346	25680		0.61		1.0E-99 X98022.1	7	H.sepiens E6-AP gene exem 2
9554	Ι.		0.86	1.05-99	11419721 NT	M	Hamo sapiens ALEX1 protein (LOC51309), mRNA
							IndOZNOZNI Scares_NFL_T_GBC_S1 Hamo septens cDNA clane IMAGE:2908371 3' straiter to TR:002711
878	22831	36285	1.89		1.0E-89 AW340174.1	EST_HUMAN	O02711 PRO-POL-DUTPASE POLYPROTEIN;
11473	1_	]	1.89		7427514 NT	¥	Horno sapiens hundingtin Interacting protein 1 (HIP1), mRNA
11473	24416		1.89		7427514 NT	¥	Homo sepiens huntingtin Interacting protein 1 (HIP1), mRNA
11705					1.0E-69 AB023222.1	¥	Homo sapiens mRNA for KIAA1005 protein, partial ods
							Homo saplens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
12253	25079		90.0		1.0E-99 AF240786.1	뒫	genes, complete cds
-	13123	26021	1.83		1.0E-100 AL163247.2	۲	Homo seplens chromosome 21 segment HS210047
2	13123		1.19		1.0E-100 AL163247.2	¥	Humo sepiens chromosome 21 segment HS210047

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Table 4
Single Exon Probes Expressed in Bone Marrow

Ingle Exoli Flobes Explessed III Dolle Mallow	Top Hit Descriptor	Homo sepiens Testis-specific XK-related protein on Y (XKRY), mRNA	Hamo septems Testis-specific XK-related protein on Y (XKRY), mRNA	xv/8b11x1 NCI_CGAP_Bm63 Homo saplens cDNA clone IMAGE:2824605 3'	Hamo sapiens chromosome 21 segment HS21C006	Homo sepiens chromosome 21 segment HS21C049	EST02975 Fetal brain, Stratagene (cat#636206) Homo sapiens cDNA clone HFBCR32	Homo sepiens X-linked enhidrotitic ectodermal dysplasia protein gene (EDA), excn 2 and flanking repeat rectors	G confile DNA for ZNF80 cene homolog	RC3-HT0625-040500-022-b09 HT0625 Homo sapiens cDNA	Homo septiens DKFZP588M0122 protein (DKFZP588M0122), mRNA	Homo sepiens DKFZP586M0122 protein (DKFZP586M0122), mRNA	UI-H-BI1-efik-607-0-UI.s1 NCI_CGAP_Sub3 Hamo sepiens dDNA clane IMAGE:2722164 3'	qf62709.xf Soeres_testis_NHT Hamo septens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA	Periori Cystatin;	Homo sapiens mRNA for KIAA1168 protein, partial cds	Rat mRNA for short type PB-cadherin, complete cds	Homo septens KIAA0957 protein (KIAA0957), mRNA	Homo sapiens RGH2 gene, retrovhus-like element	Homo sapiens myotubutarin-related protein 1a mRNA, partial cds	Homo sepiens folicle stimulating harmone receptor (FSHR) mRNA	Homo sapiens small optic lobes (Drosophila) homotog (SOLH) mRNA	Homo sapiens smell aptic lobes (Drosophila) homolog (SOLH) mRNA	601863164F1 NIH_MGC_67 Hamo septens cDNA clane IMAGE:4080699 67	xa82701.x1 NG_CGAP_CML1 Hamo septens cDNA clone IMACE:2573305 3' similar to gb:X12433	PROTEIN PHPS1-2 (HUMAN);	AU118182 HEMBA1 Hamo sepiens cDNA clane HEMBA1003046 5	Homo septiems NF-E2-related factor 3 gene, complete cds	Human mRNA for plasma inter-alpha-trypsin Inhibitor heavy chain H(3)	Homo saplens ER to nucleus signalling 1 (ERN1) mRNA	Homo sepiens ER to nucleus signelling 1 (ERN1) mRNA	Homo septens hect domain and RLD 2 (HERC2), mRNA	AU140214 PLACE2 Homo septens cDNA clone PLACE2000137 5	AU136800 PLACE1 Hamo sepiens cDNA clane PLACE1005089 5"
ZOII FIODES EX	Top Hit Detathese Source			T_HUMAN	H IN	H] IN	EST_HUMAN E	I &		T HUMAN			T_HUMAN		HUMAN	H	NT K		H	H NT				HUMAN		HUMAN	EST_HUMAN A	H						EST_HUMAN A
Aligie I	Top Hit Acession No.	11418230 NT	11418230 NT	1.0E-100 AWZ75237.1	1.0E-100 AL163206.2	2		•		_	361685	7861685 NT	1.0E-100 AW207655.1			.1		11418976]NT		1	4503782 NT	5032104	5032104 NT	Ţ		2	1	1	(14690.1	4567568 NT	4557568	5729867 NT	1	
	Most Similar (Top) Hit BLAST E Value	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100 AL 163249.	1.0E-100 T05087.1	4 0E-400 AE003538	1 0F-100 X89631 1	1.0E-100 BE180609.	1.0E-100	1.0E-100	1.0E-100		1.0E-100	1.0E-100 AB032994	1.0E-100 D83349.1	1.0E-100	1.0E-100 D11078.1	1.0E-100 AF057354.	1.0E-100	1.0E-100	1.0E-100	1.0E-100 BF244218.		1.0E-100/	1.0E-100 AU118182	1.0E-100 AF135116.	1.0E-100 X14690.1	1.0E-100	1.0E-100	1.0E-100	1.0E-100/	1.0E-100 AU136800.
	Expression Signal	1.3	1.3	79.0	2.62	96'0	2.53	92.6	48	4.1	4.33	4.33	1.23		1.49	0.98	1.25	1.98	3.1	1.48	1.94	3.58	3.58	1.71		99.0	1.6	1.29	6.0	0.89	0.89	1.1	4.85	0.81
	ORF SEQ ID NO:	28106	20106	28128	26197						27017	27018				27906		28728		30154	30172	31012	31013	31338		31850	69028	32113	21228	35228	32596		828Z8	33039
	SEQ D	13187	13187	13203	13272	13409	13432	49544	13583	13581	14067	14057	14582		14588	14908	15268	15711	16089	17267	17283	18136	18136	18467		18682	18877	18929	19023	18359	18359	19636	19703	19780
	Probe SEQ ID NO:	88	88	87	170	317	343	267	8	510	1024	1021	1540	,	- - - - - - - - - - - - - - - - - - -	1881	2264	2717	3031	4238	4284	2127	5127	2985		5586	9829	5839	2882	2829	2829	9299	6846	6704

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Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor	y38c08.s1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134 3'	Homo sepiens Rho GTP asse activating protein 6 (ARHGAP6), transcript variant 4, mixiva	ae33b08.r1 Gessler Wilms turnor Homo sepiens cDNA clone IMAGE:897387 5' similar to 1R:G487418 G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN.;	accisbo8.rl Gessler Wilms tumor Homo sepiens cDNA clone IMAGE:897587 5' similar to TR:G487418	G487418 ACLIN FILAMEN I FASSOCIALED FROTEIN.;	MKT-I NUORG-DOUG-UG-OCO I NOUGO FIGURO SERVERO CATAN	TI-INCAR-CROBUCC-CUR-DOD INCOME DESIGN COLOR	Human mKNA for kaney epidemen grown racial (COT) presules	Homo sapiens Kad50 (Kad50) mKNA, complete dos	Homo sapiens Kad50 (Kad50) mKNA, compliand cus	601647357F1 NIH_MGC_61 Hamo sapiens CDNA clone IMACHE3831310 o	Homo sepiens chromosome 21 segment HS210003	AU116851 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5	AU116951 HEMBA1 Hamo sapiens aDNA clane HEMBA1000343 6	Homo sapiens mRNA for KIAA1485 protein, partial cds	wr37g09.x1 NCI_CGAP_Pr28 Homo espiens cDNA chone IMAGE:2489620 3" similar to contains element	MER22 repetitive element;	PAID-BN0065-100300-001-c06 BN0066 Homo septems cDNA	AU127720 NT2RP2 Hamo septens CDNA clone NT2RP2001918 5	Homo sepiens mRNA for KIAA1628 protein, pertial cds	Homo sapiens mRNA for KIAA1626 protein, partial cds	hhasc11.y1 NCI_CGAP_GU1 Hamo sapiens cDNA clone IMACE:23085395 b	hh83c11.y1 NCI_CGAP_GU1 Hamo sepiens aDNA clane IMAGE::2868396 o	AV732101 HTF Hamo sepiens dDNA dane HTFBIG01 5	802020554F1 NCI_CGAP_Bm67 Homo saplens cDNA clone IMAGE:4136163 5	Human andogancus retrovirus HERV-K, pd gane	MR0-BN0070-270300-008-h11 BN0070 Hamo saplens cDNA	H.sapiens CD97 gene exon 4	H.sapiens CD97 gene excn 4	Homo sapiens 14q32 Jegged2 gene, complete cds; and unknown gene	Homo sepiens 14q32 Jegged2 gene, complete cds; and unknown gene	Homo sepiens chromosome 21 segment HS210047	Homo sapiens gogin-like protein (GLP) gene, complete cds
Top Hit Detablese Source	EST_HUMAN M		EST HUMAN G	Т	┪	7	HOMAN			П	EST_HUMAN 6		EST_HUMAN A		T F	Г	EST HUMAN IN	EST_HUMAN P	T_HUMAN		NT IN			EST_HUMAN /	EST HUMAN		EST_HUMAN N		NT	IN	- LN		<u> </u>
Top Hit Acession No.		7382479 NT	1 0F-100 AA496841.1		_	-	_		-		-	2	AU116951.1	1.0E-100 AU116951.1	1.0E-100 AB040918.1		1.0E-100 A1972388.1	AW998611.1	1.0E-100 AU127720.1	1.0E-100 AB046846.1	1.0E-100 AB046848.1	1.0E-100 AW630487.1		1.0E-100 AV732101.1	1.0E-100 BF347519.1	1.0E-100 Y10391.1	1.0E-100 BF327292.1	1.0E-100 X94633.1	1.0E-100 X94633.1	1.0E-100 AF111170.3	1.0E-100 AF111170.3	1.0E-100 AL163247.2	1.0E-100 AF286285.1
Most Similar (Top) Hit BLAST E Value	1.0E-100 R10887.1	1.0E-100	1 05-100		1.0E-100 AA496841	1.0E-100	1.0E-100 BF378478.	1.0E-100 X04571.1	1.0E-100 U63139.1	1.0E-100 U63139.1	1.0E-100 BF103853	1.0E-100	1.05-100	1.0E-100	1.0E-100		1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100		1.0E-100
Expression Signal	1.36	1.08	86		0.96	1.12	1.12	6.82	0.62	0.52	11.86	5.3	0.59	0.59	3.34		24	202	1.06	228	220	1.47	1.47	0.48	2	1.58	7.51	1.78	1.78	3.57		1.96	2
ORF SEQ ID NO:	33190	33478	33462	3	33463	33401	33402	33410	34323	34324	35266		35763					34511		36331	36332		L	36764			37593			L			
SEQ ID	19896	L	<u>.</u>	. 1	20145	20062	20082	l	20929	l		L	L		1		22822		_		Į.	1_	L	┸		L	1_			_			Ш
Probe SEQ ID NO:	8843	7500	9	812	7019	2070	82 82	7078	0882	7880	8877	200	8920	880	8850		8	0788	8842	8942	8042	10203	10203	10384	10836	10024	1111	11618	11618	1681	188	11712	11989

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Single Exon Probes Expressed in Bone Marrow

ingle Exon Proces Expressed in Bone Marrow	Top Hit Descriptor	Homo sepiens obase gene, exan 12	601588031F1 NIH_MGC_7 Homo sepiens cDNA done IMAGE:3940423 5	Homo septions gluteritione S-transferase finds 2 (GSTT2) and gluteritione S-transferase theta 1 (GSTT1) genes, complete cds	7q88h03.x1 NCJ_CGAP_Lu24 Homo sepiens cDNA clone IMAGE: 3' similar to TR:Q21897 Q21897 COSMID R151, [2] TR:Q9UA08;	Homo saplens SHS-domain binding protein 1 (SH3BP1), mRNA	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA	Homo espiens SEC14 (S. cerevisiae) like 2 (SEC14L2), mRNA	Homo sapiens SEC14 (S. cerevisiae)-Ilie 2 (SEC14L2), mRNA	Homo sapiens mRNA for KIAA0448 protein, partial cds	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA	Homo saplers pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo septiens phosphoribosylghydnamide formyltransferase, phosphoribosylghydnamide synthetase, phosphoribosylghydnamide synthetase, phosphoribosylghydnamide synthetase, (GART) mRNA.	Homo saplens of cardiac alcha-myosin heavy chain gene	602156474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297291 5	ag89e09.x1 Soares_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:1843336 3'	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA	Homo saplens butyrophilin, subfamily 2, member A1 (BTN/2A1), mRNA	Homo sapiens KIAA0589 gene product (KIAA0589), mRNA	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	Homo saptens carboxypeptidase A1 (pencreatic) (CPA1) mRNA	RC3-ST0281-160600-016-h09 ST0281 Hamo saplens cDNA	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA	H.sapiens EWS gene, excn 5	Homo sepiens RIBIR gene (partial), excm 12	Homo sapiens RiBilR gene (partial), exan 12	Homo sapiens genomic downstream Rhesus box	Homo sapiens gamma-glutamytransferase 1 (GGT1) mRNA	601458631F1 NIH_MGC_66 Hamo sapiens cDNA clone IMAGE:3862086 5	EST377629 MAGE resequences, MAGI Homo sepiens cDNA	Homo sapiens RIBIIR gene (pertial), exon 12
XOII FIODES E	Top Hit Database Source	Ę	EST_HUMAN	Ę	EST HUMAN											T_HUMAN	EST_HUMAN o	_					T_HUMAN		± N	NT TN	NT TN	N			EST_HUMAN E	
aelBuic	Top Hit Acession No.	AJ131034.1	<b>-</b>	¥-:	•	11545732 NT	11417974 NT	7110714 NT	7110714 NT	1.0E-101 AB007815.2	7110734 NT	7110734 NT	7857454 NT	4503914 NT		Ĺ		5921460 NT	5921460 P	7862183 NT	7862183 NT	4502996 NT	BE843070.1	5729892 NT					4885270 NT		_	
	Most Similar (Top) Hit BLAST E Vatue	1.0E-100	1.0E-100 BE791491	1.0E-100 AF240786.	1.0E-100 BF448548	1.0E-100	1.0E-100	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101 Z20656.1	1.0E-101 BF681218.	1.0E-101 AI221878.1	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101 AJ237744.	1.0E-101 AJ237744.1	1.0E-101 AL252312.1	1.0E-101	1.0E-101 BF035327.	1.0E-101 AW965556.	1.0E-101
	Expression Signal	3.03	1.65	15.03	232	2.58	8.6	1.19	1.19	2.63	6.85	6.85	1.48	288	12	7.23	0.78	1.34	1.34	1.12	1.12	1.58	1.07	1.17	6.3	2.07	207	13.42	1.69	2.49	1.73	203
	ORF SEQ ID NO:	00986	38601	22986		31789	31691	26118	26119	28676	26702	26703	26776	26868	28929	26994	27051	27594	27595	27778	zm	27987	28107	28387	28646	28763	28764		29194		29367	28763
	Exan SEQ ID NO:	24996	24997	25025	25851	25233	25015	13195	13196	13750	13767	13767	13831	13910	13977	14038	14101	14619	14819	14790	14790	14984	15089	15891	15621	15745	15745	16025	16271	16309	1644	15745
	Probe SEQ ID NO:	12127	12128	12177	12307	12488	13084	78	78	687	705	705	772	854	924	186	1055	1586	1586	1761	1761	1962	2072	2357	2622	2763	2753	2967	3216	3255	3382	841

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Top Hit Database Source	Homo sapiens RIBIIR gene (partial), exon 12	Homo sepiens ASHZL gane, complete cds, similar to Drosophila ash2 gane	Homo sepiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA	HUMAN EST377212 MAGE resequences, MAGI Homo septens cDNA	Homo sepiens cytopiesmic finker 2 (CYLN2), mRNA	Homo sepiens cytoplesmic finker 2 (CYLN2), mRNA	Homo sepiens carbonic anhydrase VII (CA7), mRNA	Homo sepiens hypothetical protein FLJ22087 (FLJ22087), mRNA	Homo sepiens Kruppel-type zho finger protein (PEC3) mRNA, alternative spiloe form 4, partial cds	Homo espiens Kruppel-type zho finger protein (PEG3) mRNA, alternative splice form 4, partial cds	EST_HUMAN   wA55f12.x1 NCL_CGAP_Ges4 Homo septems cDNA clone IMAGE:2833487 3'	Г	EST_HUMAN RC1-BT0313-220700-018-f12 BT0313 Homo septens cDNA	EST_HUMAN   601121621F1 NIH_MGC_20 Homo septens cDNA chare IMAGE:3345899 6	EST_HUMAN 601121621F1 NIH_MGC_20 Homo septens oDNA clone IMAGE:3345888 5	EST_HUMAN   601764686F1 NIH_MGC_63 Homo septens cDNA clane IMAGE:3996837 5	ht/14g10.y1 NCI_CGAP_GU1 Homo septens cDNA done IMAGE:2868578 & striller to gb:J03143 EST_HUMAN INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);	hin74g10,y1 NCI_CGAP_GU1 Home sepiens cDNA clone IMAGE:288678 6' striiter to gb:J03143 EST_HUMAN INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);	EST_HUMAN PIR:S54640 S54640 YD8335.03c protein - yeast;	Home expiens mRNA for KIAA1351 protein, pertial ods	Homo septens mRNA for KIAA1351 protein, pertital cds	Human mRNA for pancreatic gamma-glutamytransferase	Humen mRNA for pencreate gamma-glutamytransferase	Homo septens gamma-glutamytransferase 1 (GGT1), transcript variant 3, mRNA	HUMAN 601472808T1 NIH_MGC_68 Homo septens cDNA clone IMAGE:38759533'	EST HUMAN 601472808T1 NIH_MGC_68 Hamo septens dDNA dane IMAGE:3876963 3'	Homo sepiens potassium channel, subfamily K, member 10 (KCNK10), mRNA	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA	LEST_HUMAN KERATIN, TYPE I CYTCGKELETAL 18 (HUMAN);
	Ę	ž	5921460 NT	<b>N</b>	اـــا	7427512 NT	7427512 NT	34 NT	780 NT	N	Ā	EST	EST	EST	EST	EST	EST	EST	EST	EST	토	¥	¥	Ŋ	9845492 NT	EST	EST	10863960 NT	11420127 NT	EST
Top Hit Acessian No.	1.0E-101 AJZ37744.1	1.0E-101 AB02Z785.1	59214	F924460 NT	AW965139.1	74275	74275	11430734 NT	11545780 NT	1.0E-101 AF208970.1	1.0E-101 AF208970.1	1.0E-101 AW008475.1	1.0E-101 BE267384.1	1.0E-101 BF330759.1	1.0E-101 BE275821.1	1.0E-101 BE275821.1	1.0E-101 BF029174.1	1.0E-101 AW630070.1	1.0E-101 AW630070.1	1.0E-101 AA036800.1	AB037772.1	1.0E-101 AB037772.1	X60069.1	X60069.1	98454	1.0E-101 BE619667.1	BE619667.1	10863		1.0E-101 AI570283.1
Most Similar (Top) Hit BLAST E Vatue	1.0E-101	1.0E-101	1.0E-101	1.0E-101		1.05-101	1.0E-101	1.0E-101	1.05-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.05-101	1.0E-101	1.0E-101	1.05-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101 X60069.1	1.0E-101 X60069.1	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	_
Expression	203	4.58	1.54	1.54	2.08	3.69	3.59	1.16	1.18	4.82	4.82	7.39	1.78	6.3	1.07	1.07	6.11	0.83	0.83	0.83	0.82	0.82	19.42	19.42	18.13	13.91	13.91	0.61	1,98	0.56
ORF SEQ ID NO:	28782	29839	30983	30864	31371	32420	32421	33202		33863	33864	34040		34327	34621	34622	34766	35053	35054	35768	36094	36095	34544			36520	36521	L		
SEQ ID	15745	16830	18082	18082	18 28 28	19198	19196	19806	20453	20505	20505	20674	20774	20832	21214	21214	21359	21683	21653	22329	22638	22638	24139	21139	82923	23041	23041	23179	23694	23728
Probe SEQ ID NO:	3411	3880	5072	5072	339	6118	6118	8853	7488	7542	7542	7117	8282	2882	8245	8246	888	888	\$6	9364	9885	5886	7186	9817	9838	1916	10115	10254	10773	10807

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Table 4
Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	1677411.x1 NCI_CGAP_Ges4 Homo sepiens oDNA cione IMAGE:2184309 3' similer to gb:M28328 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);	601680823F1 NIH_MGC_83 Hamo sapiens aDNA dane IMAGE:3950887 5	601680825F1 NIH_MGC_83 Homo capiens cDNA clone IMAGE:3950887 5	branched-chain aipha-leab acid dehydrogenase complex E1 alpha subunit [human, Genomic, 195 nt, seconant 8 of oi	organists or of	CO 125/25 Bottle marrow from Septems during a semiliar to detection 1	QVI-U tube-zauzubas-eut D tube frants septers u.m.	Homo sapiens phosphatidy(inosital 4-kinase 230 (p/4K230) mRNA, complete cds	Homo sepiens chromosome 21 segment HS21C103	Homo sepiens down-regulated in edenoma (DRA) mRNA	Human endogenous retroviral DNA (4-1), complete retroviral segment	Homo sepiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA	Homo septens solute center family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA	601288982F1 NIH_MGC_21 Homo septems cDNA done IMAGE:3629801 5	am60c10.x1 Johnston frontal contex Homo septens cDNA done IMAGE:1539954 3' similar to	SW:GC86_HUMAN Q08379 GOLGIN-95.;	em60c10.x1 Johnston frontal contex Homo sapiens cDNA clone IMAGE:1538954 3' similær to	SW:GC885_HUMAN Q08379 GOLGIN-85;	Homo sepiens PRKY excn 7	Homo sepiens KIAA0187 gene product (KIAA0187), mRNA	AU141005 PLACE4 Hamp septems aDNA dane PLACE4000650 5"	AU141005 PLACE4 Homo sapiens cDNA done PLACE4000850 5	Homo sapiens chromosome 21 segment HS21C007	601107843F1 NIH_MGC_16 Homo septens cDNA clone IMAGE:3343882 5	y32c04.r1 Scares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140834 5	Homo saplens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, excn 7	Homo septems HSC54 mRNA for heat shock cognate protein 54, complete ods	Homo sapiens histone deacetylase 7 (HDACT), mRNA	Homo sepiens histone deacetylass 7 (HDAC7), mRNA	Homo septems hect domain and RLD 2 (HERC2), mRNA	ar62709.x1 Barsteed colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' sertiler to TR:Q13137 Q13137 NDP62.;	UI-H-BIS-6[1-4-10-0-UI.srl NCI_CGAP_Sub5 Hamo sapiens cDNA clone IMAGE:2736835 3'
	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	Ę	T	T	LHOWAN	Į,			NT	¥		EST_HUMAN		EST_HUMAN		EST_HUMAN	NT		EST_HUMAN	EST_HUMAN	F	EST_HUMAN	EST_HUMAN	¥	N	ķ	¥	Z	T HUMAN	П
28.60	Top Hit Acessian No.	V570288.1	E973648.1	3E973648.1	4 200000	2002/1.1	1.0E-101 AA321316.1	W838051.1	F012872.1	L163303.2	4557534 NT	M0978.1	11437146 NT	11437146 NT	1.0E-102 BE408447.1		V1124699.1		VI124669.1	/13932.1	TN 979197	AU141005.1	\U141005.1	NL163207.2	3E251310.1	<b>366488.1</b>	AF067133.1	AB034951.1	7706398 NT	7705398 NT	11433046 NT		1.0E-102 AW451643.1
	Most Similar (Top) Hit BLAST E Vetue	1.0E-101 AI570283.1	1.0E-101 BE973648.	1.0E-101 BE973648.	700	1.05005 101-30.1	1.0E-101	1.0E-101 AW939051	1.0E-102 AF012872.1	1.0E-102 AL163303.2	1.0E-102	1.0E-102 M10978.1	1.0E-102	1.0E-102	1.0E-102		1.0E-102 A1124689.1		1.0E-102 AI124669.1	1.0E-102 Y13932.1	1.0E-102	1.0E-102	1.0E-102 AU141006.	1.0E-102 AL163207.2	1.0E-102 BE251310.	1.0E-102 R66488.1	1.0E-102 AF067133.	1.0E-102 AB034951.	1.0E-102	1.0E-102	1.0E-102	1.0E-102 Al459825.1	1.0E-102
	Expression Signal	0.56	0.64	0.0	8	8,3	162.1	7.64	0.73	5.2	1.07	4.8	227	227	200.41		1.36		1.36	67.0	1.48	3.24	3.24	1.83	1.95	+	1.52	3.3	3.45	3.45	96.0	2.74	0.5
	ORF SEQ ID NO:	37230	37349	37350	į	8/700	38650		26064	26351	26781	27114	27268	27269	27423		28352		28353		28047	28120	29121	30170	30358	31045	31460		32163		32169		
	Exan SEQ ID NO:	23728	23834	23834		241/8	24955	25387	13161	13430	13835	14163	14308	14308	14450		15329		16329	16095	16135	16207	16207	17289	17467	18167			L	Ľ	L	l _	
	Probe SEQ ID NO:	10807	10914	478		120	12083	12735	41	24	778	1119	1273	1273	1417		2318		2318	3037	3078	3150	3150	4260	444	5157	5445	5842	5882	2882	5880	6425	7283

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	Top Hit Descriptor	801581505F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831241 5	601277215F1 NIH_MGC_20 Homo septens dDNA clone IMACE=3618243 6	Homo sapiens mRNA for KIAA0960 protein, partial cds	Homo sepiens mRNA for Centeurin-alpha2 protein	AV710738 Cu Homo sepiens cDNA clone CuAAKD03 5	Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA	QV3-NT0025-210600-236-h08 NT0025 Homo sepiens cDNA	601501107F1 NIH_MGC_70 Hamo sapiens aDNA clane IMAGE:3903145 67	AV694817 GKC Hamo septems aDNA dane GKCEEF11 5"	AV894817 GKC Homo sapiens cDNA done GKCEEE11 5'	Homo sepiens mRNA for KIAA0454 protein, partial cds	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5	601283770F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3605536 5	w63b08x1 NCI_CGAP_Ktd12 Homo septens cDNA olone IMAGE:23979713' straiter to contains MER4.t1	MER4 MER4 repetitive element;	AV755842 BM Homo sepiens cDNA clone BMFAUD08 5	yd13d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5	yd 13d07,r1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5	AU124629 NT2RM4 Hamo sepiens cDNA clane NT2RM4000309 6"	Homo sepiens phospholipid scremblase 1 gene, excn 1 and 5 flanking region	Homo sepiens myomesh (M-protein) 2 (1651D) (MYOM2), mRNA	Homo septens myomestn (M-probain) 2 (165tid.) (MYOM2), mRNA	RC-BT074-260469-014 BT074 Homo sapiens cDNA	RC-BT074-280489-014 BT074 Homo sepiens cDNA	on57h04.s1 Scares_NFL_T_GBC_S1 Homo sapients cDNA clone IMAGE:1560823 3' shrifar to SW:CAV2_HUMAN P51636 CAVEOLN-2. [1] :	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA	Homo sapiens UDP giycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA	RC8-ET0072-150600-011-P01 ET0072 Homo seplens cDNA	Human chromosome 16 creatine transporter (SLO6A8) and (CDM) paralogous genes, complete cds	Human unconventional myosin-ID (MYO1F) gene, partial cds	Hamo sepiens chromosome 21 segment HS21C080	X07c12x1 NCI_CGAP_Co20 Homo sepiens cDNA clone IMAGE::2660038 3
	Top Hit Database Source	EST HUMAN 6	EST_HUMAN 6	NT F	H	THUMAN		EST_HUMAN C		EST_HUMAN A	EST_HUMAN A	TN TN	EST HUMAN 0		<b>&gt;</b>	EST_HUMAN N	EST_HUMAN /	EST_HUMAN Y	EST_HUMAN )	EST_HUMAN /	NT IN			EST HUMAN F	EST_HUMAN F	EST HUMAN			T_HUMAN	¥	NT.	IN TN	EST_HUMAN )
	Top Hit Acession No.	Ţ	1	1	1	1	10947053 NT	1.0E-102 BE783051.1	1	1	-	1	Ţ	-		1.0E-102 AI762859.1	-			.1	1.0E-102 AF153715.1	11425430 NT	11425430 NT		1.0E-102 AB05037.1	1.0E-102 AA970788.1	4507822 NT	4507822 NT	1.0E-102 BF359243.1	U41302.1	U57053.1	1.0E-102 AL163280.2	1.0E-102 AW300862.1
-	Most Similar (Top) Hit BLAST E Vatue	1.0E-102 BE729323.	1.0E-102 BE386108.	1.0E-102 AB023177.	1.0E-102 A.1238994.1	1.0E-102	1.0E-102	1.0E-102	1.0E-102 BE910555.	1.0E-102 AV694817.	1.0E-102 AV694817	1.0E-102 AB007823.	1.0E-102 BE388063.	1.0E-102 BE389063.		1.0E-102	1.0E-102 AV765842	1.0E-102 T70393.1	1.0E-102 T70383.1	1.0E-102 AU124829.	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102 U41302.1	1.0E-102 U57053.1	1.0E-102	1.0E-102
	Expression	0.75	0.77	0.54	8.85	264	0.58	3.61	0.94	122	122	0.74	0.73	0.73		0.56	0.80	2.15	2.16	3.86	0.71	0.43	0.43	က	3	1.15	236	2.36	2.7	4.74	5.67	2.49	4.15
	ORF SEQ ID NO:	33658	33693	33818	33889	34208	34505	34953	35035			35340	35679	35680		36062		36082		38163		37221	37222				37887						31746
	Een SEQ ID NO:	20314	20341	20459	20540	20830	21108	21533	21613	21806	21806	21916	22249	22249		22610		$\mathbf{I}_{-}$	22629	22707	23870	l	23719		23755	L					1_		25380
	Probe SEQ ID NO:	7343	7374	\$	7578	988/	8168	8565	8845	6838	6888	8950	8363	828		9096	888	929	9296	9768	10748	10798	10798	10835	10835	10806	11410	11410	11732	12019	12079	12182	12727

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID S	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Velue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
13028	26576		1.59	1.0E-102 J05235.1		NT	Human gamma-glutamyi transpeptidase mRNA, complete cds
2	13188	28107	4.14	1.0E-103	1.0E-103 BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Hamo septens cDNA dane IMAGE:3902305 5
٤	13188	28108	1.14	1.0E-103	1.0E-103 BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5
<del>2</del>	13216	28140	9.55	1.0E-103 D87078.2	D87078.2	NT	Homo septems mRNA for KIAA0235 protein, perital cds
88	13310		4.18	1.0E-103	5453793 NT	NT	Homo septens nuclecter protein (KKE/D repeat) (NOP55) mRNA
286	14033	28985	1.02	1.0E-103	1.0E-103 AJZ78348.1	Į	Homo septens mRNA for pregnancy-essociated plasma protein-E (PAPPE gene)
1248	14284		18.75		1	EST_HUMAN	601485368F1 NIH_MGC_69 Hamo septems cDNA clone IMAGE:3887878 67
1600	14632		2.39	1.0E-103	1.0E-103 AF012872.1	NT	Homo sepiens phosphatidylinosital 4-kinase 230 (pi4K230) mRNA, complete ods
1992	15013	28018	1.4	1.0E-103	4502428 NT	ΙN	Homo sepiens bane marphagenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
1992	15013	28019	1.4	1.0E-103	4502428 NT	M	Homo septems bane marphagenetic protein 8 (asteogenic protein 2) (BMP8) mRNA
2313	15325	81482	0.93	1.05-103		EST_HUMAN	AU134891 PLACE1 Homo sepiens aDNA dane PLACE1000985 5
2457	15461	28484	1.66	1.0E-103	1.0E-103 AF060668.1	NT	Homo saplens promyelocytic leukemia zinc fingar protein (PLZF) gene, complete cds
2801	15601	28622	1.07	1.05-103	1.0E-103 BF528379.1	EST_HUMAN	602041882F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4170429 5
2601	15801	28623	1.07	1.05-103	1.0E-103 BF528379.1	EST_HUMAN	602041882F1 NCI_CGAP_Bm67 Hamo sapiens cDNA clane IMAGE:4179429 5
26.7	15626	ORARO	5	1 0F=403 N32770 1	V82770 4	NAMILH TRE	we1d08.s1 Soares placents 8to6weeks 2NbHP8to6W Homp sapiens cDNA clone IMAGE:259599.3"
	1838			1.0E-103	1.0E-103 BE744722.1	EST HUMAN	601573113F1 NIH MGC 9 Hamo sepiens aDNA dane IMAGE:3834315 5
3391	16440	29368			1.0E-103 AW298245.1	EST HUMAN	UI-H-BWO-gt-h-11-0-UI.s1 NCI_CGAP_Sub6 Homo saplens cDNA clone IMAGE:2733165 3'
8453	16489				1.0E-103 AB040892.1	F	Homo sepiens mRNA for KIAA1459 protein, partial cds
3767	16805			L		TN	Macaca mulatta cyclophilin A mRNA, complete cds
				1	,		ab10d12.s1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:840407.3' stmilar to contains
88	5 8 8 8			1	_	ESI HUMAN	GENERAL LIKTO I ESPECIOVE GENERALI,
384	1889			_1	114308/6 N	N.	THIRD SQUARES INSTRUCTION IN THE PARTY OF TH
4628 828	17087			1.0E-103 T23683.1	123683.1	ESI HUMAN	SECTION DATES AND THE SECTION SECTION SECTION OF THE PARTICULAR SECTION OF THE SE
4858	17875		0.83	1.0E-103	1.0E-103 BE900203.1	EST HUMAN	6016/3135F1 NIH_MGC_Z1 Hamo sapiens attiva ciane imala=33603603 0
8044	19126	32332	96.0		1.0E-103 BF569527.1	EST_HUMAN	602186023F1 NIH_MGC_45 Hamo eaplens cDNA clane IMAGE:4310573 5
6062	19133	32342	1.67	1.0E-103	1.0E-103 AF179995.1	NT	Homo septens septin 2 (SEP2) mRNA, partial cds
8888	19466	32712	0.73	1.0E-103	11435053 NT	N	Homo sepiens KJAA0440 protein (KJAA0440), mRNA
8889	19466	32713	0.73		11435053 NT	¥	Homo sepiens KIAA0440 protein (KIAA0440), mRNA
6602	19661				1.0E-103 AW954568.1	EST_HUMAN	EST388838 MAGE resequences, MAGC Homo septens cDNA
6602	19681				AW964	EST_HUMAN	EST366636 MAGE resequences, MAGC Homo septems cDNA
6847	19705				10947051	Z.	Homo sepiens entyrin 2, neuronal (ANK2), transcript variant 1, mRNA
6746	25867				_	EST_HUMAN	aj28e03.s1 Sogres_testis_NHT Homo sapiens CDNA clone 1391452.3
6787	19842	33125	0.98		1.0E-103 AF053460.1	F	Homo sepiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4

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igie Extil Flobes Extra esseu III Dolle Mail Ow	Top Hit Descriptor	tm58k05x1 NCI_CGAP_Bm25 Homo sepiens cDNA done IMAGE-2162289 3' sémiler to TR-Q13769 Q13769 ANONYMOUS. ;	tin58b05.x1 NCL_CGAP_Bm25 Hamo sepiens cDNA clane IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS. ;	Homo sepiens dystrophin (muscular dystrophy, Duchenne and Becker types), Includes DXS142, DXS164, DXS208, DXS230, DXS239, DXS289, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA	Homo septiens dystrophin (muscular dystrophy, Ducherne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS288, DXS289, DXS270, DXS272 (DMD), transcript variant Dp427m,	mRVA	Hamo sepiens ribosomel protein L3-like (RPLSL), mRNA	Homo sepiens KIAA0851 gene (pertial), XT3 gene and LZTFL1 gene	EST377849 MAGE resequences, MAGI Homo septems cDNA	601571537F1 NIH_MGC_65 Hamo septens aDNA clane IMAGE:3838545 67	tm38b05.x1 NCI_CGAP_Bm25 Homo sepiens dDNA done IMAGE:2162289 3' similar to TR:Q13789 0133780 ANONYMOLIS	TO ALL THE COLOR OF THE COLOR O	tmbedocat NCI_CCAPBm26 Homo septens canna come invice-2162289 3 similer to incut 3769 Q13789 ANONTAROUS.;	EST27193 Human Brain Homo saplens cDNA 5' end similar to None	AU140344 PLACE2 Homo septens cDNA clone PLACE2000374 5	AU140344 PLACE2 Hamo sapiens aDNA clane PLACE2000374 5	7180603.X1 Scenes_NSF_F8_9W_OT_PA_P_S1 Homo septens cDNA clone IMAGE:3525984.3" striller to SW-PTNF HUMAN 0.16825 PROTEIN_TYROSINE PHOSPHATASE D1 :	Homo septens triple functional domain (PTPRF Interacting) (TRIO), mRNA	Homo sepiens triple functional domain (PTPRF Interacting) (TRIO), mRNA	nd13c02.s1 NCI_CGAP_Ov1 Homo septens cDNA clone IMAGE:800162 3' similar to gb:1.02426 28S PROTEASE SUBUNIT 4 (HUMAN);	ae84d12.s1 Stratagene schizo brein S11 Homo sapiens cDNA clone IMAGE:970871 3' stmiler to gb:X03747_cds1 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-1 (HUMAN);	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)	EST376749 WAGE resequences, WAGH Homo sapiens cDNA	au § 1904. y 1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE 22518326 5' similar to TR: 015046 015046 KJAA0338;
KOII FIOUGS EX	Top Hit Database Source	EST_HUMAN Q1	EST_HUMAN Q1						EST_HUMAN ES	EST_HUMAN 60	E C	T	EST_HUMAN Q	EST_HUMAN ES	EST_HUMAN. AL	EST_HUMAN A		Y SHOT		HUMAN			EST HUMAN E	
Single	Top Hit Acession No.	1.0E-103 Al590071.1		6082282 NT		5032282 NT	11431100 NT		1.0E-103 AW965778.1	1.0E-103 BE748158.1		1.UE-103 AIBSUO/ 1.1	1.0E-103 AI590071.1		1.0E-103 AU140344.1	L		1.0E-103 8005821	6005921 NT	1.0E-103 AA581088.1		-	19.1	
	Most Similar (Top) Hit BLAST E Value	1.0E-103	1.0E-103	1.05-103		1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	20, 10,	3030:	1.0E-103	1.0E-103 T31080.1	1.05-103	1.0E-103	4 05 400	1.0E-103	1.0E-103	1.05-103	1.0E-103	1.0E-103 Z37976.1	1.05-103	1.0E-103
	Expression Signal	1.47	1.47	£.7		1.73	1.62	1.06	2.68	3.47	8	3.08	3.69	0.43	0.92	0.92	8,	288	288	1.43	0.48	128	1.81	10.03
	ORF SEQ ID NO:	33229	33230			31276	18218	33589	33768	ŀ		40242	34385		35359	35360	06444	35865	35866			L		
	Exen SEQ ID NO:	19931		18356		18356	18393	20255	20404	20519	1	20988	20888	21600	21834	21834	1	22427	22427		1		L	1 1
	Probe SEQ ID NO:	6879	6879	7024		7024	7181	7234	7437	7558		င်ဂွန	8051	8632	8888	8968	73.00	9463	9463	858	7758	10418	10459	10598

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Deliabase Source	Top Hit Descriptor
11004	23970	37494	1.64	1.0E-103	1.0E-103 BE549708.1	EST_HUMAN	7b41f03.x1 NCI_CGAP_LL24 Home sepiens cDNA clone IMAGE:3230813 3' similer to gb:M69043 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN (HUMAN);
11085	24046	37568	3.89	1.0E-103	1.0E-103 AI792758.1	EST_HUMAN	obzatočijá NCI_CGAP_LLIS Hamo seplens cDNA clone INAGE:1522283 5' stritler to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
11183				1,0E-103	11424061 NT	F	Homo expiens AXL receptor tyrosine Idnase (AXL), mRNA
11183			1.89	1.0E-103	11424061 NT	¥	Homo sepiens AXL receptor tyrosine kinase (AXL), mRNA
11341	24291		1.48	1.0E-103	1.0E-103 BE671418.1	EST HUMAN	7e50f08.x1 NCI_CGAP_LL24 Homo sepiens cDNA clone IMAGE:3285927 3' shrifer to gb:,405272 INOSINE- 5-MONOPHOSPHATE DEHYDROGENASE 1 (HUMAN);
11570		38066	9	1.0E-103	1.0E-103 BE886279.1	EST_HUMAN	601506347F1 NIH_MGC_71 Homo septems cDNA clone IMAGE:3908147 67
11702			2.59	1.0E-103	1.0E-103 AU138283.1	EST_HUMAN	AU136283 PLACE1 Homo sepiems cDNA clone PLACE1003923 5
11774	23929	37450	79.7	1.0E-103 LA3610.1	L43610.1	Ę	Homo espiens polycystic kidney disease (PKD1) gene, exone 27-30
11980	24857		1.47	1.0E-103	1.0E-103 AB024759.1	NT	Hamo sepiens TSA305 gene, exan 16
12047		38516	2.25	1.0E-103	1.0E-103 BE644611.1	EST_HUMAN	7e88er10.x1 Sceres_NSF_FB_9W_OT_PA_P_S1 Homo septens cDNA clone IMAGE:3287810 S' struiter to contains MER29.t3 MER29 repetitive element;
4.2.78	25026		88	4 OF 403	1 DE. 103 AF224689 1	Ę	Homo sapiens mannosidase, beta A, fysosomei (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) censes, complete case
12208	Т.		1.85	1.0E-103	11528291 NT	E	Homo sepiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12410	25183	31820	4.32	1.0E-103	1.0E-103 AB011399.1	F	Homo sepiens gene for AF-8, complete cds
238	13338	28280	1.65	1.0E-104	1.0E-104 AL037549.3	EST_HUMAN	DKFZp564H1072_r1 584 (synanym: httpx2) Hamo saptens cONA clane DKFZp564H1072 5
88	13336		1.65	1.0E-104	1.0E-104 AL037549.3	EST_HUMAN	DKFZp584H1072_r1 584 (synanym: http:// Hamo saptens cDNA clane DKFZp584H1072 5
1905	14929		1.86	1.0E-104	4502428 NT	M	Homo sapiens bane marphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2203	15218	28238	252	1.0E-104	1.0E-104 AA132975.1	EST HUMAN	zo22o06.s1 Strategene colon (#637204) Homo septems cDNA clone IMAGE:567626 3' similar to gb.Z14116_ma1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
27.4	L			1.0E-104	1.0E-104 BE744828.1	EST_HUMAN	801577480F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926438 5
7752				1.0E-104	1.0E-104 BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sepiens cDNA
72277	15385		1.02	1.0E-104	BF334221.1	<b>EST_HUMAN</b>	RC1-CT0249-110900-214-f12 CT0249 Homo saplens cDNA
2444	15450		2.43	1.0E-104	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2882	15941	23858	7.18	1.0E-104	1.0E-104 M34671.1	M	Human lymphocytic antigen CDS9MEM43 mRNA, complete ods
2927	15985		2.84	1.0E-104 Y11151.1	Y11151.1	LN.	H.sapiens gene encoding phenylpyruvate fautomerase II
8277	16831	29252	16.0	1.0E-104	1.0E-104 AU133828.1	EST_HUMAN	AU133926 OVARC1 Hamo sapiens cDNA clone OVARC1000936 5
3402	16451		1.88	1.0E-104	1.0E-104 AA319436.1	EST HUMAN	EST21668 Adrenel gland tumor Homo sepiens cDNA 6' end
3615				1.0E-104	1.0E-104 AB033102.1	¥	Homo sepiens mRNA for KIAA1276 protein, partial cds
3615		29578		1.0E-104	1.0E-104 AB033102.1	Ę	Homo sepiens mRNA for KIAA1276 protein, partial cds
3863	17003		0.94	1.0E-104	1.0E-104 AB032998.1	Ę	Homo sepiens mRNA for KIAA1172 protein, partial cots

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Probe SEO IO NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vetue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10808	23729	37231	5.11	1.0E-104	1.0E-104 AU130765.1	EST_HUMAN	AU130765 NTZRP3 Homo sepiens cDNA clone NTZRP3001398 57
10917	23837	37353	4.5	1.0E-104	1.0E-104 U68535.1	NT	Human beta4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25
10831	13851		0.82	1.0E-104	11427757 NT	TN	Homo septens KIAA0649 gene product (KIAA0649), mRNA
11629	24567	38129	3.00	1.0E-104	1.0E-104 BE720191.1	EST_HUMAN	RCO-HT0885-310700-021-b09 HT0885 Homo septens cDNA
11629	24567	38130	3.09	1.0E-104	1.0E-104 BE720191.1	EST_HUMAN	RC0-HT0885-310700-021-b09 HT0885 Homo septens cDNA
11658	24592	38165	3.48	1.0E-104	1	EST_HUMAN	602141215F1 NIH_MGC_46 Hamo sapiens cDNA clane IMAGE-4302507 5
12888	25548		1.43	1.0E-104	1.0E-104 BE383882.1	EST_HUMAN	601312181F1 NIH_MGC_44 Hamo sapiens cDNA clone IMAGE:3658676 5
278	15810	26302	1.61	1.0E-105	4502166 NT	¥	Homo sepiens emyloid beta (A4) precursor protein (protesse nextin-II, Abzheimer disease) (APP), mRNA
425	13120	28018	878	1.0E-105		¥	Homo sepiens Meist (mouse) hamolog (MEIS1) mRNA
989	13863	28578	3.89	1.0E-105	1.0E-105 AF032897.1	NT	Homo septens potassium channel subunit (HERG-3) mRNA, complete cds
<b>8</b> 8	13683	77832	3.89	1.0E-105	1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1689	14720		233	1.0E-105	1.0E-105 AB020981.1	ĮN.	Hamo sepiens mRNA for cyclin B2, complete ods
1837	14884	27862	1.47	1.0E-105	1.0E-105 AL 163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1943	14967	27964	2.09	1.0E-105 D50918.1		TA	Human mRNA for KIAA0128 gene, partial cds
2189	15214	28234	2	1.0E-105	1	EST_HUMAN	EST20609 Spieen I Homo sapiens cDNA 5 end similar to autoimmune antigen Ku, p70/p80 subunit
2731	15726		1.07	1.0E-105	1.0E-105 AA584808.1	EST_HUMAN	no10d05.s1 NCI_CGAP_Phet Hamo sepiens cDNA clane IMAGE:1100265 3'
3018	16076		3.14	1.0E-105	1.0E-105 AJ229041.1	TN	Homo sapiens 959 lib contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3362	18412	22336	1.11	1.0E-105	7304922 NT		Homo sepiens bromodomein edjacent to zho finger domain, 28 (BAZ2B), mRNA
3362	16412	29337	1.11	1.0E-105	304922		Homo septens bromodomain adjacent to zinc finger domain, 28 (BAZ2B), mRNA
4125	17158	30048	3.14	1.0E-105	1.0E-105 AW961688.1		EST373781 MAGE resequences, MAGG Homo sapiens cDNA
4773	17788	30684	0.69	1.0E-105	1.0E-105 BE868881.1	EST_HUMAN	601445823F1 NIH_MGC_65 Hamo sepiens cDNA clane IMAGE:3850156 5
4773	17788	30686	0.69	1.0E-105	1		601445823F1 NIH_MGC_65 Homo sepiens cDNA done IMAGE:3850156 5
. 4788	17810	30702	1.65	1.0E-105	1.0E-105 AA698335.1	EST HUMAN	z44g02.s1 Scenes_fetal_liver_splean_1NFLS_S1 Hamo sapiens aDNA dane IMAGE:433682.3"
4976	17991		4.04	1.0E-105	2	NT	Hamo sepiens chranosame 21 segment HS210008
5147	18158	31036	1.21	1.0E-105		NT	Homo sapiens mRNA for KIAA0798 protein, partial cds
5403	18506	31383	0.7	1.0E-105	1.0E-105 AF016704.1	NT	Homo sepiens E6-AP ubiquitin-protein ligase (UBE3A) gene, excn 2
5471	18572		1.02	1.0E-105	11420134 NT	۲	Homo sepiens Retine-derived POU-domain factor-1 (RPF-1), mRNA
7089	20023	33324	1.57	1.0E-105	1.0E-105 BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sepiens cDNA clone IMAGE:4130334 5
7089	20023	33326	1.57	1.0E-105	1.0E-105 BF314302.1	EST HUMAN	601801028F1 NIH_MGC_19 Hamo septens aDNA clane IMAGE:4130334 5
7174	18405	31203	3.49	1.0E-105	11419196 NT	NT	Homo sepiens GTP ase activating protein-like (GAPL), mRNA
7174	18405	31204	3.49	1.0E-105	9616	N.	Homo sepiens GTPase activating protein-like (GAPL), mRNA
222	20245	33579	0.56	1.0E-105	.1	EST HUMAN	EST36398 MAGE resequences, MAGB Homo sepiens cDNA
7501	20466	33827	0.69	1.0E-105	1.0E-105 BE902616.1	EST_HUMAN	601677279F1 NIH_MGC_21 Horno sapiens cDNA clone IMAGE:3960019 5

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	Top Hit Descriptor	Human mRNA for dbl proto-oncogene	EST02975 Fetal brain, Stratagene (cat/808206) Homo septiens curve done Hi-BCA32	ws50c10.x1 NCI_CGAP_Bm25 Homo septens cDNA clone IMACE:25000225 3' similar to SW:ACSA_PENCH P38333 ACETYL-CCENZYME A SYNTHETASE;	RC1-CN0008-070100-011-e05 CN0008 Homo saplens cDNA	UI-H-BIOP-ADI-D-12-0-UI.s1 NCI_CGAP_Sub2 Homo sepiens cDNA clone IMAGE:27117823	QV2-OT0062-140300-083-d09 OT0062 Homo sapiens cDNA	QV2-OT0062-140300-083-d09 OT0062 Hano sapiens GUNA	601443755F1 NIH MGC 65 Hamo saptens GUNA Gane INFACE 3047004 3	80144375571 NIH MGC 65 Hamo septens alona date image: 3047604 3	Homo sapiens SMARCA4 isoform (SMARKCA4) gene, complete cos, ausmauvery spiloso	Homo septens COLAAB gene for e8(IV) collegen, excn 31	Homo sapiens Ran binding protein 11 (LOC51194), mRNA	w/74f07.x1 Soares_frymus_NHFTh Homo sapiens cDNA clone IMAGE:2536301 3' similar to TK:P87692	P87882 PROTEASE;	76/86/10.x1 NCI_CGAP_Kid11 Homo septiens cDNA clone IMAGE:35/4291 3' semiller to 1 K:P9/00U P9/00U	KINI.	Hamo sapients game to critical as early services	Homo septems gene for Smea 3, excrt 2 end 3	ULHE-BNO-akt-g-07-0-ULH NIH MGC 30 Hamb septens duny dans Impressor 3	tg78c01 x1 NC CGAP Ut1 Hamp sapients duyla dame livacie: 221 Julio 3	EST377829 MAGE resequences, MAGI Homo sapiens CLNA	Human ditydrofolate reductase pseudogene (pst-html)	Human dihydrofolate reductase pseudogene (partion)	Human epidermal growth factor receptor (EGTK) precursor-minny, even 4, parvia wis	Homo sapiens type IV collagen alpha 5 chain (COLAA5) gene, exon 41	ng41co5.s1 NCI_CGAP_Co3 Homo sapiens cDNA done IMAGE:837362 3' similar to contains element	LIKS repeative element;	ng41c05.s1 NCI_CGAP_CGS Hamo septens curva dane IMAGE-8575525 5 seitles to cultura sections are included in 1783 servetting element :	NAPA-HTM-65-140200-040 HTM-65 Homo saniens cDNA	Union contains at the first of the first of (GSTT1), mRNA	11.0110 coprising gramman and school of the	rights sapiets Aria not delicated to the control of
Ships could into a sign	Top Hit Databese Source	П	EST_HUMAN	EST_HUMAN	Г	HUMAN			HUMAN	EST HUMAN	M	Į.			EST_HUMAN		HUMAN		7			EST_HUMAN	Ę	Ϋ́	M	M		EST_HUMAN	MAY TO HOD	TOT LINAM	ביין	Z	시
D SERVICE OF THE PROPERTY OF T	Tap Hit Acession No.			7	-	-	1.0E-105 AW882372.1	1		1			7705836 NT		1.0E-105 AW027554.1		1.0E-105 BF430921.1	1.0E-105 AB004924.1	1.0E-105 AB004924.1	1.0E-106 AW 503208.1	1.0E-106 AISS5065.1	1.0E-106 AW985568.1	J00146.1	J00148.1	U48724.1	U04510.1		1.0E-106 AA527448.1		1.0E-100 AA32/446.1	1.0E-106 BE144286.1	4004184 IN	1.0E-108 AF003528.1
	Most Similar (Top) Hit BLAST E Vetue	1.0E-105 X12558.1	1.0E-105 T05087.1	1.0E-105	1 0E-105 AW840817	1.0E-106/	1.0E-105	1.0E-105	1.0E-105	1.0E-105 BE887783.	1.0E-105 AF254822	1.0E-105 D83548.1	1.0E-105		1.0E-105		1.0E-105	1.0E-105	1.0E-105	1.0E-106	1.0E-108	1.0E-108	1.0E-106 J00146.1	1.0E-108 J00148.1	1.0E-108 U48724.1	1.0E-108 U04510.1		1.0E-108				1.0E-106	
Ì	Expression Signal	-8 8	6.09	1.52	0 75	3.19	0.91	ю.	0.76	0.78	4.59	1.61	2.83		281		2.56	1.5	1.5	1.76	1.59	223	3.07	1.71	4.6	1.01		4.27		4.27	1.52	3.89	1.07
	ORF SEQ ID NO:	34572	34743	98432	1			١	١						38388		38457	38572			26235					Ĺ		27839				28359	28539
	SEO ID NO:	21162	21331	24.700	2004B	2320	22520	22520	22810	22810	24220	24504	24540		24786	1	24861	24975	Ĺ.,	1_		L.		1_	ı			14847			_1	15336	15515
Ì	Probe SEQ ID NO:	8492	888	77.6	1 8	200	898	8558	9Z88	9268	41278	11584	14814		11914		11984	12104	12/04	152	208	5,5	209	808	4742	1735		1820		<del>2</del>	2132	2325	2512

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	Top Hit Descriptor	AU116850 HEMBA1 Hamo saplens cDNA clone HEMBA1000129 5	601594331F1 NIH_MGC_9 Hamo sepiens cDNA clone IMAGE:3948463 5	601594331F1 NIH_MGC_9 Hamp sapiens cDNA clane IMAGE:3948463 5	er68a07.x1 Berstead aorta HiPLRB6 Homo sapiens cDNA done IMAGE:2127732 3' similar to gb:X06233 CALGRANULIN B (HUMAN);	601282717F1 NIH_MGC_44 Homo septens cDNA clone IMAGE:3604483 5	601282717F1 NIH_MGC_44 Hamo septens cDNA clone IMAGE:3604463 5	NG2805.X1 NCI_CGAP_KId11 Homo sapiens cDNA clone IMAGE:2283832 3° similar to SW:ICAB_HUMAN C005084 69 KD ISLET CELL AUTOANTIGEN;	w.038c03.x1 Soares_Dieckgraefe_colon_NHCD Homo sepiens cDNA clone IMAGE:2522308 3' similar to TR:070273 070273 ETS HOMOLOGOUS FACTOR;	CM4-L T0059-150200-088-e08 LT0059 Hamo sapiens cDNA	0067e08.s1 NCI_CGAP_GCB1 Homo septems cDNA clone IMAGE:1354790 3'	c67e08.s1 NCI_CGAP_GCB1 Homo sepiens cDNA clone IMAGE:1354790 3*	cn03a04.y/ Normal Human Trabecular Bone Cells Homo sapiens cDNA ctone NHTBC_cn03a04 random	tm41f02.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.t3 TAR1 PTR5 repetitive element ;	the 1702 x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.t3	AN 282287E1 NIH MCC. At Home senions cDNA close IMAGE-3804217 5	MARTATATA IN MCC. 20 Home seniors cDNA close IMAGE:385403 6	601671674F1 NIH MGC 20 Homo saplens cDNA clone IMAGE:3954403 5	np57b10.s1 NCI_CGAP_Br2 Homo sepiens cDNA clone IMAGE:11303953'	np57b10.s1 NCI_CGAP_Br2 Hamo septens cDNA dane IMAGE:1130396 3'	RC0-CT0318-201199-031-e11 CT0318 Homo sapiens cDNA	Homo sepiens multimenin (MMRN), mRNA	Homo sapiens multimenth (MMRN), mRNA	DKFZp434F0712_r1 434 (synonym: htess) Homo saptens cDNA clone DKFZp434F0712 5	Homo sepiens chronosome 21 segment HS21C002	601453461F1 NIH_MGC_68 Hamo sapiens cDNA clane IMAGE:3857368 5	601453461F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857366 5	Human ryanodine receptor mRNA, complete ods	Human ryanodine receptor mKNA, complete cds
	Top Hit Database Source	EST_HUMAN /	EST_HUMAN	EST HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN		EST_HUMAN	Г	EST_HUMAN	EST HUMAN	EST HUMAN		EST HOMBA	NAME OF THE PERSON OF THE PERS	Т	Π		T_HUMAN			EST_HUMAN			T_HUMAN	Ę	¥
	Top Hit Acession No.	1.0E-106 AU116850.1	1.0E-106 BE741408.1		U523088.1	L	1.0E-106 BE387960.1	N654123.1	V991109.1	1.0E-106 AW838831.1	1.0E-106 AA825307.1	1.0E-106 AA825307.1	1.0E-106 AI750447.1	1 0F-108 AI479569 1	7 00.00	1.UE-100 AH/8008.1	3E308234.1	1.0E-100 BF02/310.1	1.0E-106 AA604417.1	1.0E-108 AA604417.1	1.0E-106 AW383299.1	11436432 NT	11436432 NT	1.0E-106 ALC39888.1	1.0E-106 AL163202.2	1.0E-106 BF032755.1	BF032755.1	J05200.1	105200.1
	Most Similar (Top) Hit BLAST E Value	1.0E-106	1.0E-108	1.0E-106	1.0E-106 AI523086.1	1.0E-106	1.0E-106	1.0E-106 AI654123.1	1.0E-106 AI981109.1	1.0E-106/	1.0E-108	1.0E-106	1.0E-106	1 0F-108		1.0E-100	1.0E-106 BE308234.	1.0E-100	1.0E-106	1.0E-106	1.0E-106	1.0E-108	1.0E-106	1.0E-106	1.0E-106	1.0E-106	1.0E-106	1.0E-106 J05200.1	1.0E-106 J05200.1
	Expression Signal	0.63	5.05	5.05	108.87	0.78	0.78	3.3	0.53	0.87	247	2.47	1.55	1 84		1.87	1.22	0.92	5.48	5.48	1.68	0.6		0.40	3.52	4.84	4.84		2.76
	ORF SEQ ID NO:	34463	34699				ľ								1			30836											37880
	Exan SEQ ID NO:	21068		21286		21942	1			22372	22468	22468	22585	<u> </u>			23284	2000	28528	23523	1_	<u>.</u>	L.		L			H	24346
	Probe SEQ ID NO:	8119	8317	8317	8515	8976	8976	9054	0906	9407	9502	8502	9641	7820	5	9784	10361	10444	10601	10801	10848	10653	10653	10827	1094	11242	11242	11402	11402

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Probe SEQ ID NO:	SEO (D NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Velue	Top Hit Acession No.	Top Hit Detabese Source	Top Hit Descriptor
11738	24622	38200	3.21	1.0E-106	1.0E-106 BE257385.1	EST HUMAN	601108219F1 NIH_MGC_16 Homo septems CDNA clone IMAGE:3348897 67
12250	25763		8.02	1.0E-106	1.0E-106 AW410405.1	EST_HUMAN	finoSh11x1 NIH_MGC_17 Homo sapiens cONA clone IMAGE-2961644 5
12481	25229	34796	9.58	1.0E-108	1.0E-108 BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sepiens cONA clone IMAGE:3918524 5
12481	25228	31797	3.58	1.0E-106	1.0E-106 BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Hamo sepiens aDNA clane IMAGE:3918524 5"
12687	25354		4.48	1.0E-106	1.0E-106 BE695905.1	EST_HUMAN	RC1-CT0249-090800-024-d05 CT0249 Homo septens cDNA
287			4.28	1.0E-107	5.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
264			1.85	1.0E-107		NT	Human IFNAR gene for interferon alpha/beta receptor
189		26616	3.38	1.0E-107	1.1	N.	Homo septems NY-REN-25 amigen mRNA, partial cds
814	13872	26820	277	1.0E-107	1.0E-107 X60450.1	Z	Human IFNAR gene for Interferon alpha/beta receptor
887	13942	26900	1.31	1.0E-107	1.0E-107 X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
0/6	14022	26975	12.86	1.0E-107	1.0E-107 AF154121.1	IN	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1283	14318		1.8	1.0E-107	-	Į.	Homo sepiens BAZ1B mRNA for brancdomain adjacent to zinc finger domain 1B, complete cds
1573	14606	27579	3.83	1.0E-107	1.0E-107 BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-e05 HT0540 Homo septens cDNA
1767	14798	27781	2.54	1.0E-107	1.0E-107 AF138275.1	NT	Homo septems cathepsin Z precursor (CTSZ) gene, exon 3
1857	14883	27879	96.0	1.0E-107	1.0E-107 AB007922.2	NT	Hamo sapiens mRNA for KIAA0453 protein, partial cds
1857	14883	27880	0.96	1.0E-107	2.2	NT	Homo espiens mRNA for KIAA0453 protein, pertial cds
2218	15232	28256	1.11	1.0E-107	1.0E-107 U13729.1	NT	Human dipeptid) peptidase IV (CD26) gene, excn 20
0282		28401	1.02	1.0E-107	1.0E-107 AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sepiens cDNA
0282	15378	28402	1.02	1.0E-107	1.0E-107 AW842451.1	EST_HUMAN	PAMI-CN0031-190100-001-d03 CN0031 Homo saplens oDNA
2540		28568	1.12	1.0E-107	1	EST_HUMAN	601507619F1 NIH_MGC_21 Homo sepiens cDNA done IMAGE:3842309 5
2540		28567	1.12	1.0E-107	1.0E-107 BE732460.1	EST HUMAN	601567619F1 NIH_MGC_21 Homo sepiens cDNA clone IMAGE:3842309 5
3019	16077	28997	3.8	1.0E-107	.1	EST_HUMAN	PMM-CN0031-190100-001-d03 CN0031 Homo sepiens cDNA
3019		28998	3.8	1.0E-107	1.0E-107 AW842451.1	EST_HUMAN	PMH-CN0031-190100-001-d03 CN0031 Homo septems cDNA
3116		29083	3.16	1.0E-107	TN 7802083	N <sub>T</sub>	Homo sapiens SMT3 (suppressor of mili two 3, yeast) homolog 2 (SMT3H2), mRNA
6888	16879	29782	4.78	1.0E-107	1.0E-107 AF020671.1	NT	Homo sepiens mydubularin (MTM1) gene, exan 9
2708	18801	31978	0.56	1.0E-107	.1	EST_HUMAN	EST381115 MAGE resequences, MAGK Homo septems cONA
5965	19050	32251	3.4	1.0E-107	1.0E-107 BE867469.1	EST_HUMAN	601442558F1 NIH_MGC_65 Hamo septens cDNA clane IMAGE:3846494 5
6976	20198	33627	0.56	1.0E-107	8005008 NT	NT	Homo sapiens A kinase (PRKA) anchor protein 10 (AKAP10), mRNA
7107	20041	33343	0.63	1.0E-107	11431469 NT	N <sub>T</sub>	Homo sepiens general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD) (GTF3C1), mRNA
7107	20041	33344	0.63	1.0E-107	11431469NT	¥	Homo sepiens general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD ) (GTF3C1), mRNA
7588		33809	1.16	1.0E-107	1.0E-107 AW503913.1	T_HUMAN	UHIF-BNO-eff-08-0-U.: 1 NIH_MGC_50 Hamp septems cDNA clone IMAGE:3079310 5

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Single Exon Probes Expressed in Bone Marrow

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Probe SEQ ID NO:	Exem SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
2605	18701	31674	2.27	1.0E-108	1.0E-108 BE803016.1	EST_HUMAN	601444822F1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:3848980 5
9209	19119		8'0	1.0E-108	1.0E-108 AF012623.1	Ŋ	Homo eaplans familial mental retardation protein 2 (FMR2) gene, exon 20
6117	19195	32419	26'0	1.0E-108	1.0E-108 BF334851.1	EST_HUMAN	PMA-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
62862	18335	32567	6.27	1.0E-108	1.0E-108 AF284717.1	Ę	Homo sepiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6262	18335	32568	6.27	1.0E-108	1.0E-108 AF264717.1	Ę	Homo sepiens FYVE domain-containing dual specificity protein phosphetese FYVE-DSP2 mRNA, complete cds
6392	19468	32708	122	1.0E-108	1.0E-108 AJ133269.1	Ę	Homo septens caveolin-1/-2 locus, Config1, D7S522, genes CAV2 (exons 1, 2a, end 2b), CAV1 (exons 1 and 2)
94 94 94		32419		1.0E-108	1.0E-108 BF334851.1	EST_HUMAN	PMA-CT0403-240700-001-c10 CT0403 Homo septems cDNA
6773	10828	33110	0.67	1.05-108	1.0E-108 AF016708.1	NT	Homo sapiens E8-AP ubiquitin-protein ligase (UBE3A) gene, excn 4
6773		33111	0.67	1.0E-108	1.0E-108 AF016706.1	NT	Homo septems E8-AP ubiquitin-protein ligase (UBE3A) gene, excn 4
7365	20335	33685	5.42	1.0E-108	11431857 NT	Į,	Homo sepiens G protein-coupled receptor, family C, group 5, member B (GPRCSB), mRNA
7673	20631	33995	1.98	1.0E-108	4758333 NT	F	Homo seplens defea 6 faith ecid desaturase (FADSD6) mRNA
7718	20875	34041	1.13	1.0E-108	1.0E-108 BE252607.1	EST_HUMAN	601113471F1 NIH_MGC_16 Homo sapiens cDNA clone INACE:3354064 6
7749	20702	34069	89'0	1.0E-108	1.0E-108 BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Bm67 Homo saptans cDNA clone IMAGE:4181037 5
7749	20702	34070	89'0	1.0E-108	1.0E-108 BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Brn67 Homo septens cDNA clone IMAGE:4181037 5
8140	24086	34485	250	4 OF-408	11422/55 NT	5	Homo sapiens cyclic fibrosis transmembrane conductance regulator, ATP-binding cassettis (sub-family C, member 7) (CFTR), mRNA
8388	L			1.8	1.0E-108 AF083500.1	Z	Homo seplens connective tissue growth factor-like protein precursor, mRNA, complete ods
8462	L	34835	5.44	1.0E-108	1.0E-108 AW 408694.1	EST HUMAN	UHIF-BMD ads e-12-0-Ul. 1 NIH MGC 38 Homo sepiens aDNA dane IMAGE:3062878 6
8452		34836		1.0E-108	AW408694.1	EST_HUMAN	UHIF-BIMD eds-e-12-0-UI.r1 NIH_MGC_38 Homo septems cDNA done IMAGE:3082878 5
<b>2</b>	22367	35800	0.93	1.0E-108	1.0E-108 AF203977.1	¥	Homo sapiens ETS-family transcription factor EHF (EHF) mRNA, complete cds
1448	22405	35842	0.48	1.0E-108 N44974.1	N44974.1	EST_HUMAN	y35h10 r1 Scares melenocyte 2NbHM Homo septens cDNA clone IMAGE:273283 5' similar to PIR:A45773 A45773 kelch protein, long form - fruit fly;
40003	20000	27770	296	4 05.400	TA 38185111	5	Homo sepiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sepiens) (LOC63446), mRNA
11027	1_	34439	2.14	105-108	1.0E-108 BE53527.1	EST HUMAN	801058769F1 NIH MGC_10 Homo sapiens cDNA done MAGE:3446361 6
11177	18353	31298	1.04	1.0E-108 Y12490.1	Y12490.1	¥	Homo expiens mRNA for Golgi-associated microtutute-binding protein (GMAP-210)
11602		38099	3.33	1.0E-108	1.0E-108 AW966185.1	EST_HUMAN	EST378258 MAGE resequences, MAGI Homo septens cONA
11653	24580	38160	1.75	1.0E-108	1.0E-108 AV708790.1	EST HUMAN	AV708790 ADC Hamo sepiems aDNA clane ADCAEE03 6"
11653		38161	1.75	1.0E-108	1.0E-108 AV708790.1	EST_HUMAN	AV708790 ADC Homo septems cDNA clone ADCAEE03 5"
11698	24663		2.05	1.0E-108	11441465 NT	N	Homo sepiens G protein-coupled receptor 48 (GPR48), mRNA
11757	24685	38265	1.6	1.0E-108 D63539.1	D63539.1	74	Homo sepierts COL 4A6 gene for a6(IV) collagen, exon 28

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	Top Hit Descriptor	Homo septens mRNA for RJ00037 protein, partial ods	602018571F1 NCI_CGAP_Bm67 Homo septens cDNA clone IMAGE:4154297 51	II.2-UM0077-280400-079-D06 UM0077 Homo sapiens cDNA	Humen mRNA for KIAA0220 gene, partial cds	Homo sepiens hypothetical protein FLJ11316 (FLJ11316), mRNA	Homo sepiens reficulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA	Homo sepiens tetratricopeptide repeat domain 2 (TTC2) mRNA	Homo sepiens mRNA for KIAA0999 protein, partial cds	Homo sapiens mRNA for KIAA0889 protein, partial cds	Homo sapiens chromosome 21 segment HS21C049	Homo sapiens nuclectar phosphoprotein B23 (NPM1) mRNA, complete cds	Homo sapiens nucledar phosphoprotein B23 (NPM1) mRNA, complete cds	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959836 5	601186922F2 NIH_MGC_15 Hamo septens cDNA clane IMAGE:2859636 5	Homo sepiens mRNA for KIAA0018 protein, partial cds	Homo sepiens chromosome 21 segment HS210084	Homo sapiens SNF5/INH gene, excn 6	ow85s01.x1 Soares_fetal_liver_spieen_1NRLS_S1 Homo sapiens cDNA clone IMAGE:1854538 3' striifar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN ;	ow65a01.x1 Scares_fetal_liver_spleen_1NFLS_S1 Homo septens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN.;	Homo sapians guanylate cyclasse activator 1A (rethra) (GUCA1A) mRNA	J2819F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2818 6' similier to ZINC FINGER PROTEIN ZNF43	CARS-NINDO09-190400-150-f10 NIND009 Homo sepiens cDNA	CARS-NIND009-190400-150-f10 NIND009 Homo septems cDNA	Homo sepiens retinal dehydrogenase homolog isoform-1 (ROH) mRNA, complete cds	Homo sapeins adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10	Homo sapains adenosine monophosphate deaminase 1 (AMIPD1) gene, exons 8-10	MR0-HT0209-110400-108-604 HT0209 Homo septens cDNA	ts88608.x1 NCI_CGAP_GC6 Homo septens cDNA clone IMAGE:2238330 3' stmilar to WP:F53A2.8 CE16100 ;	nu83c12.s1 NCI_CGAP_P/22 Homo septiens cDNA done IMAGE:1218282.3" similar to SW:GTT2_HUMAN P30712 GLUTHATHIONE S-TRANSFERASE THETA 2;
	Top Hit Detabase Source			EST_HUMAN III	H TN				NT H		H	H			EST_HUMAN 6	NT H		H	EST HUMAN T			T_HUMAN	EST_HUMAN C	EST HUMAN C	F			EST_HUMAN A	EST HUMAN	
28.5	Top Hit Acession No.	1	1	1.0E-109 AW803116.1		11422488 NT	11438391 NT	4507712 NT		1	2			3E293673.1	3E293673.1		2		A1022328.1	A1022328.1	4504208 NT	N85190.1	AW893192.1	1.0E-109 AW883182.1	1.0E-109 AF240598.1	M37928.1	M37928.1	1,0E-109 BE146144.1	1 OE-109 AI655417.1	1.0E-109 AA682274.1
	Most Similar (Top) Hit BLAST E Vatue	1.0E-108 AK024447	1.0E-108 BF346356.	1.0E-109	1.0E-109 D86974.1	1.0E-109	1.0E-109	1.0E-109	1.0E-109 AB023216.	1.0E-109	1.0E-109 AL 163249.	1.0E-109 M28699.1	1.0E-109 M28899.1	1.0E-109 BE293673	1.0E-109 BE283673	1.0E-109 D13843.2	1.0E-109 AL163284	1.0E-109 Y17123.1	1.0E-109 AI022328.	1.0E-109 Al022328.	1.05-109	1.0E-109 N85190.1	1.0E-109 AW893192	1.0E-109	1.0E-109	1.0E-109 M37928.1	1.0E-109 M37928.1	1.0E-109	1.0E-109	1.0E-109
	Expression	5.14	11.97	217	6.88	1.51	1.97	22	13.45	13.45	86.0	23.68	24.33	12	12	1.63	268	2.69	3.42	3.42	1.84	1.81	1,33	1.33	 8	0.92	0.82	23	497	1.33
-	ORF SEQ ID NO:	31800		26067		26245	26251			26582	27013	27204	27204	27540	27550		28294	28300	28654		١,	28040							3008	
	SEQ ID NO:	25236	25467	13164	13185	13320	13328	13540	13667	13667	14062	14246	14248	14577	14577	14916	15287	15276	15629	1	1	i	16448	16448	1	1	<u> </u>	1	<u> </u>	1 i
	Pabe SEQ ID NO:	12483	12864	4	29	83	82	467	8	8	101	1207	1208	至	154	188	8822	2362	3630	2830	2631	3071	3300	8888	3530	3572	3672	3856	4474	4189

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26661         32323         0.83           18783         0.83           18650         32709         0.67           19650         32800         0.67           19767         33477         0.62           20167         33477         0.62           2047         33477         0.62           20764         34140         3.31           20769         34142         6.45           20769         34142         6.45           2159         35017         1.08           2159         35017         1.08           22052         35474         17.25           22052         35474         17.25           22053         3613         0.65           22565         36005         1.78           22565         3613         0.65           22565         36230         2.5           22775         38230         2.5	24711	T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN	ye48e08.11 Scares Infert brein 1NIB Homo sepiens cDNA chore IMAGE:53057 67 AU1377282 PLACE1 Homo sepiens dJNA chore PLACE1006169 5 G021384469F1 NIH_MGC2 R3 Homo sepiens cDNA chore IMAGE:4272822 57 Homo sepiens placerated protein 11 (serine proteins) Homo sepiens placerated protein 11 (serine proteins) FOLHT0615-200400-022-d04 HT0615 Homo sepiens cDNA RCI-HT0615-200400-022-d04 HT0615 Homo sepiens cDNA Human interleution 4 (IL-4) gene, complete cds Human gene mapping to chomosome 13 PMo-B10340-091289-002-005 B10340 Homo sepiens cDNA chore IMAGE:3882124 67 B01428477F1 NIH_MGC_B Homo sepiens cDNA chore IMAGE:3882124 67 B01428477F1 NIH_MGC_B Homo sepiens cDNA chore IMAGE:382210 67 B01289780F1 NIH_MGC_B Homo sepiens cDNA chore IMAGE:3820030 57 B01289780F1 NIH_MGC_B Homo sepiens cDNA chore IMAGE:3820030 57 B01289780F1 NIH_MGC_B Homo sepiens cDNA chore IMAGE:3820030 57 B01289780F1 NIH_MGC_B Homo sepiens cDNA chore IMAGE:3820030 57 B01289780F1 NIH_MGC_B Homo sepiens cDNA chore IMAGE:3820030 57 B01289780F1
24088 37616 2.42 24088 37617 2.42		EST_HUMAN (R	601063020F1 NIH_MGC_10 Homo septens CDNA clone IMAGE:3446369 5 601063030F1 NIH_MGC_10 Homo septens CDNA clone IMAGE:3449399 5
24116 37642 31.85		T	602080724F2 NIH_MGC_81 Homo septens cDNA clone IMAGE:4245341 5

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ngle Exon Probes Expressed in Bone Marrow	Top Hit Descriptor	AU121370 HEMBB1 Hamo saplens cDNA clone HEMBB1002890 5	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA	zb08b12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to PIR:S43989 S43969 p54-beta stress-activated protein kinases - rat;	Int23f05.x1 NCI_CGAP_LL24 Home septens cDNA clone IMAGE:2865969 3' similar to TR:092124 Q92124 YGR183W MRNA HOMOLOGUE, COMPLETE CDS. ;	602039003F1 NCL_CGAP_Bm64 Hamo sapiens cDNA clone IMAGE:4186753 5	602035003F1 NCI_CGAP_Bm64 Hamo sepiens aDNA clane IMAGE:4186763 6	ase4207.rd Scenes_NhHMPu_S1 Homo septens cDNA clone IMAGE:823624 6	Homo sapiens SNF6/INI1 gane, exon 8	Hamo explerts SNFWINI gene, exan o	Homo sepiens gene for AF-6, complete cds	Homo sepiens delodinase, lodothyronine, type II (DIO2), transcript variant 2, mRNA	Homo sepiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA	Homo sepiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA	Homo sepiens delodinasa, todothyronina, type II (DIO2), transcript variant 2, mRNA	Human mRNA for inward rectifier potassium channel, complete cds	Human dystrobravin (DTN) gene, excn 20	Homo sepiens celebrain receptor-like (CALCRL) mRNA	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds	601237545F1 NIH MGC 44 Hamo sapiens cDNA clone IMAGE:3609683 5	UHHBIA 603-0-01.81 NG CGAP SUBS HOMO SEPIERS CLINA CAME IMACET 3083/04 3	Homo sepiens chandrottin suffere proteogrycan 4 (metanoma-associated) (CSPC44), mitches	Homo sepiens BAZ18 mRNA for bromodomein edjecent to zinc itrger domein 15, complete ous	Homo sapiens Bruton's tyrosine kinase (BTK), apha-U-galactoskiase A (S-A), L44-the mossoma protein [L44L] and FTP3 (FTP3) genes, complete cds	Homo sapiens pregnancy zone protein (PZP), mRNA	Homo sepiens pregnancy-zone protein (PZP), mRNA	Human autoimmune antigen small nuclear ribonucleoprotein E pseudogene	ouszenou Sogree_NFL_T_GBC_S1 Homo expiens cDNA clone IMAGE:1627983 3' similigr to SW:N121_RAT P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121;	AU117812 HEMBA1 Hamo septens aDNA dans HEMBA1002241 5	Homo sepiens KIAA1002 protein (KIAA1002), mRNA	601118/10F1 NIH_MGC_17 Hamb sapiens GUNA dane IMAGE::3UZB330 5
xon Probes E	Top Hit Databese Source	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	F	Į.	Ę	M	M	KT	NT	Ŋ	Nī	NT	NT	EST_HUMAN	EST_HUMAN	Ϋ́	Į.	Ę	Į	¥	Į,	EST_HUMAN	EST_HUMAN	٦	EST_HUMAN
Single E	Top Hit Aoesslan No.	1.0E-109 AU121370.1	4502838 NT	W16510.1	3E045580.1	1.0E-109 BF339540.1	1.0E-109 BF339540.1	1.0E-109 AA490558.1	17123.1	/17128.1	1.0E-109 AB011399.1	7549804	6803073 NT	5803073	7549804	387291.1		5031620 NT	1.0E-110 AB032253.1	1.0E-110 BE379477.1	1.0E-110 BF508896.1	4503088 NT	1.0E-110 AB032253.1	178027	11438041 NT	12	ł	1.0E-110 AI017213.1	1.0E-110 AU117812.1	7682441 NT	1.0E-110 BE289408.1
	Most Similar (Top) Hit BLAST E Value	1.0E-109	1.0E-109	1.0E-109 W16510.1	1.0E-109 BE045580.	1.0E-109	1.0E-109	1.0E-109	1.0E-109 Y17123.1	1.0E-109 Y17123.1	1.0E-109	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110 D87291.1	1.0E-110 U84550.1	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110	4 0E-440 178027 4	1 OF-110	1.0E-110	1.0E-110 M15918.1	1.0E-110	1.0E-110	1.0E-110	1.0E-110
	Expression Signal	1.65	282	5.45	89.	2.03	203	1.65	21	2.24	1.85	0.89	4.69	4.69	1.73	1.8	13.41	1	0.72	1.35	1.85	1.05	0.88	3	1.65	1.65	880	2.11	4.29	1,94	223
	ORF SEQ ID NO:	37860	38240	38189	38380	38597	38588	38607		28300	31774	28022	26061	28082	28022	26316	28517	27181	27282	27958			27282		20185		30145	<u> </u>			31343
	SEQ ID	24402	1_	<u> </u>	1	L	24894	25001		16278	25374	13124	L	13159	13124	13388	13599	1	14319	14961	15090	15913	14319	48480	1		1_	<u> </u>	17705		18472
	Probe SEQ ID NO:	11459	11697	11735	11910	12125	12125	12132	12395	12613	12720	6	88	88	109	数	8Z9	1184	482	1837	2073	2853	3043	2402	300	3209	4231	4665	4884	6009	5367

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Single Exon Probes Expressed in Doire mailow	Top Hit Descriptor	247507.rf Soares_pregnant_uterus_NbHPU Homo septens dDNA clone IMAGE:505045 6' similar to gb.M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);	247b07.rf Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb.M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);	601443630F1 NIH_MGC_65 Hamo septens cDNA clane IMAGE:3847655 5	Human two-handed zinc finger protein ZEB mRNA, partial cds	qp09g12x1 NG_CGAP_Kd5 Homo sepiens cDNA done IMAGE:1817574 3' similar to gb:M28883 RAS- RELATED PROTEIN RAL-A (HUMAN);	DKFZp434C1815_r1 434 (synonym: htes3) Homo septens cDNA clone DKFZp434C1815 5	UI-H-BW0-eff-d-03-0-UI.s1 NCI_CGAP_Sub8 Hamo sapiens CDNA clone IMAGE::Z/29525 31	RC2-BN0033-160200-013-b05 BN0033 Homo sepiens aDNA	II 2-NT0101-280700-114-E03 NT0101 Homo saplens cDNA	Homo septems ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant A,	HELVA	wi68do1 x/1 NCI_CGAP_Kid12 Hamo sapiens cDNA clane IMAGE:2398466 3' similar to gb:J04813 CYTOCHROME P450 IIIA5 (HUMAN);	Homo sepiens basic transcription factor 2 p44 (bt/2p44) gene, partial cds, neuronal epoptosis inhibitory	protein (naip) and survival motor neuron protein (smn) ganes, complete cds	zn62c12.r1 Stratagene muscle 837209 Homo sapiens cDNA clone IMAGE:662774 5' similar to gtc:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);	2878903.71 NCI_COAP_GCB1 Homo septens cDNA clone IMAGE:703732 5' striller to TR:G1256410 G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR.;	2878g/03.r1 NCI_CGAP_GCB1 Hamo sepiens cDNA dane IMAGE:703732 5 similar to TR:G1256410	G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR;	Homo sepiens protein x 0001 (LOC51185), mRNA	Human beta4-Integrin (ITGB4) gene, excm 13	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA	Hamo sapiens mRNA for FLJ00045 protein, partial cds	601847132F1 NIH_MGC_55 Hamo sapiens cDNA done IMAGE:4078303 5	Human mRNA for integrin alpha-2 subfinit	Human mRNA for integrin alpha-2 subunit	Homo sepiens Trio isoform mRNA, complete cots	QV2-BT0817-270900-398-606 B   0817 Homo septems CUNA
Xon Probes E	Top Hit Database Source	EST_HUMAN 9	EST_HUMAN 9	EST_HUMAN 6	П	EST_HUMAN F		EST_HUMAN (	EST_HUMAN F	EST_HUMAN !!			EST HUMAN	Ī	NT	EST HUMAN		Г	EST_HUMAN					T_HUMAN	INT	LN LN	П	EST_HUMAN
	Top Hit Acession No.	4A151017.1	1.0E-111 AA151017.1			1.0E-111 AI344679.1	1.0E-111 AL040782.1	1.0E-111 AW 294648.1	1.0E-111 AW993165.1	1.0E-111 BF366228.1		9961253 NT	1.0E-111 AI761228.1		U80017.1	1.0E-111 AA133814.1	1 DE-111 AAZ78868.1		1.0E-111 AAZ78808.1	11431896 NT	1.0E-111 U66533.1	11420518 NT	1.0E-111 AK024453.1	1.0E-111 BF214902.1	X17033.1	1.0E-111 X17033.1	1.0E-111 AF091395.1	1.0E-111 BF333210.1
	Most Similar (ΤΦ) Hit BLAST E Vaitue	. 1.0E-111 AA151017.1	1.0E-111	1.0E-111	1.0E-111 U19969.1	1.0E-111	1.0E-111	1.0E-111	1.0E-111	1.0E-111		1.0E-111	1.0E-111		1.0E-111 U80017.1	1.0E-111	4 OF-444		1.0E-111	1.0E-111	1.0E-111	1.0E-111	1.0E-111	1.0E-111	1.0E-111 X17033.1	1.0E-111	1.0E-111	1.0E-111
	Expression	0.68	. 0	0.89	0.49	5.5	96'0	1.3	0.62	2.67		0.51	0.58		0.8	1.52	0.80		0.82	0.55	324	0.77	0.83	26.95	15.22	15.22	2.88	0.48
	ORF SEQ ID NO:	31583	31594	31986	\$2111	32453	33185	33531	33724	34000		34097	34104		34185	34402			34813						35632			36079
•	Exan SEQ ID NO:	18650	18650	L	1_	<u> </u>						20725			20817			L	21400	L		L_	<u> </u>					22625
j	Probe SEQ ID NO:	999	2995	5714	5837	67.48	6837	8268	7405	7880		7772	1		7873	8087	200	3	8431	8530	8583	8027	9738	9	8238	8238	24	2/98

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Single Exon Probes Expressed in Bone Marrow

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Single Later Propose Lapressed III Doile Mailow	Top Hit Descriptor	as58g02.s1 NG_CGAP_GCB1 Hamo sepiens aDNA done IMAGE:825170 3' similar to gb:1.08235 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);	Homo sapiens RGH1 gene, retrovins-根e element	231f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5	UHHBW0-eiq-d-07-0-UI.s1 NCI_CGAP_Sub6 Hama septens cDNA clane IMAGE:2730276 3'	ILO-CT0031-221099-113-f06 CT0031 Homo saplens cDNA	Human thrombopoietin receptor (MPL) gene, evans 1,2,3,4,5 and 6	Homo septens meningtoma (disrupted in balanced translocation) 1 (MN1), mRNA	Homo sapiens mRNA for neuredin Helpha protein, complete cds	Homo espiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA	Human steroidogenic acute regulatory protein (SVAR) gene, exon 6	Humen sterotdogenic scute regulatory protein (StAR) gene, exon 5	UHH-BIA-actg-04-0-Ui.s1 NCI_CCAP_Sub8 Hamo sapiens cDNA clane IMAGE:3086023 3'	UI-H-BI4-act-g-04-0-UI.s1 NGI_CGAP_Sub8 Hamo septems aDNA dane IMAGE:3086023 3'	Homo sepiens HTRA serine protesse (PRSS11) gene, complete cds	ZINC FINGER PROTEIN 135	Homo sepiens KIAA0440 protein (KIAA0440), mRNA	Homo septens KIAA0440 protein (KIAA0440), mRNA	w60006x1 NGL_CGAP_Kid12 Homo sepiens cDNA clone IMAGE-2400611 3'	601442674F1 NIH_MGC_66 Hamo sapiens cDNA dane IMAGE:3846868 67	Homo septens glutamate receptor, tonotropic, kainate 1 (GRIK1) mRNA	Wk45b12.x1 NCI_CGAP_P722 Homo sapiens cDNA clone IMAGE:2418335 3' similar to gb:M81650_ma1 SEMENOGELIN 1 PROTEIN PRECURSOR (HUMAN);	MR2-BT0590-090300-113-f09 BT0590 Homo sapiens cDNA	Homo sapiens glutamate receptor, tonotropic, katnate 1 (GRIK1) mRNA	Homo sepiens mRNA for KIAA1411 protein, partial cds	Home sapiens mRNA for KIAA1411 protein, partial ods	ly35d07.r1 Soares melanccyte 2NbHM Homo saplens cDNA clone IMAGE:273229 5	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	UHF-BROp-ejs-g-08-0-ULT NIH_MGC_52 Hamo septems aDNA alone IMAGE:3076668 6	UHHF-BROp-gis-g-06-0-ULr1 NIH_MGC_52 Hamo sapiens aDNA dane IMAGE:3076658 5"	601594717F1 NIH_MGC_9 Hamo saplens cDNA clane IMAGE:3948557 5	602162849F1 NIH_MGC_81 Hamo sepiens cDNA clone IMAGE:4283420 6	601142755F1 NIH_MGC_14 Hamo sapiens cDNA clone IMAGE:3506508 5
ZAULI FIODOS	Top Hit Database Source	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	M	NT	IN	IN	NT	IN	EST_HUMAN	EST_HUMAN	NT	SWISSPROT	IN	NT	EST_HUMAN	EST_HUMAN	IN	EST HUMAN	EST_HUMAN	IN	IN	NT	EST_HUMAN	IN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
aifine	Top Hit Acession No.	1.0E-111 AA504160.1	1.0E-111 D10083.1	1.0E-111 AA131248.1	1.0E-111 AW296467.1	1.0E-111 AW374340.1		11417801 NT	1.0E-111 AB035358.1	4501854 NT	U29103.1	U29103.1	1.0E-112 BF609039.1	1.0E-112 BF509039.1	1.0E-112 AF157823.1	P52742	7882125 NT	7882125 NT	AI766925.1	1.0E-112 BE866859.1	4504116 NT	1.0E-112 AI826511.1	1.0E-112 BE078073.1	4504116 NT	1.0E-112 AB037832.1	1.0E-112 AB037832.1		.1	1.0E-112 AW 502497.1	1.0E-112 AW 502437.1	1.0E-112 BE741668.1		1.0E-112 BE273103.1
	Most Similer (Top) Hit BLAST E Value	1.0E-111	1.0E-111	1.0E-111	1.0E-111	1.0E-111	1.0E-111 U68159.1	1.0E-111	1.0E-111	1.0E-112	1.0E-112 U29103.1	1.0E-112 U29103.1	1.0E-112	1.0E-112	1.0E-112	1.0E-112 P52742	1.0E-112	1.0E-112	1.0E-112 AI766925.	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112 N46048.1	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112
	Expression Signal	1.88	1.69	6:39	3.4	2.64	2.98	4.77	1.75	6.0	5.51	5.51	1.91	1.91	121	1.85	3.1	3.1	1.08	1.34	3.53	1.07	0.69	0.70	5.01	5.01	38.43	1.28	0.89	0.89	0.0	0.83	0.74
	ORF SEQ ID NO:	38832		25078	37592		82828			28580	28282	26693	26818	28819	27008	27058	27703	27704	28242	28541		28346	23849	30542	30694	30695	32027	32504	32573	32574	32687	32835	33130
	SEQ ID	23434	23462	23557	24070	24238	24330	25018	18298	13675	13677	13677	13638	13698	14054	14109	14722	14722	15222	15518	16152	16421	16938	17855	17803	17803	18844	19269		19341		19682	19846
	Prabe SEQ ID NO:	10512	10540	10635	11110	11288	11383	12168	12955	610	219	612	883	889	1003	<del>1</del> 083	1692	1692	7022	2515	3084	3374	3838	4834	4784	4784	9750	9186	8529	8929	6378	6803	6782

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			N DKFZp434M0523_r1 434 (synonym: hites3) Homo sapiens cDNA clone DKFZp434M0523 5	Homo sepiens solute center family 6 (neurotransmitter transporter, L-proline), member 7 (SLC8A7), mRNA	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC8A7), mRNA						Homo sapiens mRNA for secreted modular calcium-binding protein (smoot gene)		N PMO-CT0237-141099-001-h02 CT0237 Homo septens cDNA	Human kappa-immunoglobulin germline pseudogene (Chr22.4) vartable region (subgroup V kappa II)					Homo sapiens elf-4E-transporter mRNA, complete cds									Homo sepiens UDP-N-ecety <del>l elpha-</del> D-galactosemine:polypeptide N-ecetylgalactoseminythansferase 8 (GalNAc-T8) (GALNT8), mRNA	
Top Hit Defeaberse Source	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	¥	¥	EST_HUMAN	<b>EST_HUMAN</b>	<b>EST_HUMAN</b>	EST_HUMAN	<b>EST_HUMAN</b>	ᅜ	EST_HUMAN	EST_HUMAN	Z	<b>EST_HUMAN</b>	<b>EST_HUMAN</b>	NT.	EST_HUMAN	NT	<b>EST_HUMAN</b>	NT.	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	EST_HUMAN	¥	뉟	
Top Hit Acession No.	1.0E-112 BE273103.1	1.0E-112 BF574235.1	1.0E-112 AL043289.1	11416777 NT	11416777 NT	1.0E-112 AU118051.1	1.0E-112 BE867635.1	1.0E-112 BE867635.1	1.0E-112 BF111413.1	1.0E-112 AW863327.1	1.0E-112 AJ249900.1	1.0E-112 BE280479.1	1.0E-112 AW377670.1	1.0E-112 M20707.1	1.0E-113 AI365586.1	1.0E-113 Al385588.1	1.0E-113 M11985.1	1.0E-113 Al365586.1	1.0E-113 AF240775.1	1.0E-113 BF515218.1	1.0E-113 AJ223948.1	1.0E-113 BE780858.1	1.0E-113 AU127214.1	1.0E-113 BE789172.1	1.0E-113 BE7891721	1.0E-113 AU140291.1	1.0E-113 AP016535.1	11625737 NT	
Most Similar (Top) Hit BLAST E Value	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113		l
Expression Signal	0.74	1.23	0.68	1.62	1.62	1.83	2.58	2.58	2.18	2.83	2.36	1.7	3.58	6.59	5.37	5.37	5.76	3.01	1.20	0.89	1.16	1.54	89.68	0.54	0.54	4.18	76.0	242	
ORF SEQ ID NO:	33131	33461	33682	33879	33880	34921	ļ		38888	37621	37772	37917	38008	38563	26744	26745	26946	27548	27980	28143	28118		31626						
Exam SEQ ID NO:	19846	<b>24</b>	20332	20522	20522			ı	23178	24092	24245	24377	24459	24966	13805	13805	13394	14578	15821	15123	16204	ı	18667	Ŀ	L	L	19142	L	ı
Probe SEQ ID NO:	8782	2018	7362	7569	7559	8535	8088	8300	10253	11132	11295	11433	11518	12095	744	744		1543	1958	2106	3147	5316	<b>3970</b>	5916	<b>3916</b>	<b>8</b>	<b>609</b>	88	

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Single Exon Propes Expressed in Bone Manow	Top Hit Descriptor	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA	Homo sepiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript varient B, mRNA	Homo sepiens giutemate receptor, ionotropio, N-methyl D-espartate 2A (GRIN2A) mRNA	Hamo sapiens glutamate receptor, lonotropic, N-methyl D-espartate 2A (GRIN2A) mRNA	601152078F1 NIH_MGC_19 Hamo sapiens cDNA clone IMAGE:3508362 5	601152078F1 NIH_MGC_19 Hamo septems cDNA clane IMAGE:3508362 5	801297709F1 NIH_MGC_19 Hamo sapiens cDNA clane IMAGE:3827554 5	601297709F1 NIH_MGC_19 Hamo septens cDNA clane IMAGE:3827554 5	RC1-FT0134-280600-021-d02 FT0134 Homo sapiens cDNA	Homo saplens transmembrane protein 2 (TMEM2), mRNA	Human erg protein (ets-related gene) mRNA, complete cds	Homo sapiens RAN binding protein 7 (RANBP7), mRNA	Homo saplens RAN binding protein 7 (RANBP7), mRNA	UI-HF-BND-eld-b-12-0-UI.r1 NIH_MGC_50 Hamo sapiens cDNA clone IMAGE:3077328 5	hh81s08.y1 NCI_CGAP_GU1 Homo sepiens cDNA clone IMAGE:2889176 5' shniler to TR:060327 060327 KIAA0584 PROTEIN;	hh81409.y1 NCI_CGAP_GU1 Hamo sepierts cDNA clone IMAGE-2869176 5' similar to TR:O60327 O60327 KIAA0584 PROTEIN:	801105528F1 NIH MGC_16 Hamo septens cDNA clone IMAGE-2988388 67	nc80b03.rl NCI_CGAP_GC1 Homo septems cDNA clone IMAGE:787089 5' stmiler to SW:FEN1_HUMAN P39748 FLAP ENDONUCLEASE-1;	nc80bc3.r1 NCI_CGAP_GC1 Homo sepiens cDNA done INAGE:797089 5' similar to SW:FEN1_HUMAN	P39748 FLAP ENDONUGLEASE-1;	Homo septens mitting for mutitating resistance protein 3 (ABCX.3)	Hamo sapiens mRNA for multidrug resistance protein 3 (ABCC3)	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)	yd15c01.s1 Soares fotal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb;A21187 ALPHA-2-MACROCLOBULIN PRECURSOR (HUMAN);contains Atu repetitive element.	Homo sepiens hypothetical protein FL/20080 (FL/20080), mRNA	Homo sapiens rhabdold tumor deletion region protein 1 (RTDR1), mRNA	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
Exon Propes	Top Hit Deterbese Source	NT	. <b>L</b> N	NT	IN	EST_HUMAN	EST HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	<b>EST_HUMAN</b>	IN	TN	IN	NT	<b>EST_HUMAN</b>	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN		EST_HUMAN	LN	NT	IN	EST HUMAN	N	ŢN	TN
eignik	Top Hit Acesson No.	8961249 NT	9061249 NT	E006002 NT	F006002 NT	1.0E-113 BE282161.1	1.0E-113 BE262161.1	1.0E-113 BE382842.1	1.0E-113 BE382842.1	1.0E-113 BE772967.1	11428367 NT	1.0E-113 M21535.1	5463997 NT	5453997 NT	1.0E-113 AW500519.1	1.0E-113 AW630291.1			1.0E-113 AA680720.1		1.0E-113 AA580720.1	1.0E-114 Y17151.2	1.0E-114 Y17151.2	1.0E-114 Y17151.2	1.0E-114 T70551.1	TN 7805298	7857529 NT	6631094NT
	Most Similar (Top) Hit BLAST E Vælue	1.0E-113	1.0E-118	1.0E-118	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113		1.0E-113	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114
	Expression Signal	. 0.62	0.62	0.89	0.89	0.72	0.72	2.83	2.83	0.7	1.3	6.73	0.77	0.77	1.51	60	8	294	3.1		3.1	0.65	0.65	0.65	5.97	1.78	9	1.79
	ORF SEQ ID NO:	32587	32588	32764	32785	33865	33866	35850	35851		30299	66998	36817	36818	37948	37956					38288	28092	26083	20094	28634	27068	27319	27653
	Exan SEQ ID NO:	18352	18362	19514	18614	20506	20506	22414	22414	22697	23115	23215	23332	23332	24400	24409	24409	24530	24709		24709	13179	13179	13179	13712	14117	14351	14680
	Probe SEQ ID NO:	<b>6828</b>	9829	6449	6449	7543	7543	9450	D450	9726	10190	10280	10410	10410	11457	11466	11468	11592	11826		11828	8	8	8	84 848	1072	1316	1648

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	Top Hit Descriptor	Homo saplens nucleoporin-like protein 1 (NLP_1), mRNA	Human gene for catalase (EC 1.11.1.8) exon 2 mapping to chromosome 11, band p13	601869832F1 NIH_MGC_19 Homo saplens cDNA clone IMAGE:4100214 5	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	Human interferon-alpha receptor (HulFN-alpha-Rec) mRNA, complete cds	zq05e05.r1 Strategene muscle 937209 Homo sepiens cDNA clone IMAGE:628832 5' similar to contains MER22.t3 MER22 repetitive element;	Homo sapiens sema domain, seven frrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA	Homo sapiens sema domain, seven finombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA	Homo sapiens clathrim, heavy polypeptide-like 1 (CLTCL1), transcript variant 2, mRNA	H. sepiens isofam 1 gene for L-type calcium chemnel, exon 20	Homo sepiens sperclosteonectin, cwcv and lezal-like domains proteogrycan (testican) (SPOCK) mRNA	Homo sapiens HCMOGT-1 mRNA for sperm antigen, complete cds	AU134187-OVARC1 Homo sapiens cDNA clone OVARC1001444 5	AU134187 OVARC1 Homo septens cDNA clone OVARC1001444 5	Homo septems NF2 gene	Homo sapiens NF2 gene	Homo sepiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA	qy88db6.x1 NC _CGAP_Bm25 Hamo saplens cDNA dane IMAGE:2017163 3'	qy68d06x1 NCI_CGAP_Bm25 Hamo sepiens cDNA dane IMAGE:2017163 3'	Human neunal cell adhesion molecule CDS8 mRNA, complete cds	Homo sapiens mRNA for KIAA0561 protein, partial cds	Homo sapiens mRNA for KIAA0561 protein, partial cds	Homo sapiens mRNA for KIAA1664 protein, partial ods	788g12.x1 Scenes NSF F8_9W_OT_PA_P_S1 Home sapiens cDNA clone IMAGE:3528847 3' striitar to TR-OSI JHN8 OCI IHN8 TRANSMEMBRANE PROTEIN 2	dq03f05x1 NIH MGC 2 Hamo sapiens cDNA clone IMAGE:2846744 57	Homo sepiens tyrosine kinase pp600-src (SRC) gene, excn 12 and partial cds	Human ceruloplesmin mRNA	601449752F1 NIH_MGC_65 Hamo sapiens cDNA clone IMAGE:3853500 5	Homo sapiens chromosome 21 segment HS21C027
	Top Hit Databese Source	NT	Z	EST_HUMAN	NT	NT	EST_HUMAN	¥	Ę	¥	FA.	¥	Z.	EST_HUMAN	EST_HUMAN	NT	NT	NT	EST_HUMAN	EST_HUMAN	NT	NT	IN	NT	EST HIMAN	EST HUMAN	F	N	EST_HUMAN	Į.
	Top Hit Acesslon No.	6879073 NT	(04086.1	1.0E-114 BF206374.1	1F149773.1		1A194468.1	4506880 NT	4506880 NT	TN 1027228		4759163 NT	1.0E-114 AB041533.1	NU134187.1	4U134187.1	718000.1	/18000.1	4557600 NT	1.0E-114 AB63139.1	1.0E-114 Al363139.1		1	1	AB046784.1	4 0E-444 BE400832 4	1.0E-114 AW327456.1	AF077754.1	M13536.1	3E870004.1	1.0E-114 AL163227.2
	Most Similar (Top) Hit BLAST E Vatue	1.0E-114	1.0E-114 X04088.1	1.0E-114	1.0E-114 AF149773.	1.0E-114 J03171.1	1.0E-114 AA194468.	1.0E-114	1.0E-114	1.0E-114	1.0E-114 Z26298.1	1.0E-114	1.0E-114	1.0E-114 AU134187.	1.0E-114 AU134187.	1.0E-114 Y18000.1	1.0E-114 Y18000.1	1.0E-114	1.0E-114	1.0E-114	1.0E-114 U63041.1	1.0E-114 AB011133.	1.0E-114 AB011133	1.0E-114 AB046784.	4 OF-444 5	1.0E-114	1.0E-114 AF077754.	1.0E-114 M13536.1	1.0E-114 BE870004.	1.0E-114/
	Expression Signal	5.92	2.91	1.26	1.25	0.78	0.99	1.47	1.47	₩-	0.51	0.54	1.01	1.08	1.08	5.65	5.65	1.87	1.65	1.65	3.38	5.81	5.81	0.42	28.0	14.09	3.34	1.15	0.95	1.42
-	ORF SEQ ID NO:	27691	29119	22460	29980	30335	31110	31483	31484	31943	32665	31224		33770	33771	33824	33826	34600	34888	34889	35439	35514	36515	35744	35048		34546		36919	36942
	Exan SEQ ID NO:	14713	16205	16242	17082	17444	18236	18575	18575	18771	19423	18422	20014	20416	20418	20464	20464	ı	21475	-				81822	00566		L.,	22858	23420	23444
	Probe SEQ ID NO:	1681	3148	3187	4044	4417	6228	5474	5474	5876	6354	7191	7280	7460	7450	7499	7499	8223	8507	8507	9049	9119	9119	8853	0547	9769	9818	9066	10498	10522

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Citigle EAUT FIGURES EAUTONE MAITON	ORF SEQ Expression (Top) Hit Top Hit Acession Database ID NO: Signal Vatue	2827 37340 0.87 1.0E-114 BE171984.1 EST_HUMAN MR0-HT0559-250200-002-407 HT0559 Homo sapiens cDNA	16.04 1.0E-114 BE302888.1 EST_HUMAN	38018 3.01 1.0E-114 AV733454.1 EST_HUMAN	38019 3.01 1.0E-114 AV733454.1  EST_HUMAN	2.9 1.0E-114 11418041 NT	31725 3.55 1.0E-114 11034850 NT	5484 31728 3.55 1.0E-114 11034850 NT Homo sapiens hypothetical protein (DJ1042X10.2), mRNA	28044 2.83 1.0E-115 4758111 NT .	28165 2.37 1.0E-115	3239 3.36 1.0E-115 4557887 NT Homo septems keredin 18 (KRT18) mRNA	28313 5.22 1.0E-115 AW804759.1  EST_HUMAN	28628 1.12 1.0E-115 AISS9208.1 EST_HUMAN	9808 28627 1.12 1.0E-115 AB39208.1 EST HUMAN TITF-I INTERACTING PEPTIDE 5;	28792 0.78 1.0E-115 5174702 NT	28783 0.78 1.0E-115 5174702 NT	26795 68.69 1.0E-115 4503794 NT	27598 1.46 1.0E-115 AF229180.1 NT	27567 1.46 1.0E-115 AF229180.1 NT	Homo septiens Bruton's tyrosine lanese (BTK), eighe-D-gelectosidese A (GLA), L44-like ribosomet protein (L44L) and FTP3 (FTP3) genes, complete cds	1.7 1.0E-115 AW804759.1 EST_HUMAN	28089 2.74 1.0E-115 AJ245822.1 NT	6189 29100 2.74 1.0E-115 AJ245922.1 NT Homo septens mRNA for alpha-tubulin 8 (TUBA8 gene)	6532 29457 2.07 1.0E-115 AJ277892.1 NT Homo saptens partial TTN gene for titin	30002 4.75 1.0E-115 AB002348.2	7324 30204 0.86 1.0E-116 AL137163.1 IVT Novel human gene mapping to chomosome X	30347 3.89 1.0E-115 6912659 NT	30378 3.73 1.0E-115 4758279 NT	30616 2.63 1.0E-115 AL096867.1 NT	7723 30617 2.53 1.0E-115 AL08867.1 INT Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
-	Exam ORF S SEQ ID ID NO.	23827 37		24465 38		25974			13144 26	13235 26	13239	13386 26	13608			13846 26	13848 26	14593 27	14593 ZI	14884		16189 26	16189 28	16532 28		17324 30	17456 30	17491 30		17723 30
ŀ	Probe SEQ ID NO:	10907	11140	11524	11524	12619	12859	12859	24	130	134	202	587	687	787	787	882	L	1561	1858	23863	3432	3132	3488	4072	4295	4429	4465	4702	4702

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Table 4
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ORF SEQ Expression (Top) Hit Top Hit Accession Delabbase ID NO: Signal Value	2.1 1.0E-115 BE045880.1 EST_HUMAN PRP4 PROTEIN KINASE HOMOLOG;	38084 2.1 1.0E-115 BE046890.1 EST_HUMAN	38189 2.06 1.0E-115	1.62 1.0E-115 AF24078	28557 1.02 1.0E-116 BE275502.1 EST_HUMAN	28807 2.44 1.0E-116 4507334 NT	99:0	28044 2.89 1.0E-116 5174478 NT	28045 2.89 1.0E-116 5174478 NT	28350 1.86	Human offactory receptor off17-201-1 (OR17-201-1) gene, offactory receptor off17-32 (OR17-32) gene and offactory receptor pseudo_off17-01 (OR17-01) pseudogene, complete cds	28489 2.99 1.0E-116 AB018333.1 NT	28754 3.32	0.95 1.0F-118 1075151 HIMAN	29161 5.44 1.0E-116 L77570.1 NT	29162 5.44 1.0E-116 L77570.1 NT	30318 2.36 1.0E-116 5031954	30798 2.03 1.0E-116 Al907096.1 EST_HUMAN	31111 0.92	31326 0.92 1.0E-116 Al302062.1 EST_HUMAN	228407.rt Soeres, senescent, fibroblasts, NIDHSF Homo sepiens dDNA dane IMAGE:323245 6" similar to SW:MDHM MOUSE P08249 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR:	32845 1.8 1.0E-116 AB046856.1 NT	32846 1.8 1.0E-116 AB046856.1 NT	32723 0.95 1.0E-116 BE408097.1 EST_HUMAN	32982 0.73 1.0E-116 5729867 NT	32983 0.73 1,0E-116 5729867 NT
	38083	38084	38189		28657	26807		28044	28045	28350		28489	28754		28461	28162	30318	30798	31111	31326	32384	32845	32646	32723	32982	32983
Exan SEQ ID NO:	24527	24527		25036			13916		15034	15327	15357	15466	15829	16235		16244	l	17909	18238	18456	1978				19707	19707
Probe SEQ ID NO:	11589	11689	11726	12191	574	8	098	2013	2013	2316	2348	2462	2744	3180	3189	3189	4405	4892	5230	5351	0609	6336	6336	6408	6649	6649

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	Top Hit Descriptor	MR2-HT0379-210200-102-b04 HT0379 Homo sepiens cDNA	C02944 Human heart cDNA (Makamura) Homo sapiens cDNA clone 3NHC0567	AV716314 DCB Hamo septens cDNA dane DCBBCG06 5	EST62885 Jurkat T-cells V Homo sepiens aDNA 5" and straiter to straiter to keratin 2	EST62685 Jurket T-cells V Homo septens cDNA 5 end similar to similar to keratin 2	CM-BT043-090289-075 BT043 Homp seplens cDINA	601338268F1 NIH_MGC_63 Homo espiens cDNA clone IMAGE:3680680 6	qhoecct.x1 Scares_NFL_T_GBC_S1 Home septens cDNA clane IMAGE:1844168 S' similar to gb:X53741_ma1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);	Homo sepiens laminin, elpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA	Homo septens partial mRNA for xylosyltransferase I (XT-1 gene)	Homo septens partial mRNA for xylosythansferase I (XT-I gene)	QV4-HT0401-281289-083-c09 HT0401 Homo eapiens cDNA	CM2-CT0482-300800-349 e06 CT0482 Homo sepiens cDNA	qq41e04x1 Soeres_NhHMPu_S1 Hamo sepiens cDNA clane IMAGE:1935102 3' similar to WP:B0486.7 CE01765 ;	DKFZp76211110_r1 762 (synchym: hmel2) Hamo sapiens cDNA clane DKFZp762L1110 5	Homo sepiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, excus 13a through 15	Homo saptems ALR-like protein mRNA, pertiel ods	Human apolipoprotein B-100 (apoB) gene, eaon 10	EST369769 MAGE resequences, MAGE Homo sepiens CDNA	op32c11.s1 Sogres_NFL_T_GBC_S1 Homo sapiens cDNA done IMAGE:15/8548 3	EST188414 HCC cell line (matastasts to liver in mouse) II Homo septens cDNA 5' end simiter to ribosomal	probabilities    Company	Hand septems consigen, type if, within a (Alphut Syndring) (COLPAN), the Wall of the Syndring	DN-Zp454C1120 IT 434 (s)notyfit mess) frame sapeats curvi care Livi zpravu 1120 o	H.sapiens mRNA for TPCR16 protein	H.sepiens mRNA for TPCR16 protein	Homo sepiems Scer2 (SCAR2) gene, partial cds	Homo sepiens Scar2 (SCAR2) gene, partial cds	Homo sepiens mRNA for KIAA0866 protein, complete dos	60156265/F1 NIH MCC_20 Hamp septems curve dans tweet.socz14 o	
T IONS	Top Hit Database Source	EST_HUMAN	EST_HUMAN (	Г	П	EST_HUMAN I		EST_HUMAN (	T_HUMAN		NT	N		EST_HUMAN	EST HUMAN	Т		둫	NT	M	EST_HUMAN	EST_HUMAN		HOMAN		HOMAN	N	NT	N	۲		Т	EST_HUMAN
Olingia L	Top Hit Acessian No.	1.0E-116 BE158133.1		2	1.0E-116 AA354256.1	1.0E-116 AA354258.1		1.0E-116 BE565507.1	1.0E-116 AI216352.1	11418848 NT	1.0E-116 A.1277441.1		1.0E-116 BE159913.1	1.0E-116 BF335848.1	1 0E-118 AB87140 1	1.0E-116 AL134889.1	4826636 NT	4F124393.1	1.0E-117 AF284750.1	M19816.1	1.0E-117 AW957699.1	1.0E-117 AA978114.1		1.0E-117 AA316723.1	866964 NI	1.0E-117 AL042120.1	X89670.1	X89670.1	1.0E-117 AF134304.2	1.0E-117 AF134304.2	1.0E-117 AB020673.1	1.0E-117 BE730508.1	1.0E-117 AA323348.1
-   	Most Similar (Top) Hit BLAST E Vatue	1.05-116	1.0E-116 C02944.1	1.0E-116/	1.0E-116	1.0E-116	1.0E-116 AI904151.1	1.0E-116	1.05-116	1.0E-118	1.0E-116	1.0E-116	1.0E-116	1.0E-116	1 OF 448	1.0E-116	1.0E-117	1.0E-117	1.0E-117	1.0E-117 M19816.1	1.0E-117	1.0E-117		1.05-117	1.0E-117	1.0E-117	1.0E-117 X89670.1	1.0E-117 X89670.1	1.0E-117	1.05-117	1.0E-117	1.0E-117	1.0E-117
	Expression	208	1.50	7.19	1.32	1.32	<u>1</u> .	1.39	2.9	1.49	0.71	0.71	16:0	2.44	286	1.08	2.5	0.86	22	204	1.28	1.51		5.89	2.1	1.85	1.19	1.19	10.31	10.31	4.01	3.29	0.53
	ORF SEQ ID NO:		33417	33728	35106	Ì				1			37128				28547		ļ			<u> </u>				30521				30758	30881		31269
	SEO ID NO:	19720	20106	20377	21680	21680	21791	22258	22419	22960	23555	23555	23635	24010	24469	25840		1_	L	1_	15235	16335	l.		17398	17829	L				<u> </u>	18524	18380
	Probe SEQ ID NO:	8883	7130	7410	8712	8712	8827	9280	9455	10033	10633	10633	10713	11048	4,7,7	1200	989	4070	1228	1848	222	3281		4018	4371	4608	4755	4755	4847	4847	4977	5421	7148

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	Acession Top Hit Descriptor Acession Deterbese Top Hit Descriptor Source	Ŋ	NT.	EST_HUMAN	EST_HUMAN	1 EST_HUMAN		D834989 NT	1 EST_HUMAN	1	NT	21 EST_HUMAN	NT	1420222 NT	MT	1424835 NT	1424836 NT	i.1 NT	-1.	3.1 EST_HUMAN	4501848 NT	4501848 NT Homo sapiers ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA	,	Į	1 EST HUMAN	7857016 NT		5.1 EST HUMAN 601281947F1 NIH MGC_44 Homo saplens cDNA clone IMAGE:3604019 5	S.1 EST_HUMAN	EST_HUMAN	EST_HUMAN	¥	NT Human breakpoint cluster region (BCR) gene, complete cds
Y PIGINO	Top Hit Acession No.				1.0E-117 AV717788.1  E	-	10834989 NT	10834989 N	ŀ	1		2.1	1.0E-117 AF099033.1 N			11424835 N	11424835N	1.1	1.1	1.7	4501848	4501848 N	,		-	7857016	5174680 N	1.0E-118 BE389705.1 E	7.	1.0E-118 BE389705.1 E	1.0E-118 AW951729.1		
	Most Similar (Top) Hit BLAST E Veitue	1.0E-117 L76571.1	1.0E-117 L76571.1	1.0E-117 AV717788	1.0E-117	1.0E-117 AI950145.	1.0E-117	1.0E-117	1.0E-117 Al904151.	1.0E-117 Al904151.	1.0E-117 D16524.1	1.0E-117 BE73392	1.0E-117	1.0E-117	1.0E-117 D83778.1	1.0E-117	1.0E-117	1.0E-117 AB01154	1.0E-117 AB01154	1.0E-117 BE269856	1.0E-117	1.0E-117	4 05-447 85224880	1.0E-111 AF 181500	1.0E-118 AL045854	1.0E-118	1.05-118	1.0E-118	1.0E-118 BE38970	1.0E-118	1.0E-118	1.0E-118 U07000.1	1.0E-118 U07000.1
	Expression Signal	4.55	4.55	3.74	3.71	3.79	1.01	1.01	9.0	0.63	1.61	1.71	0.64	1.98	2.17	1.96	1.96	272	272	34.46	1.76	1.78	66	000	127	4.46	1.88	8:	1.83	1.83	1.55	2.48	2.48
	ORF SEQ ID NO:	34004	34005	34121	34122	34691	35042	35043	35144	35145	36046	36546	36713	37370	37691	37850	37851	38101	38102	<b> </b> -	38383	38394		26400	28136	26509	26923	28280	28281	28282		28760	28761
	Econ SEQ ID NO:	20641	20641	20747	20747	21280	2822	24822	21722	21722	22597	23071	25701	23854	24161	24322	24322	24542	24542		24802	24802	77090	13180	13241	13589	15854	15256	I	15256	15348	15743	15743
	Probe SEQ ID NO:	7683	7885	7785	7796	8311	8654	8654	. 8754	8764	8654	10145	10306	10834	11207	11375	11375	11604	1188	11722	11821	11921	75,58	7 7	. 8	518	93	242	2242	2242	2337	2750	2750

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Single Explication in Dolle mailor	Exam SEQ in ID NO: Signed BLASTE No. Source Survey No. Signed in Value		16285 29187 4.61 1.0E-118 Ai347694.1 EST_HUMAN   qp01f05xf NCI_CCAP_Kd5 Homo saplens cDNA done IMAGE:1816769.3'	29188 4.61 1.0E-118 AIS47894.1 EST_HUMAN	29924 0.98 1.0E-118 AB024469.1 NT	17149 30041 5.07 1.0E-118 D23680.1 NT   Human mRNA for ribosomal protein, complete cds	31508 1.86 1.0E-118 AF142624.1 NT		31984 0.66 1.0E-118 11422054 NT	18807 31985 0.66 1.0E-118 11422054 NT Homo septents re-elin (RELN), mRNA		18892 32075 0.58 1.0E-118 U08892.1 NT Hunan GS2 gene, excm 6	19047 32247 0.95 1.0E-118 11425900 NT Homo septems T-box 4 (TBX4), mRNA	19047 32248 0.95 1.0E-118 11425900 NT Homo saplents T-box 4 (TBX4), mRNA	4557732 NT	57732 NT	EST_HUMAN	1.0E-118 AL043781.1 EST_HUMAN	34179 6.13 1.0E-118 11431050 NT	Z	1 EST_HUMAN	1.0E-118 BE082865.1 EST_HUMAN	1 . EST HUMAN	1 EST_HUMAN	1 EST_HUMAN	1.0E-118 AB002381.1 NT			22037 35461 1.32 1.0E-118 4557732 NT Homo sepiens latent transforming growth factor beta binding protein 2 (LTBP2) mtRNA	1 EST_HUMAN	35825 0.63 1.0E-118/AL048474.2 EST_HUMAN	36341 2.29 1.0E-118 7657016 NT	23620 37115 0.48 1.0E-118 BE736213.1 EST_HUMAN 601307146F1 NIH_MGC_39 Hamo sapiens cuna cane inace=36416U3 o
		3178			L																												
	Probe Ex SEC ID SEC NO:	3121 16		l			L	5497 18	乚		5800		]		L			$\mathbf{L}_{-}$	1_	L	2 9088		2 02.18		8732 2		9021 2	L	L		9421 2	9951 2	10698 2

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Top Hit Descriptor	601307146F1 NIH_MGC_39 Homo sepiens cDNA clone IMAGE:3841603 5	7n17e09x1 NCI_CGAP_Bm23 Homo sepiens cDNA clone IMAGE:3564785 % similar to SW:2P3A_HUMAN P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR;	UI-H-BWO-alo-e-07-0-UI.s1 NCI_CGAP_Sub6 Homo expiens cDNA clone IMAGE:27297723	EST188814 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light	chain 1, cytoplasmic	801488614F1 NIH_MGC_70 Hamo sapiens cUNA clane IMAGE:3801563 5	601489514F1 NIH_MGC_70 Home septems cDNA clone IMAGE:3801563 5	QV0-UM0091-120900-385-b12 UM0091 Hamo saptens cDNA	QV0-UND081-120900-385-b12 UN0091 Homo sapiens cDNA	Homo sapiens flap structure-specific endonuclease 1 (FEN1), mRNA	Homo sapiens CGI-105 protein (LOC51011), mRNA	Homo sapiens mRNA for KIAA0930 protein, partial cds	Homo sepiens hypothetical protein FLJ10062 (FLJ10062), mRNA	on10b06.s1 NCI_CGAP_Lu5 Hamo sapiens cDNA clone IMAGE:1556241 3' similar to WP:E04F6.2	CE01214;	Homo sepiens glutamete receptor, tonotropic, keinate 1 (GRIK1) mRNA	AU13S389 NTZRP4 Homo sapiens cDNA clone NTZRP4001891 5'	Human neurofibromin (NF1) gene, complete cds	RC1-NN0073-250800-018-g06 NN0073 Homo sepiens cDNA	AV683731 GKC Homo sapiens cDNA done GKCDHB03 6	DKFZp782M0710_r1 762 (synonym: hmel2) Homo septems cDNA clone DKFZp762M0710 6	DKFZp762M0710_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5	qb77c09.x1 Soares_febal_heart_NbH119W Homo sepiens cDNA clone IMAGE:1706128 3' skrifar to SW:K1C1_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10;	Homo sepiens matrix metallxproteinase 28 (MMP28) mRNA, complete cds	Homo sepiens metrix metalloproteinase 28 (MMP28) mRNA, complete cds	tm23f10.x1 Scares_NFL_T_GBC_S1 Homo septems cDNA clone IMAGE:21574513'	Human c-festips proto-oncogene	EST386296 MAGE resequences, MAGM Homo septens cDNA	601592005F1 NIH_MGC_7 Home septens cDNA done IMAGE:3946081 57	601280584F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3822526 6	Homo sepiens melanama differentiation associated protein-5 (MDA5), mRNA	Homo septens KiAA0477 gene product (KiAA0477), mRNA
Top Hit Detabase Source	EST HUMAN	EST_HUMAN	EST HUMAN		EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Į,	Ā	IN.	Ę		EST_HUMAN	H	EST_HUMAN	IN	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	EST HUMAN	Ę	Z	EST_HUMAN	ᅜ	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	Ę	Ę
Top Hit Acession No.	BE736213.1	BF185407.1	=				2	.1	.1	6325465 NT	TN05607	AB023147.1	8922205 NT		.1	4504116 NT	1.1		.1	.1	.1	1	Ţ	۲.	۲.	1.		3.1	1.0E-119 BE796614.1	.1	11545921 NT	11036843 NT
Moet Similar (Top) Hit BLAST E Value	1.0E-118 BE736213	1.0E-118 BF185407	1.0E-118		1.0E-118 AA315007	1.0E-118	1.0E-118	1.0E-118 BF083687	1.0E-118 BF083687	1.0E-118	1.0E-119	1.0E-119 AB023147	1.0E-119		1.0E-119 AA916760	1.0E-119	1.0E-119 AU133399	1.0E-119 M89914.1	1.0E-119 BE938121	1.0E-119 AV683731	1.0E-119 AL 134903	1.0E-119 AL 134903.	1.0E-119 AI150703.	1.0E-119 AF315683	1.0E-119 AF315683	1.0E-119 AI476732	1.0E-119 X08292.1	1.0E-119 AW974190	1.0E-119	1.0E-119 BE615150	1.0E-119	1.0E-119
Expression Signal	0.46	2.31	0.54		6.48	1.9	1.9	1.51	1.51	1.58	1.75	. 2.88	98'0		0.68	1.12	2.79	14.68	288	1.55	0.68	0.68	7.38	0.69	0.69	*	2.67	4.98	1.3	1.15	0.5	1.1
ORF SEQ ID NO:	37116	37158						95586	99888		27034	27972	. 29087			62662	31391	31404	31411	31538	31937	31938	32563	32730	32731	32778	32836	32952	33964			36879
Eten SEQ ID NO:	23620			L		i	24765	24768	24768		15857	14973	16178		16308	17015		18526	18531	18608	18786	18788	19323	L	19483	19530	19683	19674	20600		23039	23192
Probe SEQ ID NO:	10698	10741	10899		11607	<del>1</del> 884	11884	11887	11887	12036	1038	1960	3119		3264	3975	5410	5423	5428	2208	5671	5671	6250	6416	6415	<b>8465</b>	8604	8816	7846	60 <b>0</b> 6	10113	10267

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i able 4 igle Exon Probes Expressed in Bone Marrow	Top Hit Descriptor	8832705.11 NCI_CGAP_GCB1 Homo sapiens cDNA done IMAGE:814977 5	Homo sepiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, excns 16-17	Homo sepiens hypothetical protein FLJ10208 (FLJ10206), mRNA	Homo sapiens hypothetical protein FLJ10208 (FLJ10208), mRNA	Homo septems Scd mRNA for stearcyl-CoA desaturase, complete cds	Homo sepiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, excris 16-17	Homo sepiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, excrns 18-17	602186072F1 NIH_MGC_45 Hamo sepiens cDNA clane IMAGE:4310833 51	RC3-CT0212-240889-011-f03 CT0212 Homo sapiens cDNA	Homo sapiens synaptojanin 1 (SYNJ1), mRNA	Homo sepiens intersectin 2 (SH3D1B) mRNA, complete cds	Homo sapiens intersectin 2 (SH3D1B) mPNA, complete cds	yy40g12.r1 Scares melanccyte 2NB-IM Homo sapiens cDNA clone IMAGE:273768 5	Homo sepiens cysteine-fich repeat-containing protein SS2 precursor, mRNA, complete ods	Homo sepiens dishitegrin and metalloprotease domain 10 (ADAM10) mRNA	Homo sepiens equaportn 4 (AOP4), spilce variant b, mRNA	Homo sepiens synephojenin 1 (SYNJ1), mRNA	Homo sapiens cAMP-specific phosphodiestenese 84 (PDE8A) mRNA, partial cds	Homo sepiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds	Homo sepiens stanniocalcin (STC) gene, pertial cds	Homo sepiens stanniocalcin (STC) gene, partial cds	602183884F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5	602183894F1 NIH_MGC_42 Homo sepiens dDNA clone IMAGE-4300174 5	Human P-glycoprotein (MDR1) gene, excris 6 and 7	Human P-glycoprotein (MDR1) gene, excris 6 and 7	Human TBXAS1 gene for thrombosane synthese, expn 7	Human gene for neurofilament subunit M (NF-M)	Human gene for neurofilament subunit M (NF-M)	602035352F1 NCI_CGAP_Bm64 Hamo sepiens cDNA clane IMAGE:4183333 67	Homo septems mRNA for KIAA1231 protein, pertial cds	Homo sapiens mRNA for KIAA1231 protein, pertial cds	Homo sapians mRNA, chromosome 1 specific transcript KIAA0495	Homo sepiens mRNA, chromosome 1 specific transcript KIAA0495	Homo sapiens mRNA for KIAA0465 protein, partial cds
xon Probes E	Top Hit Database Source	EST_HUMAN	NT	NT	NT	NT	NT	M	EST_HUMAN	EST_HUMAN	NT	NT	M	EST_HUMAN	NT	NT	NF	NT	NT	NT	Ŋ	Ŋ	EST_HUMAN	EST_HUMAN	N	M	NT	NT	NT	EST_HUMAN	NT	NT	Ŋ	Ę	¥
Single E	Top Hit Acession No.	1.0E-119 AA465124.1	1.0E-119 A.1297701.1	11425837 NT	11426837 NT	1.0E-119 AB032281.1	1.0E-119 A.1297701.1	1.0E-119 A.1297701.1	1.0E-119 BF569571.1	1.0E-119 AW847519.1	4507334	1.0E-120 AF248540.1	1.0E-120 AF248540.1	444873.1	1.0E-120 AF167708.1	4557250 NT	4755124 NT	4507334 NT	AF058490.1	1.0E-120 AF058490.1	1.0E-120 AF098463.1	1.0E-120 AF098463.1	1.0E-120 BF568222.1	1.0E-120 BF568222.1	W29428.1	V29428.1	334819.1	700067.1	100067.1	1.0E-120 BF337599.1	1.0E-120 AB033057.1	1.0E-120 AB033057.1	1.0E-120 AB007884.1	1.0E-120 AB007984.1	1.0E-120 AB007834.1
	Most Similar (Top) Hit BLAST E Value	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-120	1.0E-120	1.0E-120	1.0E-120 N44873.1	1.0E-120	1.05-120	1.0E-120	1.0E-120	1.0E-120	1.05-120	1.0E-120	1.0E-120	1.0E-120	1.0E-120	1.0E-120 M29428.1	1.0E-120 M29428.1	1.0E-120 D34819.1	1.0E-120 Y00067.1	1.0E-120 Y00067.1	1.0E-120	1.05-120	1.0E-120	1.0E-120	1.0E-120	1.0E-120
	Expression Signal	5.31	1.12	6.73	0.73	0.79	1.86	1.86	13.43	321	0.00	1.6	1.6	2.56	2.5	1.4	1.08	1.34	1.81	1.81	2.67	267	13.85	13.85	0.63	0.53	1.84	1.78	1.78	282	0.75	0.75	2.5	2.5	1.13
	ORF SEQ ID NO:	37026		37344	37346	87419	37870	37871			26322	27040	17041	27429	27614		85582		30297	30208	90908				32910	32911	34147	34602		35068	35138	35139	35141		35185
	Exam SEQ ID NO:	23530	23790	23831	23831	23905		24340	24476	25901	13395	14088	14088	14455	14637	14850	15537	13395	17413	17413	17712	17712	18915	18915	19643	19643	20771	21185		21643	21715			21719	
	Probe SEQ ID NO:	10608	10870	10911	1001	10985	11394	11394	11535	12486	301	1042	1042	422	1605	<u>\$</u>	2534	3318	4385	4385	4691	169H	9289	5826	6583	8899	7823	8228	8228	8675	8747	8747	8751	8751	8788

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	Top Hit Descriptor	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3825544 5	801307739F1 NIH_MGC_44 Hamo septens cDNA clone IMAGE:3625544 5	601888956F1 NIH_MGC_17 Home sapiens cDNA clone IMAGE:4122876 5	AU133205 NT2RP4 Homo septens cDNA clone NT2RP4001541 5	Novel human game mapping to chomosome 13, stmiller to rat RhoGAP	CALBT043-090298-075 BT043 Homo septems cDNA	Homo sapiens mRNA for KIAA1077 protein, partial cds	601176727F1 NIH_MGC_17 Homo septens cDNA clone IMAGE:3532015 5	601443135F1 NIH_MGC_66 Hamo septens cDNA clone IMAGE:3847281 67	601443135F1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:3847281 5	Human muscle glycogen phospharylase (PYGM) gene, 6UTR and exan 1	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens NF2 gene	AU134963 PLACE1 Hamo saplens cDNA dane PLACE1000899 5	Homo sepiens TNF receptor-essociated factor 1 (TRAF1) mRNA	Homo sapiens inosital polyphosphata 4-phosphatase, type I, 107kD (INPP4A), spilos variant e, mRNA	Homo sepiens inosital polyphosphate-4-phosphatese, type I, 107t0 (INPP4A), splice variant e, mRNA	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds	Homo sepiens serine pelmitoyi transferese, subunit il gene, complete cds; and unknown genes	Homo sepiens hHb3 gene for hair keratin, excris 1 to 9	Homo sapiens hHt3 gene for hair keratin, exons 1 to 9	Homo sapiens mRNA for KIAA1337 protein, partial cds	Homo septens mRNA for KIAA1337 protein, partial cds	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds	457b01x1 NCI_CGAP_Pan1 Homo saplens cDNA clone IMAGE:20054173	H.saplens ECE-1 gene (exon 17)	Homo sepiens synaptojanin 1 (SYNU1), mRNA	[hu09f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE;3186119 3'	601140485F1 NIH_MGC_9 Hamo septens cDNA clane IMAGE:3048820 5	Homo sepiens Xq pseudosutusomal region; segment 2/2	RC3-NN0068-270400-011-f02 NN0088 Hamo capiens cDNA	RC3-NN0068-270400-011-f02 NN0068 Homo sepiens cDNA
	Top Hit Datebase Source	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	EST_HUMAN	¥	EST_HUMAN	NT	EST HUMAN	<b>EST_HUMAN</b>	<b>EST_HUMAN</b>	LN.	IN	NT	EST_HUMAN	N	TN.	¥	5	Ę	TN	NT	NE	IN	IN	EST_HUMAN	IN	IN	<b>EST_HUMAN</b>	<b>EST_HUMAN</b>	IN	EST_HUMAN	EST_HUMAN
A	Top Hit Acession No.	1.0E-120 BE392102.1	1.0E-120 BE392102.1	3F306541.1	1.0E-120 AU133206.1	1.0E-120 AL049801.1	1.0E-120 AI904151.1	1.0E-120 AB029000.1	1.0E-120 BE296387.1	1.0E-120 BE867619.1	3E867619.1	J94774.1	11417862 NT	/18000.1	1.0E-121 AU134963.1	5032/92 NT	4755139 NT	4755139 NT		1.0E-121 AF111168.2	118208.1	/19208.1	AB037758.1	4B037758.1	<b>1F165156.2</b>	1.0E-121 Al263294.1	<b>137.1</b>	4507334 NT	1.0E-121 BE222250.1	1.0E-121 BE271424.1	1.0E-121 AJZ71736.1	1.0E-121 AW898086.1	1.0E-121 AW898088.1
	Most Similar (Top) Hit BLAST E Value	1.0E-120	1.0E-120	1.0E-120 BF306541.	1.0E-120	1.0E-120	1.0E-120	1.0E-120	1.0E-120	1.0E-120	1.0E-120 BE867619	1.0E-120 U94774.1	1.0E-120	1.0E-121 Y18000.1	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121 L78831.1	1.0E-121	1.0E-121 Y19208.1	1.0E-121 Y19208.1	1.0E-121 AB037758.	1.0E-121 AB037758.	1.0E-121 AF155156.2	1.0E-121	1.0E-121 X91937.1	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121
	Expression Signal	4.14	4.14	3.89	7.33	0.67	0.51	3.02	19.45	2.6	2.5	223	1.45	26.0	1.92	1.83	1.17	1.17	1.36	1.69	3.41	3.41	0.84	0.84	8.63	1.39	3.4	0.93	0.86	0.58	0.7	0.82	0.82
	ORF SEQ. ID NO:		36248	38505						38216		38436	31785	28113	26392	38721	28007	28008		28961			22518	29519	20848	30267		31067	31198	31801		31230	31231
	Ean SEQ ID NO:	22795	22795	23028	23044	23061	23177	89882	24404	24638	24638		25318	13191	13462	15848	15004	15004	15120	16038	16154	16154	16593	16583	16733	17385	18026	L	18445	18737			18387
ſ	Probe SEQ ID NO:	9859	8828	10102	10118	10135	10262	10436	11461	11672	11672	11963	12632	1/	378	725	288	1983	2112	2980	3097	3097	3547	3547	3690	4358	5012	5182	5340	5641	7072	7165	7155

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Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	Homo sapiens gamma-aminobutyric acid (GABA) A recaptor, alpha 2 (GABRA2), mRNA	Homo sapiens DNA for prostacyclin synthase, exon 8	Homo sapiens DNA for prostacycilin synthase, exon 8	ia05g05.y/ Human Pancreatic Islets Homo saplens cDNA 5' similar to TR:075457 075457 CYTOSOLIC PHOSPHOLIPASE A2-GAMIMA.;	ROSGOS, VI Human Pancreatic Islets Homo septens cDNA 5' similar to TR:075457 075457 CYTOSOLIC PHOSPHOLIPASE A2-GAMIMA.;	Homo sapiens COX11 (yeast) hamalog, cytochrane c addase assembly protein (COX11), mRNA	Homo sepiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele,	camplete cds	Homo sapiens chioride intracellular channel 4 like (CLIC4L), mKNA	y/74c01.s1 Sceres fetal liver spieen 1NFLS Hamo sapiens cDNA cione IMAGE:248448 3	AU119320 HEMBA1 Homo saplens cDNA clone HEMBA1005536 5	Homo sapiens T-cell lymphoma invasion and metastasts 1 (TIAMM), mRNA	Homo sepiens intersectin short isoform (ITSN) mRNA, complete cds	Homo sepiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA	Homo septiens intersectin short isoform (ITSN) mRNA, complete cds	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)	Homo seplens cysteine-tich repeat-containing protein SS2 precursor, mRNA, complete cds	Homo septens collegen, type XII, alpha f (COL12A1), mRNA	Homo sepiens collegen, type XII, alpha 1 (COL12A1), mRNA	601497032F1 NIH_MGC_70 Homo sepiens cDNA clone IMA(3E:3888338 5	601896173F1 NIH_MGC_19 Hamo saplens cONA dane IMAGE:4125234 6	601896173F1 NIH_MGC_19 Hamo sapiens cDNA clane IMAGE-4125234 5	Homo sepiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete	cds	Homo septens amyldd beta (A4) precursor protein (protesse nech-ll, Alzheimer disease) (APP), mRNA	UI-HF-BNO-411-4-03-0-UI.r1 NIH_MGC_50 Hamo sepiens aDNA clane IMAGE:3079948 51	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 6	601113567F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3354232 5	8K4GH06.s1 Sogres_bests_NH   Hamo septens CONA done IMAGE:1405339 3
	Top Hit Database Source		IN IN	IN	EST_HUMAN	EST_HUMAN					$\neg$	LHUMAN		TA		Į,	¥	TN				EST HUMAN	EST_HUMAN		Į.		T_HUMAN			EST_HUMAN
	Top Hit Acesslan No.	11436217 NT			1.0E-121 AW683858.1	1.0E-121 AW583858.1	11427788 NT		1.0E-121 AF084200.1	7330334 NT	<b>159624.1</b>	AU118320.1	11526178 NT	1.0E-122 AF114488.1	11526176 NT	1.0E-122 AF114488.1	W20707.1	1.0E-122 AF167708.1	11418424 NT	11418424 NT	1.0E-122 BE006024.1	1.0E-122 BF316170.1	1.0E-122 BF316170.1		1.0E-122 AF284717.1	4502168 NT	AW504645.1	1.0E-122 BE256039.1	1.0E-122 BE256039.1	1.0E-122 AA888671.1
	Most Similar (Top) Hit BLAST E Vatue	1.0E-121	1.0E-121 D84122.1	1.0E-121 D84122.1	1.0E-121	1.0E-121	1.0E-121		1.0E-121	1.0E-121	1.0E-121 N59624.1	1.0E-121	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122 M20707.1	1.0E-122	1.0E-122	1.05-122	1.0E-122	1.0E-122	1.0E-122		1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122
-	Expression Signal	1.67	222	222	67.0	6.0	1.87		1.52	3.61	3.42	4.22	223	3.36	21	3.20	16.66	1.02	1.67	1.67	5.11	8.15	8.15		0.91	1.03	1.4	1.31	7.59	0.6
	ORF SEQ ID NO:	34649			36630	38831			37825	37783	37815	38175	26287	28347		26897	27249	27714	27741	27742	27856				28834	30789		31904		33740
	SEQ ID	21238	21242	21242	23142	23142	24090		24096	24285	24290	24600	13363	13425	13445	13838	14262	14732	14755	14755	14858	15502	<u>.                                    </u>	L	15911	17900	<u>_</u>		i	20389
	Probe SEQ ID NO:	8383	8273	8273	10217	10217	11130		11136	11315	11340	11684	267	88	358	883	1224	1702	1725	1725	1831	2499	2489		2851	4883	5025	5643	6920	7422

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Most Shriler Top Hit Acession Database Top Hit Descriptor Source Source	0.51 1.0E-122 AA224259.1 EST_HUMAN to TR:0940370 0940370 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE;	0.61 1.0E-122 AA224259.1 EST HUMAN to TR:G940370 G940370 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE;	1.0E-122 AJZ76801.1		0.78 1.0E-122 AIS59018.1 EST_HUMAN SWAMTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.;	0.78 1.0E-122 ARREGER 1 EST HUMAN SWAMTA1 HUMAN 0.13330 METASTASIS-ASSOCIATED PROTEIN MTA1.:	1.0E-122 AL117294.1 NT	1.0E-122 AB024068.1 NT	1.6 1.0E-122 11434816 NT Homo sapiens thyroid hormone receptor interactor 11 (TRIP11), mRNA	5.83 1.0E-122 11418187 NT Homo sepiens phosphomennomulase 1 (PMIM), mRNA	3.03 1.0E-122 M20707.1 NT Human kappa-immunoglobutin garmine pseudogene (Chr22.4) variable region (subgroup V kappa II)	1.18 1.0E-129 BF345274.1 EST_HUMAN 602018068F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153670 6	1.0E-128 BF345274.1   EST_HUMAN	AL163249.2 NT	2.2 1.0E-123 5803114 NT Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mPNA	Homo sapiens phosphalidylinositid-4-phosphale 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products products	5.26 1.0E-123 4505818INT products	83.95 1.0E-123 A.1388641.1 NT Homo septens partial mRNA for immunoglobulin kappa chain variable region (IGVK gene), sample GN02	2.75 1.0E-123 M55419.1 NT Human amedogenin (AMELY) gene, 3' end of cds	NT	2.76 1.0E-123 M65419.1 (NT (Human smelogenin (AMELY) gene, 3' end of cds	3.14 1.0E-123 7705962 NT Homo sepiens RAB9-like protein (LOC61209), mRNA	6912617 NT	L34219.1 NT	1.0E-123 L34219.1 NT	1.31 1.0E-123 BE799746.1 EST_HUMAN   801591108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3845433 57
C Expression	- E	22	88	8	- 8	<u> </u>	150	8	2	╁	19	ন	2	14	12	7	핥	83	\$	\$	47	厂	R	沒	g	ß
ORF SEQ ID NO:	34471		35539			38087					27219	8 26772			27021	27241	27242	27459	3 28145	5 28146	3 28147	-	8 28239	1 31555		7 31925
	8135 21072 34471	24072	ļ	22348	12027	23831	23415	24877	24973	25063	13107 14262 27219	769 13828 26772	13828		1024 14070 27021	1243 14279 27241	1243 14279 27242	1449 14482 27459	15128		15128	2323 15334	16318		18621	18757

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	Top Hit Descriptor	AU118435 HEMBA1 Hamo sapiens aDNA clane HEMBA1003591 6"	yg84e03.11 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:202444 6' similar to SP:YAK1_YEAST P14680 PROTEIN KINASE YAK1;	Human growth harmone releasing harmone gene, exan 7	Human hBRAVONir-CAM precursor (hBRAVONir-CAM) gene, complete cds	Homo sepiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA	Homo sapiens 2-5 digosdenylate synthetase 2 (OAS2), mRNA	601152815F1 NIH_MGC_19 Homo septems cDNA done IMAGE:3508162 5	y 689d11 r.1 Soares melanocyte 2NbHM Homo sapiens cDNA clone INAGE: 268917 5' similar to PIR: 549611 S49611 protein kinase PiqoA - Phycomyces blekesleeanus;	y889d11 rf Scenes metanocyte 2NbHM Homo septens cDNA done IMAGE:288917 5' stmilar to PIR:S48811 S48811 protein kinsse PloA - Phycomices biakesteesinus :	All 131881 NT2RP3 Home services (DNA clone NT2RP3003409 5	ACTION INTELL STUDIES Explain COLOR NUMBER OF STUDIES	10151661 N. ZATA DIGING SEPTEMBER WITH GIVE SANDANG O	KC4-b (0311-231186-012-407 b) to 11 runib septemb curv	Homo sepiens mRNA for KIAA0454 protein, partial cds	Oryctolegus cunicutus New Zeafand white elongation factor 1 alpha (Rabeflaz) mRNA, complete cds	Homo sepiens Jerky (mouse) homolog-tike (JRKL), mRNA	602088791F1 NIH_MGC_83 Hamo sepiens cDNA clane IMAGE-4250879 5	602086791F1 NIH_MGC_83 Hamo septens cDNA clane IMAGE:4250879 5	Homo sapiens T-cell lymphoma trvesion and metastasis 1 (TIAM1) mRNA	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sepiens DNA for emyloid precursor protein, complete cds	Homo septens chromosome 21 segment HS21C046	zi81604.r1 Stratagane achizo brain S11 Homo capiens cDNA cione IMAGE:728719 6' similar to TR:C300482 G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;	z181b04.r1 Stratagene schizo brain S11 Homo saplans cDNA clone IMAGE:728719 6' similar to TR:G300482	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);	Human putative ribosomal protein S1 mRNA	Homo sepiens T-cell lymphoma invasion and metastasis 1 (TIAM) mRNA	Homo sapiens hypothetical protein (HSPC068), mRNA	Homo sepiens glucose transporter 3 gene, exons 9, 10, and complete ods	Homo sepiens glucose transporter 3 gene, exons 9, 10, and complete cas
artin mana artin artin	Top Hit Datebase Source	EST_HUMAN	EST_HUMAN	П	M			EST_HUMAN	EST_HUMAN		T	Т	Т	HOMAN	¥			T_HUMAN	EST_HUMAN		NT	N	M	EST HUMAN		EST_HUMAN	Ŋ	M	NT	K	뉟
28.10	Top Hit Acession No.	1.0E-123 AU118435.1	153198.1			41525833 NT	11436439 NT	1.0E-123 BE263001.1	435841.1	U2E944 4	N (404004 4	1.0E-123 AU131861.1	1.0E-123/AU131881.1	1.0E-123 AW371924.1	1.0E-123 AB007023.1	J09823.1	4504806 NT	1.0E-123 BF677292.1	1.0E-123 BF677292.1	4507500 NT	4507500 NT	D87675.1	1.0E-124 AL163246.2	1.0E-124 AA397551.1		1.0E-124 AA397551.1	1.0E-124 AF155654.1	4507500 NT	7705446 NT	1.0E-124 AF274892.1	1.0E-124 AF274892.1
	Most Similar (Top) Hit BLAST E Vatue	1.0E-123	1.0E-123 H53198.1	1.0E-123 U42224.1	1.0E-123 U65258.1	1.0E-123	1.0E-123	1.0E-123	1.0E-123 N35841.1	1 00 438844	201-101	1.05-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123 009823.1	1.0E-123	1.0E-123	1.0E-123	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124		1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124
	Expression Signal	1.97	0.83	124	0.67	6.0	1.20	1.87	0.71	27.0	0.0	6.0	0.5	1.43	2.03	31.72	0.44	5.3	6.3	1.18	1.18	0.79	211	8.04		8.04	6.08	1.34	4.34	12.68	12.68
-	ORF SEQ ID NO:	32940	33564		İ				34418				34627	٠	36205	36253		38489					28485			26884	28763		26916		
	Electron SEQ ID	19871	2023	20235	20368	20592	20847	20856	24020	8	71000	21217	21217	21847	23122	22789	23293	24905	24905	13364	13364	L	L	13754	Ĺ.	13754	13818	L	13980		14384
	Probe SEO ID NO:	8813	7188	7212	7400	7832	200	7913	808	. 8	3	8248	8248	8880	9724	88	10370	12029	12029	88	88	274	88	89		288	758	88	98 8	1349	1349

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igle Exon Probes Expressed in Boile Marrow	Top Hit Descriptor	UI-HF-BN0-aicz-b-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078846 5'	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17	hib6c06.x1 Soares_NFL_T_GBC_S1 Homo septems cDNA clone IMAGE-2280905 31	\$19603.X1 NC_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:031662 031662 YKRS PROTEIN. ;	f19603x1 NCI_CGAP_Gas4 Homo septens cDNA clone IMAGE:2141960 3' similar to TR:031662 031662 YKRS PROTEIN.;	z81b04.rl Strategene schizo brain S11 Homo septens cDNA cione IMAGE:728719 6' struitar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;	281604.71 Strategene schizo brain S11 Homo septens cDNA clone IMAGE:728719 5' striitar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);	Homo sapiens mRNA for KIAA1093 protein, pertial cds	Homo sepiens calcineum binding protein 1 (KIAA0330), mRNA	Homo sepiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sepiens mRNA for KIAA1172 protein, pertial cds	601577861F1 NIH_MGC_8 Hamo sepiens cDNA clane IMAGE:3926885 5	HA0086 Human fetal liver cDNA library Homo sapiens cDNA	HA0086 Human fetal liver cDNA library Homo sapiens cDNA	Homo sepiens ALR-tike protein mRNA, partial cds	zkä3c07.s1 Scares_pregnarit_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb>x8s867_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPOTE (HUMAN);	Homo sepiens chromosame 21 segment HS21C010	Homo sepiens KUA40744 gene product; histone deacetylase 7 (KIAA0744), mRNA	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA	Homo septiens Bruton's tyrosine kinase (BTK), alpine-D-galactosidase A (GLA), L44-like ribosomal protein	(LAAL) and FIP3 (FIP3) ganes, complete cos	Homo sapiens Usurpin-alpha mRNA, complete cds	Homo sepiens Usurpin-elpha mRNA, complete cds	zi01g09.r1 Soares_fetai_liver_spiean_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428568 5	Homo sapiens inhibin, alpha (INHA) mRNA	Homo sepiens Inhibin, alpha (INHA) mRNA	bb74f06.y1 NIH_MGC_12 Hamo sepiens cDNA clane IMAGE:3048131 5' similar to TR:095604 085604 ZINC FINGER PROTEIN.;
Xon Propes	Top Hit Database Source	EST_HUMAN		EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	NT.	IN	NT		Į.	노	Z	EST_HUMAN	IN	Ę	EST_HUMAN
Single	Top Hit Acession No.	1.0E-124 AW 503755.1		1.0E-124 AW665663.1	N446455.1	1.0E-124 AI448455.1	1.0E-124 AA397561.1	1.0E-124 AA397661.1	1.0E-124 AB029018.1	11417862	11417862 NT	1.0E-125 AB032998.1	1.0E-125 BE743922.1	1.0E-125 AI110658.1	1.0E-125 AI110858.1	1.0E-125 AF284750.1	1.0E-125 AA042813.1	4L163210.2	1.0E-125 7682270	7661867 NT		J78027.1	1.0E-125 AF015450.1	1.0E-125 AF015450.1	1.0E-125 AA011278.1	4504698 NT	4504696 NT	1.0E-125 BE018009.1
	Most Similar (Top) Hit BLAST E Vatue	1.0E-124	1.0E-124 U94778.1	1.0E-124	1.0E-124 AJ446455.1	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125		1.0E-125 U78027.1	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125	
	Expression Signal	1.76	1.53	5.85	208	2.08	9.4	4.08	1.38	1.67	1.67	10.43	5.43	1.26	1.28	234	1.61	1.16	22	1.89		1.65	2.84	284	1.78	1.19	. 1.19	1.19
	ORF SEQ ID NO:	36645	37862	38169	37479	37480	26883	26884	31749	31436	31437		26019	28632	28833	28725	20875	27003	27148				27852			28626	128827	28001
Ī	SEQ ID	23156	24333	24596	23956	23966	13754	13754	25383	25852	26862	13411	13121	13711	13711	13790	13917	14051	14198	15874		14844	14855	14855		L		18311
	Probe SEQ ID NO:	10230	11388	11680	11801	11801	12305	12305	12730	12983	12983	319	428	8	8	82,	88	8	1156	1682		1817	1828	1828	2368	200	<b>280</b>	3022

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Single Exon Probes Expressed in Bone Marrow

Single Exon Prodes Expressed in Bone Martow	Top Hit Descriptor	zi63c07.s1 Sceres_pregnant_uterus_NbHPU Homo sepiens cDNA clone IMAGE:486540 3' similar to gb:X85857_cds1 OLFACTORY RECEPTOR-LINE PROTEIN HGMP07E (HUMAN);	Homo sepiens zenc finger protein ZNF287 (ZNF287), mRNA	Homo saplens zinc finger protein ZNF287 (ZNF287), mRNA	601141152F1 NIH_MGC_9 Hamo sapiens aDNA dane IMAGE:3140798 5	Homo septems KIAA0985 protein (KIAA0985), mRNA	QV2.HT0577-010500-165-b08 HT0577 Homo saplens cDNA	601433472F1 NIH_MGC_72 Homo septens cDNA clone IMAGE:3916962 6	w.67co7.x1 NCI_CGAP_Gas4 Homo septens cDNA clone IMAGE:2256108 3' shriter to WP:C45G9.2 CE01854;	601305670F1 NIH_MGC_39 Homo septens cDNA clone IMAGE:3640097 67	601335625F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3689790 5	601335828F1 NIH_MGC_44 Homo septiens cDNA clone IMAGE:3889780 5	Hamo sapiens IGF-II gene, exan 5	Homo sapiens IGF-II gene, excn 5	601158078F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505603 5	Homo sepiens adeptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA	Humen chromosome 10 duplicated adrendeukodystrophy (ALD) gene segment containing eachs 8-10	Human chromosome 10 dupiticated adrencieulocitystrophy (ALD) gene segment containing exons 8-10	QV1+HT0838-070500-191-d12 HT0838 Homo saplens cDNA	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA	tn52b03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2171981 3' straiter to TR:Q14089 Q14089 HYPOTHETICAL PROTEIN ;	601590345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944631 57	Human mRNA for KIAA0300 gene, pertial cds	Homo sapiens HREL gene, excn 5	X59802.X1 NCI_CGAP_G884 Homo saptens cDNA done IMAGE:2822383 3' similar to TR:Q13284 Q13284 LAMBDA/IOTA PROTEIN KINASE C-INTERACTING PROTEIN. [1];	xf59f02.x1 NC]_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284 LAMBDAAOTA PROTEIN KINASE C-INTERACTING PROTEIN. [1] ;	Homo sapiens mRNA for KIAA0667 protein, partial cds	Homo sepiens myosin, heavy polypeptide 1, skeletel muscle, edutt (MYH1), mRNA
XON Probes EX	Top Hit Detablese Source	EST_HUMAN 9			THUMAN		EST HUMAN Q	EST_HUMAN 60	EST_HUMAN C	EST_HUMAN G	EST_HUMAN @	EST_HUMAN &		Ī	T_HUMAN			Ŧ	T_HUMAN	EST_HUMAN Q	EST_HUMAN H	Г		H	EST_HUMAN L	EST HUMAN L		
Single	Top Hit Acessian No.	AA042813.1	11425114 NT	11425114 NT	1.0E-125 BE315412.1	11436448 NT	1.0E-126 BE176169.1	1.1	+:	1.0E-125 BET38055.1		1.0E-125 BE562526.1			3.1	11425572 NT			1.0	1.1	F	<u> </u>	7.1	2	1.0E-126 AW131202.1	1.0E-125 AW131202.1	71	7889505 NT
	Most Similar (Top) Hit BLAST E Value	1.0E-125	1.0E-125	1.0E-126	1.0E-125	1.0E-125	1.0E-126	1.0E-125 BE89266	1.0E-125 AI679904	1.0E-125	1.0E-125 BE56252	1.0E-125	1.0E-125 X03427.1	1.0E-125 X03427.1	1.0E-125	1.0E-125	1.0E-125 U90288.1	1.0E-126 U90288.1	1.0E-125 BE18164	1.0E-125 BE181640	1.0E-125 AI565896.	1.0E-125 BE79457	1.0E-125 AB00229	1.0E-125	1.0E-126	1.0E-125	1.0E-125 AB014567	1.0E-125
	Expression Signal	1.11	1.86	1.86	1.68	1.47	1.01	3.58	0.6	99.0	1.29	1.20	5.05	5.05	1.04	0.54	0.99	0.80	12.5	126	880	0.65	0.74	254	1.97	1.97	2.99	2.08
	ORF SEQ ID NO:	29821	30498	30488	30556	85ZZE	32276	32328	32378	82728	33068	33069	33286	33297	34100	34363	35278	35279	35875	35876	36219	37242	37280	37533	37610	37611		38121
	Exam SEQ ID NO:	16911	17602	17602	17869	19058	19078	19123	19168	19481	19789	19789	19998	19998	20728	20969	21857	21857	22437	22437	22764	23740	23780	24006	24084	24084		24559
	Probe SEQ ID NO:	3872	4580	4580	4648	5973	<b>7689</b>	9041	9809	6413	6733	6733	7283	7283	7775	8032	8891	889	8738	2	8738	10819	10860	11042	11124	11124	11471	11621

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Single Exoli Plobes Expressed iii Doire mailom	ORF SEQ Expression (Top) Hit Top Hit Accession D No. Signel BLASTE No. Scurce	38128 5 1.0E-125 AF028029.1 NT	38192 1.68 1.0E-125 AW812899.1 EST_HUMAN	38236 4.32 1.0E-125 BE074287.1 EST_HUMAN	38297 4.32 1.0E-125 BE074287.1 EST_HUMAN	32127 1.48 1.0E-125 BF683645.1 EST_HUMAN	28780 6.16 1.0E-128 4758007 NT	26926 0.8 1.0E-128 X68735.1 NT	28383 0.91 1.0E-126 8923056 NT	28384 0.91 1.0E-128 8923056 NT	28828 1.41 1.0E-128 6382078 NT	29058 7.58 1.0E-126 AA160709.1 EST_HUMAN	29059 7.58 1.0E-128 AA160709.1 EST_HUMAN	28060 1.02 1.0E-128 BF510408.1 [EST_HUMAN	28061 1.02 1.0E-126 BF510408.1 EST_HUMAN	29803 0.75 1.0E-128 X53941.1 NT	29828 2.09 1.0E-128 7857038 NT	30741 1.15 1.0E-128 AF101108.1 NT	30742 1.15 1.0E-128 AF101108.1 NT	30777 1.38 1.0E-128 N34078.1 EST_HUMAN	32061 0.71 1.0E-128 T66998.1 EST_HUMAN	32672 3.23 1.0E-126 AA460075.1	32739 3.5 1.0E-126[AB040808.1 IN	32740 3.5 1.0E-126 AB040858.1 NT	34061 0.98 1.0E-126 AF257737.1  NT	34082 0.98 1.0E-126 AF257737.1 NT	34299 0.64 1.0E-128 AU136463.1 EST HUMAN	A COLOUR DOLL TO A 100 COLOUR	94502 0.00 1.0E-120 AB097745 1 NT	24588 0 02 4 0E-126 AR0377151 NT	34300	34/03 4.9 1.0E-1.20 A10006.1 N.I
																																╛
	Exan SEQ ID NO:	3 24564					5 13834	13974	15361	15361	5 15605	7 16145		8 16146	15146			L	17843	17889	7 18879			19489	2 20696	20696	L	L	I.	24170	L	21289
	Probe SEQ ID NO:	11628	11729	11830	11830	12106	776	820	2352	2352	2605	3087	3087	3088	3088	3645	3668	4826	4826	4872	5787	888	822	6422	7742	7742	2962			3 8	3 8	33

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	Top Hit Descriptor	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA	Homo sapiens chondrollin sulfate proteoghoan 2 (versican) (CSPG2) mRNA	Human FAU1P pseudogene, trinucleotide repeat regions	Human FAU1P pseudogene, trinucleotide repeat regions	Homo sepiens ribosomsi protein S2 (RPS2) mRNA	Homo sepiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA	Homo sepiens mRNA for KIAA1247 protein, partial cds	Homo septems prospero-related hamedbox 1 (PROX1), mRNA	H.saplans gene for inter-alpha-trypsin inhibitor heavy chain H1, excn 12	Homo septens phosphodiesterese 1C, calmodulin-dependent (70kD) (PDE1C), mRNA	7q88b10x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3'	601503848F1 NIH_MGC_71 Homo saptens cDNA done IMAGE:3905784 6	602042322F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179988 5	602042322F1 NCL_CGAP_Brn67 Hamo saplens aDNA dans IMAGE:4178988 57	602042322F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179988 5	Homo sepiens putetive ABC transporter (WHITE2), mRNA	Homo sapiens mRNA for KIAA1636 protein, partial cds	Homo sapiens mRNA for KIAA1636 protein, partial cds	Homo septens mRNA for KIAA0454 protein, partial cds	Homo sapiens mRNA for KIAA0454 protein, partial cds	ns04s/1.r/ NCI_CGAP_Ew/ Homo sepiens cDNA clone IMAGE:1182820 similar to TR:0961339 G951338 G4ROMOSOME SEGREGATION GENE HOMOLOG CAS.;	Homo sepiens glutamate receptor, tonotropic, N-methyl D-espantate 2D (GRIN2D), mRNA	om88h08.s1 NC _CGAP_GC4 Homo sepiens.cDNA clone IMAGE:1552383 3' similer to gicX54941 CYCLIN DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);	Homo sepiens mRNA for TRABID protein (TRABID gene)	601277828F1 NIH_MGC_20 Hama sepiens cDNA clane IMAGE:3618750 5	EST367360 MAGE resequences, MAGC Homo sapiens cDNA	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]	Novel human mRNA containing Zinc finger C2H2 type domains	Homo sepiens glubathione S-transferase theta 2 (GSTT2) and glubathione S-transferase theta 1 (GSTT1) genes, complete cds
	Top Hit Database Source			NT.	TN							T_HUMAN	П		EST_HUMAN	T_HUMAN		NT		NT		EST HUMAN		T HUMAN	Γ	T HUMAN	_HUMAN	Ę		N	IN TN
28.00	Top Hit Acessian No.	4758081 NT	4758081 NT			4506718 NT	11437455 NT	1	426673		11420965 NT	1	1.0E-128 BE614105.1	.1	.1	.1	11545923 NT	.1	.1	.1	1	Ψ.	11425254 NT	4:	-	5	-			.1	4
	Most Similar (Top) Hit BLAST E Value	1.0E-128	1.0E-128	1.0E-128 U02523.1	1.0E-128 U02523.1	1.0E-128	1.0E-128	1.0E-128 AB033073	1.0E-128	1.0E-128 X69539.1	1.0E-128	1.0E-128 BF224345	1.0E-128	1.0E-128 BF529931	1.0E-128 BF529331	1.0E-128 BF529931	1.0E-128	1.0E-128 AB046856	1.0E-128 AB046858	1.0E-128 AB007923	1.0E-128 AB007923	1.0E-128 AA639198	1.0E-128	1.0E-128 AA926959	1.0E-128	1.0E-128	1.0E-128 AW955290	1.0E-129 S37722.1	1.0E-129 S37722.1	1.0E-129 AL096880.	1.0E-129 AF240786
	Expression	2.18	2.18	9.34	9.34	31.4	1.49	123	5.05	0.64	1,94	6.42	0.69	0.53	0.53	0.63	0.62	0.49	0.49	0.5	0.5	5.1	3.42	3.84	1.48	2.69	8.88	0.89	۲	3.06	25
	ORF SEQ ID NO:	27150	27151	28117	28118	28257		28377	30609	31879	32883	33353	33986	34313	. 34314	34315	34417	34478	34477	35281	35282	36917	37552	37559	37635	37687	-	28423	26423	27745	27750
	SEO EO NO:	14200	14200	15101	15101	15233	15456	16454	17714	18720	19618	20050	20621	20822	20822	20022	21017	21076	21076	21859	21859	23418	24028	24035	24109	24156	25174	13486	13486	14761	14768
	Probe SEQ ID NO:	1158	1158	2084	2084	2219	2451	3405	4693	5624	8999	7116	1992	7883	2862	2862	8080	8139	8139	8833	8833	10498	11065	11073	11149	11202	12400	122	413	1731	1736

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Probe SEQ ID NO:	Esch SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acession No.	Top Hit Detrabese Source	Top Hit Descriptor
							Homo septems glutathione S-transferase theta 2 (GSTT2) and glutaffione S-transferase fineta 1 (GSTT1)
1736	14768					Į.	genes, complete ods
1863	14888	Z7885	286	1.0E-129	11418522 NT	¥	Homo saplens zinc imger protein (16 (expressed in tesus) (ZNF (0), mixny
3145	16202		1.33	1.0E-129 Q14585	Q14685	SWISSPROT	ZINC FINGER PROTEIN HZF10
3145	16202	29114	1.33	1.0E-129 Q14585	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3145	1_		133		Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4182			1.87		1.0E-129 AB040882.1	TN	Homo sapiens mRNA for KIAA1459 protein, partial cds
							CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYA5
4309	17338	30216	1.86		1.0E-129 AW 755254.1	LSI HOMBIN	Calibratily assurance bate o
6081	17338	30247	1.86		1.0E-129 AW766264.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo septens curin cone 4131430 similar to CMYA5 Cardiomyopathy associated gene 5
6210					1.0E-129 AJ008345.1	M	Homo septems IV/LQT1 gene
6874	1_		0.54	L	1.0E-129 BE88834.1	EST_HUMAN	601513861F1 NIH_MGC_71 Hamo sapiens cDNA clane IMAGE:3915350 5
7834	_		4.07	1.0E-129	AJ006345.1	ĮN.	Homo saplens KVLQT1 gene
7396	L				11420850 NT	¥	Homo sepiens similar to ribosomal protein S28 (H. sepiens) (LOC63694), mRNA
1111	L				1.0E-129 AF041058.1	TN	Homo septens WSCR4 gene, exons 3 and 4
1777	L		0.78		1.0E-129 AF041058.1	본	Homo sepiens WSCRA gene, exans 3 and 4
1988	21629		4.37		1.0E-129 AB014534.1	LN.	Hamo sepiens mRNA for KIAA0834 protein, peritial ads
10439		36850	0.79	1.0E-129	•	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10439				1.0E-129	11437282 NT	NT.	Homo sepiens solute carrier family 21 (organic enion transporter), member 9 (SLC21A9), mRNA
							qiqodosixi NCI_CGAP_Bm25 Homo sepiens cDNA clone IMAGE:1858959 3' similar to TR:Q14840 Q14840   process   process   Centendo 2
10878	23798	37299	0.48		1.0E-129 AI189117.1	EST_HUMAN	MI LUCEN INDUCIBLE GENE MAY.
10878	23788	37300	0.48		1.0E-129 AI199117.1	EST_HUMAN	040008.X1 NCL_CGAP_BM25 Homo septens G.NA cione IMAGE:1850859 \$ Smiller to Incul 14640 C114640 MTOGEN INDUCIBLE GENE MIG-2;
11557	1_				1.0E-129 AA625528.1	EST_HUMAN	af72707.r.1 Scares_Nht-NmPu_S1 Homo sapiens cDNA clone IMAGE:1047589 5
11630	L	33716	62	1.0E-129	11420850 NT	뇐	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63894), miRNA
4.78.RB		<u> </u>	424		1 0F-129 H83155.1	EST HUMAN	1948-06.11 Scares fetal liver spleen 1NFLS Home esplens oDNA clone IMAGE:189112 6' similar to SP-B48150 B48150 HP-25-HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS-ASIAN;
1275R	_		263	L	1.0E-129 AL120739:1	EST HUMAN	DKFZp762K171_f1 782 (synonym: hmel2) Homo sapiens cDNA clane DKFZp782K171 6
		26117			TN05530 NT	Į.	Homo saplens hypothetical protein (HSPC242), mRNA
1174	L			L	1.0E-130 AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, pertial cds
1675	<u> </u>		13.33		1.0E-130 BE275192.1	EST_HUMAN	601121985F1 NIH_MGC_20 Hamo sepiens aDNA dane IMAGE:3346368 5
1675		77688	•		1.0E-130 BE275192.1	EST_HUMAN	60112/995F1 NIH_MGC_20 Homo sapiens cDNA done IMAGE:3346368 5
2000	15021		3.15		1.0E-130 X04092.1	Z	Human gene for catalesse (E.C. 1.11.1.6) exon 9 mapping to catomoscane 11, pana p13

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	Top Hit Descriptor	Homo sapiens RET finger protein-like 1 antisense transcript, partial	601343016F1 NIH_MGC_63 Homo septems cDNA clone IMACE:3885488 5	601343016F1 NIH_MGC_63 Homo sepiens cDNA done IMAGE-3685466 5	Homo sapiens retinal dehydrogenase hamalog isaform-1 (RDH) mRNA, complete cds	601343016F1 NIH_MGC_53 Hamo saplens cDNA clone IMAGE:3685496 5	601343016F1 NIH_MGC_53 Homo septens cDNA clone IMAGE:3885488 5	UI-HF-BNO-aky-g-08-0-ULr1 NIH_MGC_50 Homo sapians cDNA clone IMAGE:3078731 6	Human T-cell receptor (V alpha 22.1, J alpha RPM/4285-variant, C alpha 1) mRNA	CMA-CN0045-180200-511-f02 CN0045 Homo septems cDNA	RC0-CT0318-201199-031-af1 CT0318 Homo sapiens cDNA	RCO-CT0318-201199-031-ar11 CT0318 Homo sapiens aDNA	Human germline immunoglobulin lambda light chain pseudogene (VII.1)	CMD-CN0045-170200-225-g03 CN0045 Homo septens cDNA	CMD-CN0045-170200-225-g03 CN0045 Homo saplans cDNA	Homo sapiens estrogen-responsive B box protein (EBBP), mRNA	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA	Homo septens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds	Homo sepiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds	Homo capiens aurora-related kinase 1 (ARK1) mRNA, complete cds	EST368312 MAGE resequences, MAGD Homo sapiens cDNA	Homo sepiens mRNA for KIAA1335 protein, partial cds	xd36e06.xf NCI_CGAP_Ov23 Hamo septems aDNA clone IMAGE:2586874.3'	Homo sapiens glutamete receptor, metabotropic 5 (GRM5) mRNA	Homo sapiens RET finger protein-like 1 entisense transcript, partial	ar68004.r1 Scense_NhHMPu_S1 Homo sepiens oDNA done IMAGE:687650 6' similar to TR:G222811   G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.;	258c04.71 Soares_NhHMPu_S1 Homo septens cDNA clone IMAGE:067590 5' struiter to TR:G222811	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.;	Homo expiens checipoint suppressor 1 (CHES1), mRNA	Homo sepiens hypothetical protein FLJ20371 (FLJ20371), mRNA	Homo sepiens hypothetical protein FLJ20371 (FLJ20371), mRNA	Homo sapiens DCRR1 mRNA, partial cds	Homo sepiens DCRR1 mRNA, partial cds
	Top Hit Database Source	ᅜ	<b>EST_HUMAN</b>	<b>EST_HUMAN</b>	NT.	EST_HUMAN	<b>EST_HUMAN</b>	EST HUMAN	F	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	TN.	<b>EST_HUMAN</b>	EST_HUMAN	TN.	Ę	٦	Þ	¥	EST_HUMAN	IN	EST_HUMAN	IN	IN	EST HUMAN		EST_HUMAN	NT	M	M	۲	Σ
28	Top Hit Acession No.	1.0E-130 AJ010230.1	1.0E-130 BE564219.1	1.0E-130 BE564219.1	1.0E-130 AF240698.1	1.0E-130 BE564219.1	1.0E-130 BE564219.1	1.0E-130 AW503580.1	M97710.1	1.0E-130 AW843983.1	1.0E-130 AW363299.1	1.0E-130 AW363299.1	X57825.1	1.0E-130 AW843875.1	1.0E-130 AW843875.1	11425446 NT	11416777 NT	1.0E-130 AF257737.1	1.0E-130 AF257737.1	1.0E-130 AF008551.1	1.0E-130 AW956242.1	1.0E-130 AB037756.1	1.0E-130 AW103454.1	4504142 NT	1.0E-130 AJ010230.1	0.0E+00 AA228128.1		AA228128.1	4885136 NT	8923349	8923349	0.0E+00 D83327.1	D83327.1
	Most Similar (Top) Hit BLAST E Value	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130 M97710.1	1.0E-130	1.0E-130	1.0E-130	1.0E-130 X57825.1	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	0.05+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D833Z7.1
	Expression Signal	8.37	1.3	1.3	1.27	4.55	4.55	1.41	1	8.22	1.63	1.53	0.63	0.89	0.89	0.88	2.06	0.55	0.55	6.0	291	1.74	1.29	1.71	1.44	2.84		264	2.59	99.0	0.66	1.8	1.8
	ORF SEQ ID NO:		28864	28865	99988	28864	28865	29912	30027	30485	31021	31022	33239	33433	33434	33452	33788	33894	33895		35563	35981		38489		26023		26024	26028	26034		26042	26043
	SEQ ID	15773	15949	15949	16636		15940		17133	17592	18142	18142	19943	20120	20120	20136	20432	20536	20536	21886	22137	22531	23218	24892	15773	13125		13125	13128	13136	13136	13143	13143
	Probe SEQ ID NO:	2781	2890	2890	3591	8778	8778	3957	4099	4669	6133	5133	<b>1</b> 688	<b>88</b>	<b>889</b>	7010	7468	7574	7574	0508	917	0898	10283	12015	13046	4		4	8	16	16	ଷ	প্ত

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i abre 4 gle Exon Probes Expressed in Bone Marrow	Top Hit Descriptor	Homo sapiens beta-tubulin mRNA, complete cds	Human heparin cofactor II (HCF2) gene, exons 1 ffrough 5	Homo sepiens RNA-binding protein S1, serine-rich domein (RNPS1), mRNA	Homo sepiens mRNA for multidrug resistance protein 3 (ABCC3)	Homo saptens mRNA for multidrug resistence protein 3 (ABCC3)	HUM516H08B Human piacenta polyA+ (TFujiwara) Homo sepiens cDNA clone GEN-516H08 5	HUM516H08B Human placenta polyA+ (TFujiwara) Homo sepiens cDNA clone GEN-516H08 6	Human ribosomal protein L7 (RPL7) mRNA, complete ods	cr48e07.x1 Jia bana mamow stroma Homo sepiens dDNA clane HBMSC_cr48e07.3"	cr48e07.x1 Jia bane manow strama Hamo sapiens aDNA clane HBMSC_cr48e07 31	Human von Willebrand factor pseudogene corresponding to eachs 23 through 34	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA	Homo sapiens protein tyrosine phosphatese, non-receptor type substrate 1 (PTPNS1) mRNA	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA	Homo sapians arriforide binding protein 1 (arrine oddase (copper-containing)) (ABP1), nuclear gene	encoding mitochandnial protein, mRNA	Homo sepiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA	Homo sapians actin, beta (ACTB) mRNA	Human polyhomeotic 1 homotog (HPH1) mRNA, partial cds	HA1347 Human fetal Ilver cDNA library Homo sapiens cDNA	Homo sapiens mRNA for KIAA1363 protein, partial cds	ts38b05.x1 NCI_CGAP_Ut4 Homo sepiens cDNA done IMAGE:2230833 3' similer to TR:Q89551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR.;	ts38b05x1 NCI_CGAP_Ut4 Homo sapiens cDNA done IMAGE:2230833 3' similar to TR:089551 089651	MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR;	yo1h08.r1 Soares melanocyte ZNbHM Homo septems CDNA clone IMAGE:270017 6	yyo1h09,r1 Soares melanocyte 2NbHM Homo saplens cDNA clone IMAGE:270017 5"	Homo sapiens neuropilin 2 (NRP2) mRNA	Homo sapiens polymensse (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA	Homo sepiens igG Fc binding protein (FC(GAMMA)BP) mRNA	ya83g04,72 Strategene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE-68310 5	ya83g04.72 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5
xon Probes E	Top Hit Defabase Source	NT.	Į.		NT	NT		EST_HUMAN		HUMAN	EST_HUMAN	M				NT		Ę	M	NT	M	EST_HUMAN	LV.	EST_HUMAN		HEMAN	EST HUMAN	EST_HUMAN	NI NI	NT	NT			EST_HUMAN
Single E	Top Hit Acession No.	AF141349.1		TN 2287889						1	0.0E+00 AW069534.1		4758977 NT	4768977 NT	4758977 NT	4758977		4501850 NT	450444 NT	5016088		0.0E+00 AJ114743.1	0.0E+00 AB037784.1	0.0E+00 AI623701.1		.1			4505458 NT	4505838 NT	4505938 NT	4503680		F56945.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00/	0.0E+00(M58600.1	0.0E+00	0.0E+00 Y17151.2	0.0E+00 Y17151.2	0.0E+00 D78804.1	0.0E+00 D78804.1	0.0E+00 L16558.1	0.0E+00	0.0E+00	0.0E+00 MB0878.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00 U89277.1	0.0E+00/	0.0E+00/	0.0E+00		0.0E+00	0.0E+00 N36040.1	0.0E+00 N38040.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 T56945.1	0.0E+00 T56945.1
	Expression Signal	61.1	78.0	4.86	213	213	127	127	25.34	11.49	11.49	1.16	4.06	4.06	2.97	2.97		0.79	18.85	80.76	16.85	2.55	1.19	0.83		0.78	0.04	0.64	0.85	5.48	5.49	0.65	0.85	0.85
	ORF SEQ ID NO:	28048	28060	28085	<b>58090</b>	28097	28085	26096	28097	26100	28101		28115	28118	28115	28116		28122		28131	28134	28141	28142	28151		28151	28152			20108	28167	28407		28175
'	Exan SEQ ID NO:	13140	13158	13162	13178	13178	13180	13180	13181	13183	13183	13186	13193	13183	13183	13183		13198	13199	13207	13210	13217	13218	13227		13227	15809	15809	13230	13236	13236	13474	13244	13244
•	Probe SEQ ID NO:	8	88	3	88	8	8	Ю	29	ষ্ট	ষ্ঠ	88	92	12	R	R		28	88	ъ	क्र	ট্	<del>1</del>	116		117	118	118	121	131	131	<u>\$</u>	141	141

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Table 4
Single Exon Probes Expressed in E

SEQ ID ORF 13283 1	<del></del>	Signal Si	Most Similar Vatus	No. No. Hit Ace No. No. No. No. No. No. No. No. No. No.	Top HR Database Source Source Source Source Source Source Source Source Source Source Source EST HUMAN EST HUMAN EST HUMAN NT NT NT NT NT NT NT NT NT NT NT NT NT	Top HR  Deathose  Source  Sour
	8 <sup>□</sup>	ORF SEO  D NO:  28188  28181  28182  28188  28188  28188  28188  28188  28188  28288  28288  28288  28288  28288  28288  28288  28288  28288  28288  28288  28288	ORF SEQ Express 28192 28192 28192 28192 28192 28192 28192 28192 282999 282999 282999 28299	ORF SEQ Expression (T Signal Bit Sequence) (T Signal B	ORF SEQ Expression (Top) Hit Acc Similar No. Signal BLAST E No. Veitus Veitus Signal BLAST E No. Veitus Sep. 14 0.0E+00 BF038381.1 28182 0.74 0.0E+00 BF038381.1 28182 0.74 0.0E+00 BE285873.1 28182 0.74 0.0E+00 BE285873.1 28182 0.85 0.0E+00 BE162832.1 28182 0.85 0.0E+00 BE162832.1 28182 0.85 0.0E+00 BE162832.1 28182 0.85 0.0E+00 BE162832.1 28182 0.85 0.0E+00 BE162832.1 282182 0.85 0.0E+00 BE162832.1 282182 0.85 0.0E+00 BE162832.1 282182 0.85 0.0E+00 BE162832.1 282182 0.85 0.0E+00 BE162832.1 282182 0.0E+00 BE162832.1 282182 0.0E+00 BE162832.1 282182 0.0E+00 BE162832.1 28221 0.0E+00 BE162832.1 28222 288.4 0.0E+00 BE162832.1 28223 0.0E+00 BE162832.1 28223 0.0E+00 BE162832.1 28223 0.0E+00 BE162832.1 28223 0.0E+00 BE162832.1 28223 0.0E+00 BE162832.1 28223 0.0E+00 BE1627308.1 28223 0.0E+00 BE1627308.1 28223 0.0E+00 BE1627308.1 282240 51.32 0.0E+00 BE1627308.1 282240 51.32 0.0E+00 BE1627308.1 282240 51.32 0.0E+00 BE167774.1 28223 0.0E+00 BE167774.1 282240 51.32 0.0E+00 BE167774.1 28223 0.0E+00 BE167774.1 282240 51.32 0.0E+00 BE167774.1 282240 51.32 0.0E+00 BE167774.1 282240 51.32 0.0E+00 BE167774.1 282240 51.32 0.0E+00 BE167774.1 282240 51.32 0.0E+00 BE167774.1 282240 51.32 0.0E+00 BE167774.1 282240 51.32 0.0E+00 BE167774.1 282240 51.32 0.0E+00 BE167774.1 282240 51.32 0.0E+00 BE167774.1 61.200.1 61.32 0.0E+00 BE167774.1 61.200.1 61.32 0.0E+00 BE167774.1 61.200.1 61.32 0.0E+00 BE167774.1 61.200.1 61.40 BE1677774.1 61.200.1 61.40 BE1677774.1 61.200.1 61.40 BE1	Database   Signal   All

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Table 4
Single Exon Probes Expressed in Bone Marrow

MOLINAL PROPERTY AND AND AND AND AND AND AND AND AND AND	Expression (Top) Hit Top Hit Acession Signel BLASTE No. Source		26249 3.11 0.0E+00 6978444 NT Mus musculus testis-epecific protein, Y-encoded-like (Tspyl), mRNA	26264 3.14 0.0E+00 5453805[NT Homo sapiens NS1-essociated protein 1 (NSAP1) mRNA	6.19 0.0E+00/AL163201.2 NT Hamp sapiens chromosame 21 segment HS21C001	FN F.	28272 2.06 0.0E+00 X89772.1 INT H.saplens mRNA for interferon alphafosta receptor (long form)	9.67		26291 1.2 0.0E+00 4507500 NT Homo sapiens T-cell Imphoma Investon and metastasts 1 (TIAM1) mRNA	0.0E+00 7706028 NT	1.55 0.0E+00 D83327.1 NT	1.75 0.0E+00[D83327.1  NT	0.0E+00 D83327.1  NT	0.98 0.0E+00 AW845283.1  EST_HUMAN	0.0E+00 4557029 NT	28315 7.75 0.0E+00 4557029 NT Homo sapiens potassium inwandly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA	3.68 0.0E+00 AB028942.1 NT	28326 15.06 0.0E+00/AB028942.1 NT Homo septems mRNA for KIAA1019 protein, partial cds	12.15 0.0E+00 4508728 NT Homo sepiens ribosomal protein S5 (RPS5) mRNA	Homo sapiens phosphoribosylghychamide formyltransferase, phosphoribosylghychamide synthetase, phosphoribosylghychamide synthetase, phosphoribosylaminotruidazole synthetase (GART) mRNA	0.0E+00 AA48000	4507162 NT	28328 22.55 0.0E+00 4507152 NT Homo sapiens SON DNA binding protein (SON) mRNA		014867 SWISSPROT	0.0E+00 O14867  SWISSPROT	4.94 0.0E+00 7657213 NT	28343 1.14 0.0E+00 7657213 NT Homo sepiens hormonally upregulated neu tumor-essociated kinase (PUNK), mRNA	26355 0.0E+00 5174574 NT (MLT4) mRNA	4505256 NT	4827057 NT	26365 1.24 0.0E+00 U71600.1 NT Human zinc finger protein zfp31 (zf31) mRNA, partial cds
	ORF SEQ Eq	26248	26249	26264		26269	28272	-	26290	26291	26293		26306	26307		26314	26315	26325	26326		26327		26328	26328	26332	26341	26342	26343	26343	26355	26356	26360	26365
	Exem SEQ ID NO:	224 13323	225 13324	239 13338	240 13339		249 13346	257 13354	269 13365		13367	282 13377	283 13378	283 13378	284 13379	Ш	283 13387	304 13398	305 13399	306 15838	307 13400		309 13402	310 13402	314 13408	327 13418	327 13418	328 13419	329 13419	344 13433	345 13434	348 13437	351 13440
	Probe SEQ ID NO:							ľ		,	,,,	7	"	~	["			l s	"	<u>"</u>		ľ	<b>"</b>	("	·"	·"		,	Ĺ	.,,		,	**

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Table 4
Single Exon Probes Expressed in Bone Marrow

Top Hit Descriptor	Hamo septens dirromosome 21 segment HS21C001	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA	EST27054 Carebellum II Homo sapiens cDNA 5' end	601111520F1 NIH_MGC_16 Hamo septens cDNA clane IMAGE:3352348 6	Homo sepiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA	Homo sapiens 5-hydroxy/tryptamine (serotoxin) receptor 1B (HTR1B) mRNA	Homo septems kenetin 18 (KRT18) mRNA	Homo septems kerattin 18 (KRT18) mRNA	Homo sapiens chromosome 21 segment HS210046	Hamo sepiens chramosame 21 segment HS210046	Hamo sapiens chromosome 21 segment HS21C046	Homo sapiens mRNA for KIAA1209 protein, partial cds	AU132898 NT2RP4 Homo espiens aDNA done NT2RP4000837 6	601274951F1 NIH_MGC_20 Homo saplens cDNA clone IMAGE:3015758 5	PMC-DT0065-130400-002-c06 DT0065 Hamo sapiens cDNA	Novel frumen gene mapping to chamosame 1	Homo sapiens PC326 protein (PC326), mRNA	II.2-FT0159-070800-120-F07 FT0159 Homo sepiens cDNA	Homo septens chromosome 21 segment HS21C010	QV2-BT0635-160400-142-H05 BT0635 Homo septens cDNA	601784858F1 NIH_MGC_53 Homo septens cDNA clone IMAGE:3986988 5	Homo sepiens mRNA for KIAA1476 protein, partial cds	Hamo sepiens transcription elongation factor B (SIII), polypeptide 1-tite (TCEB1L) mRNA	Homo sepiens guenine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mrtvA	Homo sepiens guantine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mYNA	Homo sapiens enillin (LOCS4443), mRNA	Homo saptens artillin (LOC54443), mRNA	Homo sapiens entitin (LOC54443), mRNA	Homo sepiens X-linked antikinditic ectodermel dysplasia protein gene (EDA), exon 2 and flanking repeat	regions	ULH-BI1-ech-h04-0-U.s1 NCI_CGAP_Sub3 Homo sepiens cuna cione imace::2/138313	Hamo sepiens RGH1 gene, retrovirus-like element	Homo sepiens ubiquinol-cytochrome c reductase, Rieske Iron-suffur polypeptide 1 (UQCRFS1), nuclear game encoding mitochondrial protein, mRNA	
Top Hit Database Source	¥		EST_HUMAN E	T_HUMAN						±	¥	E	EST_HUMAN /	EST HUMAN	Г	Z		EST_HUMAN I	- L	EST_HUMAN	EST_HUMAN			,							EST HUMAN	NT		
Top Hit Acession No.	0.0E+00 AL163201.2	57879	0.0E+00 AA3242621		4504532 NT	4504532 NT	4557887 NT	4557887 NT	AL163246.2	0.0E+00 AL1632462	0.0E+00 AL163246.2				-		R923855 NT	0.0E+00 BF373403.1	0.0E+00 AL163210.2				F006030 NT	4504038 NT	4504036	B923831 NT	8623831	8623831		-	0.0E+00 AW135324.1	0.0E+00 D10083.1	TN 0474763	
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	- CO-	1-2
Expression	121	6.45	0.75	1.25	3.47	3.47	284	2.84	2.68	6.81	6.81	3.92	183	1.58	1.88	1.47	0.0	0.82	532	1.15	1.91	223	10.84	4.48	4.46	0.00	12	1.2		5.14	1.55	254	et c	
ORF SEQ ID NO:		28452			26466	29467	26475	26478	26482	26483	28484								28511	28515							28536				28546		7.530	
Exen SEQ ID NO:	13517	13519	13524	13525	13641	13541	13546	13546	13557	13558	13558	13586	13568	13578	15842	13579	13580	13584	1350	15843	13603	13609	13612	13613	13613	13615	13616	<u> </u>		13620	13628			2000
Probe SEQ ID NO:	44	448	15	452	88	88	474	474	\$	285	485	8	9	202	505	808	209	613	520	223	533	823	2	545	542	\$	35	55		999	<b>558</b>	883	2	8

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Top Hit Acession Detablesse Top Hit Descriptor	Ŋ	T_HUMAN	23631 NT	8923691 NT	4501854 NT	0.0E+00 AF221712.1 NT Homo sapiens Smad- and Olf-Interacting zinc finger protein mRNA, partial cds	0.0E+00 AF221712.1 NT Homo sepiens Smad- and Off-Interacting zinc finger protein mRNA, partial cds	1 NT	0.0E+00 AB037807.1 NT Homo sapiens mRNA for KIAA1386 protein, partial cds	6806918 NT	6806918 NT	6806978 NT	6806918 NT	6806918 NT	0.0E+00]AA389486.1 EST_HUMAN   ZISOco7.r1 Sogres_testis_NHT Homo sapiens cDNA clone IMAGE:728732 5	0.0E+00 D11078.1 NT Homo septiens RG+D gene, retrovirus-like element	0.0E+00 W78811.1 EST_HUMAN gb:A21187 ALPHA-2-MACROCALOBULIN PRECURSOR (HUMAN);	2.0E+00 W78811.1 EST HUMAN (ab-A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);	4885526 NT		5031624 NT	MT	0.0E+00 AF108389.1 NT Homo sapiens sodium/calcium exchanger isoform NaCe3 (NCX1) mRNA, complete cds	N	4826947 NT	0 4826947 NT Homo septens protein kinasa, X-linked (PRICX) mRNA	X57147.1 NT	504424 NT		7657468[NT	0.0E+00 AA614537.1 EST_HUMAN INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);
원 원	J04068.	BF10480				AF2217	AF2217	AF1497.	AB0378						AA3894	D11078	W78811.	W78811.				U05235.	AF10838	AF10836			X57147.		AB02901		AAB145
Most Similar (Top) Hit BLAST E Valus	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	15.19	1.83	0.77	0.77	0.69	1.6	1.6	1.86	1.63	0.85	1.65	1.65	1.34	1.34	1.35	4.61	1.86	186	5.61	2.78	2.3	3.11	0.99	68'0	4.84	4.94	3.3	9.58	4.6	17.63	15.52
ORF SEQ ID NO:		28585	28587	26588	26591	26597	26598	26805	26808	26609	26810	26811	28812	26613	26823	28827	26830	26831		28843	26846	26850	26653	79997	26659	26660		26673	26877	26892	26708
SEQ ID	13668	13871	13673	13873	13878	13681	13681	13688	13690	13692	13683	13693	13894	13894	13702	13708	13710	13710	13713	18720	18722	13726	13720	13729	13734	13734	15846	13746	13751	13760	13772
Probe SEQ ID	ह	흏	8	8	611	916	918	623	959	129	828	828	83	623	828	8	\$	4	8	758	929	659	88	88	88	88	675	88	88	88	710

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Sion Top Hit Datebese		¥	2192 NT	NT Homo sepiers ALR-tites protein mRNA, partial cds		5800 NT	THE PARTY OF THE P	Z.	Ę		¥	ź	2749 NT	ᅜ	EST_HUMAN	EST_HUMAN 1989908.r1 Scares breast 2NiHBst Homo sepiens cDNA clone IMAGE:154046 5	2086 NT	Z	H965 NT		INT Human mRNA for KIAA0184 gene, pertial cds		¥	M					57886 NT	NT	Mī	N	03854 NT Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
8 .	480675.1	A60675.1		0.0E+00 AF284760.1	0.0E+00 AF284750.1		0.05-00 05-2410/7.1	0.0E+00 AFZZ6990.2	0.0E+00 AF228980.2	103764.1	103764.1	0.0E+00 AB037780.1	691	330512.1	0.0E+00 BE869735.1	348915.1	503	0.0E+00 AB011399.1	Ø	380008.1	<b>D80006.1</b>	099772.1	0.0E+00 AB020717.1	AB020717.1	517	450	785	785	455	0.0E+00 AF108830.1	0.0E+00 AF108830.1	0.0E+00 AF108830.1	450
Most Similar (Top) Hit BLAST E Value	0.0E+00 M80875.1	0.0E+00 M60675.1	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.00	0.0E+00.	0.0E+00	0.0E+00 J03764.1	0.0E+00 J03764.1	0.0E+00	0.0E+00	0.0E+00 D30612.1	0.0E+00	0.0E+00 R48915.1				0.0E+00 D80008.1	0.0E+00 D80006.1	0.0E+00 XB9772.1	0.0E+00	0.0E+00	00+30'0	0.0E+00	0.0E+00	0.0E+00					
Expression Signal	4.91	4.91	22	4.69	4.69	11.38	2.31	2.00	2.00	0.88	0.88	2.01	0.86	3.03	1.78	3.68	2.14	1.88	277	2.38	2.38	2.72	3.38	3.38	10.76	9.83	1.58	2.57	1.82	3.12	3.12	1.34	2.16
ORF SEQ ID NO:	28710	26711	26720	26726	26727	28730	8/8	28761	26762	28764	28765	26768	28767	26769	26770	26774	26775	26783	26787	26799	26800	26804	28808	50892	26815		26836	26837			26846	26847	
Estan SEQ (D NO:	13776	13776	13786	13791	13791	13783	25/25	13817	13817	13819	13819	13822	13823	15850	13825	13829	13830	13838	13842	13852	13852	13857	13861	13861	13865	13866	13883	13884	13888	13891	1389H	13892	13897
Probe SEQ ID NO:	714	714	2	8	8	E	8	191	767	759	758	28	8	18	786	E	77	130	8	783	288	8	88	8	28	88	825	8	88	뛇	훯	88	8

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igle Exon Probes Expressed in Bone Marrow	Top Hit Descriptor	Homo sapiens T-cell lymphoma investon and metastasts 1 (TIAM1) mRNA	Homo sapiens T-cell lymphoma invesion and metastasis 1 (TIAM1) mRNA	Homo sapiens sodiun/myo-inosital cotransporter (SLCSA3) gene, complete cds	Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo saplens mRNA for KIAA1019 protein, partial cds	Homo sapiens SON DNA binding protein (SON) mRNA	Homo sepiens mRNA for KIAA1019 protein, partial cds	Homo sapiena ribosomel protein S5 (RPS5) mRNA	Homo septems mRNA for KIAA0910 protein, partial ods	Homo sapiens mRNA for KIAA0910 protein, partial cds	nj88407.s1 NCI_CGAP_Pr10 Hamo sepiens dDNA clane IMAGE:987453	nj88d07.s1 NCI_CGAP_Pr10 Hamo sepiens cDNA clane IMAGE:397453	802085579F1 NIH_MGC_83 Hamo sapiens cDNA clane IMAGE:4248915 5"	Homo sapiens hormonally upregulated neu fumor-associated kinase (HUNK), mRNA	Homo sapiens hormonally upregulated neu fumor-essociated kinase (HUNK), mRNA	Homo sepiens hormonally upregulated neu furnor-associated kinase (HUNK), mRNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo saplens chromosome 21 segment HS21C003	QV0-BT0703-280400-211-g11 BT0703 Homo saplens cDNA	QV0-BT0703-280400-211-g11 BT0703 Homo saplens cDNA	Hamo sapiens chromosome 21 segment HS21C003	Homo sepiens laminin receptor 1 (67/IO, ribosomal protein SA) (LAMR1), mRNA	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA	Homo sapiens alpha-1-antichymotrypsin precursor, mRNA, partial ods	Homo septens kellistatin (P14) gene, exons 1-4, complete cds	Homo sapiens of cardiac alpha-myosin heavy chain gene	Homo sapiens of cardiac alpha-myosin heavy chain gene	Homo sapiens of cardiac elpha-myosin heavy chain gene	Homo sapiens of cardiac alpha-myosin heavy chain gene	Homo septens mRNA for KIAA0994 protein, pertial ods	Homo sapiens mRNA for KIAA0394 protein, partial cds	Human ras inhibitor mRNA, 3' end	Human ras inhibitor mRNA, 3' end	Human ras inhibitor mRNA, 3' end
xon Probes EX	Top Hit Detabers Source	NT H			H H								HUMAN	HUMAN						EST_HUMAN O	EST HUMAN Q				¥I, IN					土 L					Ĭ
Single F	Top Hit Acression No.	4507500	4507500 NT	0.0E+00 AF027153.1	0.0E+00 AB028942.1	0.0E+00 AB028942.1	4507152 NT		4506728	0.0E+00 AB020717.1	0.0E+00 AB020717.1		0.0E+00 AA533272.1	0.0E+00 BF677694.1	7667243 NT	7657213	7657213	7657213	0.0E+00 AL163203.2	0.0E+00 BE089592.1	0.0E+00 BE089582.1	0.0E+00 AL163203.2	4504958 NT	4504958 NT	0.0E+00 AF089747.1						0.0E+00 AB023211.1	1.1			
	Most Similar (Top) Hit BLAST E Vatue	0.0E+00	0.0E+00	0.0E+00/	100+30 <sup>-</sup> 0	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00 [_28101.1	0.0E+00 Z20656.1	0.0E+00 Z20656.1	0.0E+00 Z20656.1	0.0E+00 Z20656.1	0.0E+00	0.0E+00	0.0E+00 M37190.1	0.0E+00 M37190.1	0.0E+00 M37190.1
	Expression Signal	13	123	1.78	4.48	4.48	10.69	4.54	14.11	1.18	1.18	1.8	8.1	10.08	1.57	1.57	1.95	1.95	0.86	1.72	1.72	1.69	63.74	24.73	0.71	2.39	0.84	0.04	0.63	0.63	2.68	2.68	0.68	8.74	0.72
	ORF SEQ ID NO:	76867	26858		26969	26870	26871	20872	20873	20878	26877	26878	26879		26880	26881	26882	26883	26906	26911	26912	26921			26927	26928	26930	26931	26932	28933	26950	28951	28957		26920
	SEO ID NO:	13900	13900	13907	13911	13911	13912	13913	13914	13918	13918	13919	13919	13920	13924	13824	13925	13825	13947	13954	13954	13864	13973	13973	13975	13978	13978	13978	13979	13979	13889	13999	14005	14006	14007
	Probe SEQ ID NO:	\$	\$	821	188	<b>38</b>	988	857	88	23	288	88	88	88	888	88	888	88	882	88	88	88	88	83	228	88	83	528	88	928	88	8	256	883	<b>8</b> 8

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Single Exon Probes Expressed in Bone Marrow

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Г			_				П				7	_1	_			П		ı	7	$\neg$	7		7			$\Box$			_	Т	7	7	$\neg$
	Top Hit Descriptor	Homo septens thyrotrophic embryonic factor (TEF), mRNA	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA	0898603.51 NCL_CGAP_GG3 Homo saplens cDNA clone IMAGE:16134043'	os98e03.s1 NCI_CGAP_GC3 Hamo saplens aDNA clone IMAGE:16134043'	Homo sapiens KIAA0929 protein Msv2 Interacting nuclear target (MINT) homolog (KIAA0929), mRNA	Homo sapiens mRNA for PSP24, complete cds	PM2-GN0014-050900-001-f02 GN0014 Hamo septens cDNA	PM2-GN0014-050900-001-f02 GN0014 Homo septens cDNA	PM2-CN0014-050900-001-f02 GN0014 Homo sepiens cDNA	Homo sapiens partial o-fgr gene, exons 2 and 3	Homo septens partial c-fgr gene, excris 2 and 3	Homo sepiens chromodomein protein, Y chromosome-lite (CDYL) mRNA	Human beta-fubulin (TUB4q) gene, complete cds	Human beta-tubulin (TUB4q) gene, complete cds	Human beta-tubulin (TUB4q) gene, complete cds	Homo sepiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds	Homo saplens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds	Homo sepiens 14q32 Jegged2 gene, complete cds; and unknown gene	Homo sepiens 14432 Jegged2 gene, complete cds; and unknown gene	Homo sepiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo septens 14q32 Jegged2 gene, complete cds; and unknown gene	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA	es88g07.s1 Strategene fetal retina 837202 Homo septens cDNA clone IMAGE:838236 3' similar to SW-PRS8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8;	EST51/24 WATM1 Hamo sapiens cDNA clone 51/24 similar to DNA-DIRECTED RNA POLYMERASE II	(alignment Ser and Pro with BLASTx or p)	EST51/24 WATM! Home sepiens cONA clone 51/24 similar to DNA-DIRECTED RNA POLYMERASE II	(alignment set and fro with BLAS (x of p)	Homo sepiens TRAF family member-associated NFKB activator (TANK) mRNA	Homo septens TRAF family member-associated NFKB activator (TANK) mRNA	Homo sepiens hypothetical protein FLJ11198 (FLJ11196), mRNA	Homo sapiens heat shock 70kD protein 9B (mortalin-2) (HSPA9B) mRNA
	Top Hit Defeaberse Source	IN.	LN	EST_HUMAN	<b>EST_HUMAN</b>	¥	¥	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	MT	TN	TN	NT	NT	NT	M	NT	N	M	NT	MT	NT	EST HUMAN		EST_HUMAN		EST HUMAN	¥	¥	F	¥
	Top Hit Acession No.	4507430 NT	4507430 NT	0.0E+00 Al001948.1	0.0E+00 Al001948.1	7857286 NT	0.0E+00 AB030568.1	0.0E+00 BF366974.1	0.0E+00 BF366974.1	0.0E+00 BF366974.1	(52207.1		4757969 NT	J83668.1	J83668.1	J83668.1	0.0E+00 AF198490.1	0.0E+00 AF198490.1	0.0E+00 AF111170.3	0.0E+00 AF111170.3	0.0E+00 AF111170.3	0.0E+00 AF111170.3	7881685 NT	5803114	0.0E+00 AA458890.1		V43182.1			4759249 NT	4759249	B922833 NT	4758569 NT
	Most Similar (Top) Hit BLAST E Vatue	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X52207.1	0.0E+00 X52207.1	0.0E+00	0.0E+00 U83668.1	0.0E+00 U83668.1	0.0E+00 U83668.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00 N43182.1		0.0E+00 N43182.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	0.83	0.83	224	2.24	10.17	2.04	1.86	1.86	1.86	3.55	3.55	2.25	1.17	13.38	10.52	2.58	5.29	1.28	1.82	1.71	1.65	242	121	1.58		0.78		0.78	1.2	1.2	3.19	24
	ORF SEQ ID NO:		19692	_	28969	76971	26981		88692	58685	28892	26993		27008	600/2	600/2			27015	27015	27015	27016	27019				Zvozz			27029	27030		27046
	SEQ ID NO:	14008	14008	15855	16866	14017	14027	14035	14035	14035	14037	14037	14048	14056	14057	14057	14060	14060	14084	14084	14064	14065	14068	14072	14073		14076		14076	14077	14077		14095
	Probe SEQ ID NO:	926	926	2963	888	985	976	88	<b>788</b>	7884	986	986	88	1006	1007	1008	1011	1012	1016	1017	1018	1019	1022	1026	1027		1030		1030	1031	1031	1034	1049

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ngie exon Prodes expressed in Borie Maitow	Top Hit Descriptor	Homo seplens cacherin 6, K-cacherin (fetal lidney) (CDHB) mRNA	Homo sepiens cedherin 6, K-cedherin (fetal kidney) (CDH8) mRNA	Homo sepiens hypothetical protein FLJ20865 (FLJ20895), mRNA	Homo septens hypothetical protein FL/20666 (FL/20695), mRNA	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)	Homo septens hypothetical protein FL/20080 (FL/20080), mRNA	Homo sapiens alkylation repair, alkB homolog (ABH), mRNA	Hamo septems Death associated protein 3 (DAP3) mRNA	MRO-BN0115-200300-003-h08 BN0115 Homo sepiens cDNA	Homo sepiens potassium channel, subfamily K, member 9 (KCNK9), mRNA	Homo sepiens potessium chennel, subfamily K, member 9 (KCNK9), mRNA	Homo sepiens protein kinasa, X-linked (PRKX) mRNA	Homo sapiens protein kinase, X-linked (PRKX) mRNA	Homo sepiens ribosomal protein S27a (RPS27A) mRNA	Homo sepiens hypothetical protein FLJ20309 (FLJ20309), mRNA	Homo sapiens DNA for Human P2XM, complete cds	Homo septens DNA for Hunen P2XM, complete ods	Homo septens similar to rat Integral membrane glycoprotein POM121 (POM121L1), mRNA	Homo sepiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA	Homo saptens Npw38-binding protein NpwBP (LOC51729), mRNA	H.saplens ART4 gene	H.sapians ART4 gene	qb22df0.xf Soares_pregnant_uterus_NbHPU Homo saptens cDNA ctone IMAGE:1697011 3'	Homo sapiens mRNA for KIAA0903 protein, partial cds	Homo sepiens chandraffin suffete proteogilycen 2 (versicen) (CSPG2) mRNA	Homo espiens chandratiin sulfate proteoglycan 2 (versican) (CSPG2) mRNA	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA	Homo sapiens glutamate decarboxylase 1 (brain, 67tD) (GAD1), transcript variant GAD25, mRNA	Homo sapiens glutamate decarboxylase 1 (brain, 67tD) (GAD1), transcript variant GAD25, mRNA	Homo septens mRNA for KIAA1414 protein, pertial cds	Homo sepiens keratin 18 (KRT18) mRNA	Homo sepiens Na+/r+ exchanger isoform 2 (NHE2) mRNA, complete cds	Horno sepiens muft. (E. coli) hornolog 3 (MLH3), mRNA	Homo sepiens ALR-like protein mRNA, pertial cds
xon Propes t	Top Hit Detrebesse Source	FX	Į.	Z	Z	NT	NT	MT	L	EST_HUMAN	IN	M	NT	NT	. LN	LN	NT	IN	Ę	Z	NT	NT	NT	EST_HUMAN	Ä			M	NT	Z	N	NT			IN
	Top Hit Acession No.	4826672 NT	4826672 NT	8923624 NT	8923624 NT	A.1245922.1	1N 2023087 NT	6174384 NT	4758117 NT	0.0E+00 BE005208.1	7706134	7706134 NT	4826947 NT	4826947 NT	4506712	TN 0625298		0.0E+00 AB002059.1	7657468	7857468 NT	7708500			0.0E+00 AI147850.1	0.0E+00 AB020710.1	4758081 NT	4758084 NT	9966844	7305076 NT	7305076 NT	0.0E+00 AB037835.1	4557887 NT	0.0E+00 AF073289.1	57336	0.0E+00 AF284750.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00 XB5826.1	0.0E+00 X95828.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/
	Expression Signal	213	2.13	3.18	3.18	28.45	0.82	3.85	1.91	262	5.54	5.54	0.98	96.0	33.54	234	8.07	20.89	523	6.23	1.84	0.76	0.78	1.25	1.68	3.19	3.19	0.89	8.28	8.26	1.08	1.21	0.64	1.24	1.18
	ORF SEQ ID NO:	27060	27061	27065	27068	Z7067		27071	27082	27092	27118	27117	27127	27128	27129	27131	27134	27135	27136	27137	27140	27141	27142	27143	27145	27154	27155	27156	27167	27168	27171	27180	27191		27225
	SEQ ID NO:	14111	14111	14115	14115	14118	14118	14120	14128	14142	14165	14185	14177	14177	14178	14180	14183	14185	14188	14186	14189	14190	14190	14191	14183	14202	14202	14203	14213	14213	14218	14223	14238	14252	14268
	Probe SEQ ID NO:	200	1066	1070	1070	1071	£201	1075	1084	1098	1121	1121	1134	1134	1135	1137	1140	1142	1143	1143	1147	1148	1148	1149	1151	1160	1160	1161	1172	1172	1175	1182	1198	1214	1230

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ACTIVITY DESCRIPTION OF THE PROPERTY OF THE PR	Most Similar Top Hit Acession (Top) Hit Top Hit Acession ID NO: Signal BLASTE No. Source	27228 1.18 0.0E+00 AF284750.1 NT	27227 1.6 0.0E+00 AF284750.1  NT	27228 1.7 0.0E+00 AF284760.1 NT	27253 6.18 0.0E+00 AF109718.1  NT	27254 0.98 0.0E+00 4503098 NT	27280 0.73 0.0E+00 4505740 NT	2.04 0.0E+00[Y18000.1 INT	27275 46.44 0.0E+00 4506718 NT	27284 4.02 0.0E+00 AF084479.1  NT	27288 1.08 0.0E+00 AB040940.1  NT	27289 1.08 0.0E+00 AB040840.1  NT	27302 2 0.0E+00 5174748 NT	27303 2 0.0E+00 6174748 NT	27304 2 0.0E+00 6174748 NT	3.46 0.0E+00/AF098156.1 NT	27316 1.26 0.0E+00 7857629 NT	27317 1.28 0.0E+00 7857529 NT	27322 6.23 0.0E+00 5803146 NT	27323 0.81 0.0E+00 4508004 NT	27324 6.68 0.0E+00 5803146 NT	27325 33.1 0.0E+00 4508004 NT	27327 4.74 0.0E+00 AB011149.1 NT	27328 5.7 0.0E+00 7681965 NT	27329 8.47 0.0E+00 7881985 NT	27330 6.14 0.0E+00 8567387 NT	27331 5.14 0.0E+00 8587387 NT	27344 2.17 0.0E+00 M14123.1 NT	27410 1.34 0.0E+00 A.250014.1 NT	1.79	27422 32.64 0.0E+00 6042208 NT	27430 1.31 0.0E+00 4505646 NT	27431 1.31
	ORF SEQ ID NO:	27228	12272	82242	27253	27254	27280		27275	27284	27288	277289	27302	27303	27304		27316	27817	27322	27323	27324	27325	27327	27328	6Z£1Z	27330	27331				1		
	Exam SEQ ID NO:	14268	14269	15861	14287	14288	14297	14306	14314	14321	14327		L	14339	14339		16863	15863		14356	14357			14361	14362	14363	14363	L	<u> </u>	L			Ш
	Properties (No. 10)	1230	1231	1232	1251	1252	1282	1271	1279	1286	1282	1292	1303	1303	  \$3	1304	1314	1314	1319	1320	1322	1323	1325	1326	1327	1328	1328	1340	1407	1415	1416	1423	1423

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	Top Hit Descriptor	Homo saplens KIAA1114 protein (KIAA1114), mRNA	Homo septens KIAA1114 protein (KIAA1114), mRNA	Homo saplens partial AF-4 gene, exons 2 to 7 and Alu repeat elements	Homo sapiens alpha1-6fucosyltransferase (alpha1-6FucT) gene, exon 7	Human nabulin mRNA, partial cds	Human nebulin mRNA, partial cds	Novel human gane on chromosome 20	Novel human gene mapping to chamosame 1	Human mRNA for KIAA0240 gene, partial cds	Homo saplens calcineunh binding protein 1 (KIAA0330), mRNA	Homo sapiens KJAA0170 gene product (KJAA0170), mRNA	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA	Horno sapiens RFB30 gene for RING finger protein	Homo sepiens IHIDC for hamolog of Drosophila headoase (LOC51696), mRNA	4 as34s03_r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815116 5	Cercopithecus aethiops cyclophilin A mRNA, complete cds	Cercopithecus eathlops cyclophilin A mRNA, complete cds		LEST388206 MAGE resequences, MAGN Hamo sapiens cDNA	Homo sepiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete ds	Human T-cell receptor gamma chain VJCI-CII region mRNA, complete cds	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA	Homo sapiens transmembrane glycoprotein (GPNMAB) mRNA	Homo sapiens KIAA0857 protein (KIAA0857), mRNA	Homo saplens TNF-Inducible protein CG12-1 (CG12-1), mRNA	Human transglutaminase mRNA, complete cds	Homo saplens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sepiens ribosomal protein L5 (RPL5) mRNA	Human laminin receptor (2H5 epitope) mRNA, 5' end	Homo sapiens titin (TTN) mRNA	Hamo sepiens titin (TTN) mRNA	Homo seplens chondroitin sulfate proteoghoan 4 (metanoma-essociated) (CSPG4), mRNA
	Top Hit Detabase Source	LN.	¥	Į	NT	Ν	NT	F	NT	FN	M	F	Ę	¥	E	<b>EST_HUMAN</b>	F	NT TN	EST_HUMAN	EST_HUMAN	· 坛	F	 	Ä	ΝT	NT.	Ŋ	NT	¥	NT.	NT	T	Ę	Ę
28.5	Top Hit Accession No.	TN05565 NT	IN 595502/2	0.0E+00 AJ238083.1	0.0E+00 AF038280.1	0.0E+00 US5837.1		1	0.0E+00 AL137764.1	0.0E+00 D87077.1	1N 2457 NT	TN 681965 NT	7661965 NT	0.0E+00 Y07829.2	7706434 NT	0.0E+00 AA481172.1	0.0E+00 AF023860.1	Ţ	0.0E+00 AW976097.1	0.0E+00 AW976097.1	0.0E+00 U780Z7.1		4505404 NT	4505404 NT		7856972	M98478	4507720 NT	TN 0277200 NT	4508654 NT	M14199.1	4607720 NT	4507720 NT	4503098 NT
	Most Similar (Top) Hit BLAST E Vatue	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	229	2.20	18.81	2.94	1.01	1.01	3.14	25	1.59	5.38	1.7	1.7	<u>4</u>	211	1.94	29.64	29.54	1.37	137	222	225	204	2.04	3.31	7.04	2.45	124	124	19.78	26.31	0.94	0.94	10.15
	ORF SEQ ID NO:	27434	27435	27436	27445	27456	27457	27464	27465	27470	27473	27475	27478		27516	27532	27536	27537	27540	27541		27544	27645	27546	27647	<b> </b>	27653	27555	27666		27557	27571	27572	27573
	SEQ:D	14458	14458	14460	14468	14480	14480	14490	14492	14496	14489	14501	14501	14502	14545	14561	14567	14567	14569	14569	14571	14572	14573	14573	14574	14575	14581	14584	14684	15871	14585	14696	14596	14598
	Probe SEQ ID NO:	1426	1426	1427	484	1447	1447	1457	1459	1463	1468	1468	1468	1468	1513	1528	4634	<u> </u>	1538	1538	1538	1530	1540	1540	1541	1542	1548	1551	1561	1552	1563	1563	1563	1565

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Table 4
Single Exon Probes Expressed in Bone Marrow

Single Exoli Plobes Expressed in Doile mailow	Top Hit Database Source	Ϋ́	5921460 NT Homo septers butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA	5924460 NT · Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA	EST_HUMAN	1 EST HUMAN	1 NT	1 NT					NT	EST_HUMAN	INT	.1 NT	7.1 EST_HUMAN	1 EST_HUMAN	.1 EST_HUMAN	EST HUMAN	758513 NT	IN I	NT	NT	4557887 NT Homo septems kerettin 18 (KRT18) m/2NA	7657065 NT Hamo septems viets evitar expthroblestosis virus E28 ancogene related (ERG), mRNA	.1 EST_HUMAN	1 EST HUMAN	EST_HUMAN	
IIG Mail Ow		ene	rophilin, subfamily	rophilin, subfamily	mo sapiens oDN	mo sepiens cDN	A for KIAA1472	polymenase zeta	V0589 gene produ	10569 gene produ	shock 70kD prob	shock 70kD prote	nnei mRNA	adult brain N2b4	VA for KIAA1609	VA for KIAA1609	O-UI.st NCI_CG	89-004-b11 HT0	99-004-b11 HT0	NSF FB 9W (	atopoietic-derived	al receptor gamm	protein 7 (ZFP7)	protein 7 (ZFP7)	tin 18 (KRT18) m	s avian erythrobla	GAP_Lu24 Ham TEIN TYROSINE	GAP_LI24 Ham TEIN TYROSINE	breest 3NbHBst M.TRANSPEPTI	breast 3NbHBst M.TRANSPEPTI
ST III POSSOITA		i.sapiens hH2B/e g	forno sapiens buty	forno sapiens butyr	1V690831 GKC Ho	1V690831 GKC Ho	formo sapiens mRN	forno sepiens DNA	tomo sapiens KIA/	tomo sepiens KIA/	lomo sapiens heat	lomo sapiens heat	luman sodium cha	P76c05.srl Soares	lomo sapiens mRN	forno septens mRN	JIH BIS alwood	WR0-HT0168-1911	VIRO-HTD166-1911	wg81b07.x1 Soares TR:Q62788 Q6278	Homo sepiens hem	Homo sapiens T-ce	Human zino-finger	Human zho-finger	Homo sapiens kera	Homo sapiems v-eta	hutidogaainoa_c Wiktp-1 like prot	hu11d06x1 NCI_C MIKP-1 LIKE PROT	yo59608.rt Soeres GAMIMA-GLUTAM	yo59e08.rl Sogres GAMMA-GLUTAM
AUII FIUDES E				•		T_HUMAN								HUMAN																
	Top Hit Acessian No.	283738.1	5921460	5021460	0.0E+00 AV680831.1	1	1	F157478.1	7662183	7862183	5729876	5729876			.1	.1	7.1	.1	.1		758513	1			4557887	7657065	3E222374.1		1301321	130132.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00 Z	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AV690831.	0.0E+00 AB040905	0.0E+00 AF157478	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M91803.1	0.0E+00 H26973.1	0.0E+00 AB046829	0.0E+00 AB046829	0.0E+00 AW444837	0.0E+00 BE144384	0.0E+00 BE144384	0.0E+00 AI768104.	0.0E+00	0.0E+00 AF057177	0.0E+00 M29580.1	0.0E+00 M29580.1	0.0E+00	0.0E+00	0.0E+00 BE222374	0.0E+00 BE222374	0.0E+00 H30132.1	0.0E+00 H30132.1
	Expression Signal	9.8	1.81	1.84	1262	12.62	2.54	1.24	4.83	4.83	28.28	26.26	1.58	7.01	. 231	231	1.04	1.19	1.19	1.84	1.44	3.61	1.72	1.72	1.53	212	1.27	127	6.17	5.17
-	ORF SEQ ID NO:	27589	27890	27591	27592	27383	27598	27597	27800	27601	27802	27603	27805	27821	27632	27633	27849	27682	27883	27687	27688	27889	27883	27694	27606	776977	27700	7770	27705	27.706
	SEQ ID NO:	14616	14617	14817	14618	14618	15872	14624	14626	14626	14628	14628	14630	14845	14655	14655	14678	14705	14705	14709	14710	14711	14714	14714	14718	14717	14724	14721	14723	
	Probe SEQ ID NO:	1583	1584	1584	1585	1585	1588	1592	1594	1594	1596	1596	1508	1613	1622	1622	164	1673	1673	1877	1678	1679	1683	1683	1685	1689	9	089	1683	1683

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AND EACH PROBLEM IN DOING MAILOW	Top Hit Descriptor Source	EST_HUMAN   qf43f09.x1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'	NT H.septens H2B/h gene	NT H.saplens H2Bih gene		NT Homo sepiens WNT16 protein (WNT16) mRNA, complete ods		T Homo sepiens pericentriciar material 1 (PCM1) mRNA	NT Human hepatocyte growth factor gene, excn 15	NT Human hepatocyte growth factor gene, exon 15		NT Homo septiens WAVE2 mRNA for WASP-fernity probsh, complete cds	NT TCR zeta [human, Genomic/mRNA, 365 nt, segment 1 of 8]							NT Human CSF-1 receptor (FMS) gene, complete ods, and (SMF) gene, partial cds	EST_HUMAN - Izd68g09.r1 Soares_fetal_heart_NINHH19W Homo sepiens cDNA clone IMAGE:345684 57		EST_HUMAN   zn65c09.s1 Strategene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:563056 3'	NT Human ribosomal protein L21 mRNA, complete cds	NT Human mRNA for KIAA0333 gene, partial ods	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA	Homo sepiens activating transcription factor 4 (tex-responsive enhancer element B67) (ATF4) mRNA	Homo sepiens activating transcription factor 4 (tex-responsive enhancer element B67) (ATF4) mRNA			NT Homo sapiens mRNA for KIAA1152 protein, partial cds	NT Homo sepiens mRNA for KIAA1152 protein, pertial cds
	Top Hit Acessian No.	0.0E+00 AI149890.1			5031748 NT	0.0E+00 AF169983.1 N	8923841 NT	5453865 NT			4826973 NT	0.0E+00 AB028542.1 N		4557538 NT	11545911 NT	0.0E+00 AF273841.1 N	4506718 NT	4557558 NT	4557556 NT		0.0E+00 W76571.1 E	4505332 NT	0.0E+00 AA113030.1 E		0.0E+00 AB002331.1 N	4602284 NT	4502284 NT	4502284 NT	8005855 N	6005855 NT	0.0E+00 AB032978.1	0.0E+00 AB032978.1 IN
	Most Similar (Top) Hit BLAST E Veitue	0.0E+00,	0.0E+00 Z80780.1	0.0E+00 Z80780.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M75980.1	0.0E+00 M75980.1	0.0E+00	0.0E+00	0.0E+00 S94400.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U63963.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U14967.1	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00	0.0E+00,	0.0E+00
	Expression Signal	0.94	7.28	7.28	28.3	0.91	5.35	1.03	96'0	96'0	1.37	20.03	259	76.0	121	2.63	35.79	242	242	205	1.32	3.9	1.13	14.85	5.94	6.64	6.64	884	6.56	6.58	1.34	1.34
	ORF SEQ ID NO:		27708	602.22		12112	27724	12172	27731	27732	27736	27743		27762	27759	27775		27821	27822	27825		27829	27830	27846	27848	27849	27850	27851	27872	27873	27883	27884
	SEO E	14725	14728	14726	14729	14739	14740	14743	14748	14746	14760	14756	14758	14767	15876	14789	15877	14833	14833	14835	14838	15878	14839	14851	14853	14864	14854	14854	14877	14877	14887	14887
	Probe SEQ ID NO:	1685	1686	1696	- 689	1708	1710	1713	1716	1716	1720	1728	1728	1737	1744	1760	1800	1805	1805	1807	1830	1811	1812	1824	1826	1827	1827	1827	1851	1851	1861	1861

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Table 4
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ngie Exon Probes Expressed in Bone Marrow	Top Hit Descriptor	Homo sepiens potassium voltage gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA	Human retinal degeneration slow (RDS) gene, exan 1	Human retinal degeneration slow (RDS) gens, excn 1	UI-H-BIT-effn-F-07-0-UI.s1 NCI_CGAP_Sub3 Homo sepiens cDNA clane IMAGE:2722333 3'	UI-H-BI1-afn-f-07-0-UI.61 NCI_CGAP_Sub3 Hamo sapiens aDNA clane IMAGE-2722333 3'	601179164F1 NIH_MGC_20 Hamo septens cDNA clane IMAGE:3547239 5	601179164F1 NIH_MGC_20 Homo septens cDNA clone IMAGE:3547239 5	Homo sapiens nuclear protein (NP220), mRNA	Homo saplens nuclear protein (NP220), mRNA	Homo sapiens RAD1 (S. pombe) homotog (RAD1) mRNA, and translated products	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds	Human transgutaminasse mRNA, complete cds	Human transglutaminase mRNA, complete cds	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA	Homo saptens transforming growth factor, beta 3 (TGFB3), mRNA	Homo sapiens death receptor 6 (DR6), mRNA	Homo septions glutethione S-transferase thete 2 (GSTT2) and glutethione S-transferase thete 1 (GSTT1)	gares, comprete cus	United applications by producing the state of Company Application and Company	Homo carbone hielifina ammonia basa (HAI) mRNA	Homo earlane Molidine emmonia hace (HAI) mRNA	CECURGO POPULATION OF THE PROPERTY OF THE PROP	Harro septens an unicomitie at septement Pozitousz	Homo sapiens nebulin (NEB), mRNA	Homo sepiens nebulin (NEB), mRNA	Homo sapiens actinin, atpha 4 (ACTN4) mRNA	Homo sapiens actinin, elpha 4 (ACTN4) mRNA	Homo septems mRNA for KIAA0790 protein, partial cds	Homo sepiens mRNA for KIAA0790 protein, partial cds	Human TFEB protein mRNA, partial ods
xon Probes E	Top Hit Detraberse Source	NT.		N <sub>T</sub>	NT	П			HUMAN					NT	IN	NT					Z	1						NT				NT	
Single	Top Hit Acesslan No.	4826783 NT	4826783 NT			0.0E+00 AW207280.1	0.0E+00 AW207280.1	0.0E+00 BE277466.1	0.0E+00 BE277465.1	7857390 NT	7857390	4506384 NT	4606384 NT	0.0E+00 AF157478.1		V98478.1	4507484 NT	4507464	7867038 NT		0.0E+00 AF240786.1	1.2cocciv	TIMICOCOOON	TV 2020001	TOTO TOTO	0.0E+00 AL1632522	8400716 NT	8400716 NT	4826638 NT	4828638 NT	1	1.1	
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00 U07147.1	0.0E+00 U07147.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M98478.1	0.0E+00 M98478.1	0.0E+00	0.0E+00	0.0E+00		0.05+00/	0.0E+00 M33032.1	0.05	0.00	O.UC.	0:0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M33782.1
	Expression Signal	3.28	3.28	6.86	6.86	1.48	1.48	3.46	3.48	0.83	<b>68.0</b>	2.02	2.02	1.13	1:41	1.41	2.02	2.02	1.08		5.63	287	04.	8 8	8.	60	1.81	1.81	2.97	297	1.05	1.05	1.59
	ORF SEQ ID NO:	27886	27887	27888	27889	27892	27893	27912	27913	27958	27957	27959	27960		27970	17872	27978	27979	27981				2000	00007	2007		28010	28011	28012	٨	28025		28030
	Exan SEQ ID NO:	14890	14890	14891	1489A	14894	14894	14917	14017	14960	14960	14083	14963	14972	15881	16881	14977	14977	14979		14981	14680	70001	100	B	1505	15007	15007	15008	15008	15018	15018	15024
	Probe SEQ ID NO:	1865	1885	1888	1886	1869	1869	1892	1892	1886	1836	1930	1839	1948	1940	1949	1854	28	1857			3 3		2 2	CVAL	1984	1986	1986	1987	1987	1897	1997	2003

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2008 2008 2008 2008 2008 2008 2008 2008	Example 15026 15026 15026 15026 15026 15026 15026 15030 1503	28031 28032 28033 28034 28034 28037 28038 28039 28048 28048 28048 28048 28148 28112 28124 28128 28128 28128 28128	Signal 1.38 1.18 1.18 1.18 1.18 1.18 1.18 1.18	Most Similar (Top) Hit A BLAST E NATURE OF HOD M33782.  0.0E+00 M33782.  0.0E+00 AW19302  0.0E+00 0.0E+00 AW19302  0.0E+00 AF27384  0.0E+00 AF27384  0.0E+00 AF27384  0.0E+00 AF27384  0.0E+00 AF27384  0.0E+00 AF27758  0.0E+00 AF27758  0.0E+00 AF27758  0.0E+00 AF27758  0.0E+00 AF27758  0.0E+00 AF27758  0.0E+00 AF27758  0.0E+00 AF27758  0.0E+00 AF27758  0.0E+00 AF27758  0.0E+00 AF277758  0.0E+00 AF277758  0.0E+00 AF277758  0.0E+00 AF277758  0.0E+00 AF277758  0.0E+00 AF2777758  0.0E+00 AF2777758  0.0E+00 AF2777777777777777777777777777777777777	6. Coession 6. Coession 7. Coe	HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN	Human TFEB protein mRNA, partial ods  JEBBOT X1 NCL CGAP_Part Homo sapiens cDNA clone IMAGE-2678913 3'  JEBBOT X1 NCL CGAP_Part Homo sapiens cDNA clone IMAGE-2678913 3'  JEBBOT X1 NCL CGAP_Part Homo sapiens cDNA clone IMAGE-2678913 3'  Homo sapiens calcinourin binding protein 1 (KIAA0330), mRNA  Homo sapiens acalcinourin binding protein 1 (KIAA0330), mRNA  Homo sapiens graves for semenogelin I and semenogelin II  Haptons applens graves for semenogelin I and semenogelin II  Homo sapiens MRNA for KIAA1513 protein, partial cds  Homo sapiens MRNA for KIAA1513 protein, partial cds  Homo sapiens SIMCY (SIMCY) gene, complete cds  Homo sapiens GNCY (GNCY) Homo sapiens cDNA done IMAGE-3138320 G  G0192204F1 NIH MCC_19 Homo sapiens cDNA done IMAGE-3138320 G  G0192204F1 NIH MCC_19 Homo sapiens cDNA done IMAGE-3138320 G  G0192204F1 NIH MCC_19 Homo sapiens cDNA done IMAGE-3138320 G
868	11		235	0.0E+00 L00820.1 0.0E+00 L00820.1		П	Human plasma membrane calcium ATPase Isoform 2 (APT282) mRNA, comiete cds Human plasma membrane calcium ATPase Isoform 2 (APT282) mRNA, comiete cds
7 2 2 8 7 2 2 8	$\pm 1.1 \pm 1$			0.0E+00 0.0E+00 0.0E+00	4758489 4.1 3.1	T HUMAN	Homo sepiens GTP binding protein 1 (GTPBP1) mRNA QV1-GN0065-140600-318-c10 GN0065 Homo sepiens cDNA Homo sepiens X-linked juvenile refinoschists protein (XLRS1) gene, exon 6 and complete cds 60167266F1 NIH MGC_20 Homo sepiens cDNA done IMAGE:3954786 6
27.28	15143	28160	1.42	0.0E+00	0.0E+00 BE072624.1	EST_HUMAN	PMD-B I 0547-210300-004-F04 B I 0547 Homo sapiens c.JNA

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Probe SEQ ID. NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Moct Similar (Top) Hit BLAST E Vætue	Top Hit Acession No.	Top Hit Defetationse Source	Top Hit Descriptor
2310	16322	28344	211	0.0E+00	0.0E+00 Al078404.1	EST_HUMAN	0209007x1 Soares_fetal_liver_splean_1NFLS_S1 Homo sepiens cDNA clone IMAGE:1674828 3'
2312		28346	1.43	0.0E+00	0.0E+00 AA428001.1	EST_HUMAN	zv?Ber11.r1 Sceres_itotal_fetus_Nb2HFB_9w Homo septiens cONA ctone IMAGE:759740 67
2312	l		1.43	0.0E+00	0.0E+00 AA428001.1	EST_HUMAN	ZVPBe11.11 Scenes_total_fetus_Nb2HF8_9w Homo septens cDNA clone INAGE:759740 5
2314		28349	221	0.0E+00	0.0E+00 BF347039.1	EST HUMAN	602021846F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157339 5
2315	14572	27544	1.36	0.0E+00	0.0E+00 M16768.1	NT	Human T-call receptor gamma chain VJCH-CIII region mRNA, complete cds
2320			1.09	0.0E+00	0.0E+00 L02840.1	IN	Homo sapiens potassium channel Kv2.1 mRNA, complete cds
2321	15332	28356	1.57	0.0E+00	6325466 NT	NT	Homo sapiens flavin containing monocygenase 3 (FMO3), mRNA
7827	15338	28361	1.83	0.05+00	0.0E+00.BE678085.1	EST HUMAN	722262x1 NCI_CGAP_CLL1 Homo septens cDNA clone IMAGE:3295370 3' similar to TR:094939 094639 KIAA0857 PROTEIN:
888			5.18	0.0E+00		K	Homo sepiens phosphorylese kinese elpha subunit (PHKA2) gene, exon 32
2831	L		211	0.0E+00	Al825542.1	<b>EST_HUMAN</b>	157-08-x1 NCI_CGAP_U/2 Homo sepiens cDNA clone IMAGE:2283182 3'
2338			1.78	0.0E+00		Į,	Homo sepiens sperm specific entigen 2 (SSFA2), mRNA
2338	15347		1.78	0.0E+00	5803178 NT	LN LN	Homo sepiens sperm specific antigen 2 (SSFA2), mRNA
2342	15352		1.44	0.0E+00	7862007	NT	Homo sepiens KIAA0218 gene product (KIAA0218), mRNA
2342			1.44	0.0E+00	7882007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2346	15355	728377	26'0	0.0E+00	0.0E+00 D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2346	15355		26'0	0.0E+00	0.0E+00 D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2358		28386	3.77	0.0E+00	5174678 NT	NT	Homo saptens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2360			1.88	0.0E+00	0.0E+00 AU131142.1	EST_HUMAN	AU131142 NT2RP3 Hamo sepiens CDNA clane NT2RP3002064 5
2361			8.67	0.0E+00	0.0E+00 BE794028.1	EST_HUMAN	601596843F1 NIH_MGC_7 Hamo sepiens cDNA clane IMAGE:3941003 5
2362	1 3	28391	1.23	0.0E+00	0.0E+00 AW867076.1	EST_HUMAN	MR1-SN0033-120400-002-e04 SN0033 Horpo septens cDNA
2363			3.7	0.0E+00	7862017 NT	NT	Homo septens KIAA0244 protein (KIAA0244), mRNA
2364			227	0.0E+00	1N 2648374	NT	Homo sapiens haces-8-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2364	15372	78394	2.27	0.0E+00	4758497 NT	NT	Homo sapiens hease-8-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
	·						Homo sepiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genee, complete cds; and cytochrome P450
2365	15373		6.34	0.0E+00	0.0E+00 AF280107.1	NT	polypeptide 6 (CYP3A6) gene, partial cds
2367	15375		13.47	0.0E+00	0.0E+00 AU118082.1	EST_HUMAN	AU118082 HEMBA1 Hamo sepiens cDNA clane HEMBA1002839 5
2367	15375	70582	13.47	0.0E+00	0.0E+00 AU118082.1	EST HUMAN	AU118082 HEMBA1 Homo sepiens cDNA clone HEMBA1002839 5'
2367	16375		13.47	0.0E+00	0.0E+00 AU118082.1	EST_HUMAN	AU118082 HEMBA1 Hamo sapiens cDNA clone HEMBA1002839 5'
2368		68282	98.0	0.0E+00	TN 6808268	NT	Homo sapiens hypothetical protein FLJ20081 (FLJ20081), mRNA
2424	15431	28453	1.11	0.0E+00	0.0E+00 AU119582.1	EST_HUMAN	AU118582 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5
2426	15433		4.37	0.0E+00	0.0E+00 Al042035.1	EST HUMAN	ακθύδο2.xt Soares_NhHMPu_S1 Homo septens cDNA ctone IMAGE:1660683 3' stmiler to TR:008682 C08662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE;

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	Top Hit Descriptor	Homo sepiens adilican mRNA, complete cds	601173831F1 NIH_MGC_17 Hamo sapiens aDNA dane IMAGE:3529159 5	Homo sapiens mRNA for KIAA1415 protein, partial cds	Homo sepiens mRNA for KIAA1416 protein, partial ods	UHHBW1-emp-f-12-0-ULs1 NG_CGAP_Sub7 Hamo septens cDNA clane IMAGE:3070631 S'	602152853F1 NIH_MGC_81 Hamo septens cDNA clone IMAGE:4283812 5	timigido8.x1 NCI_CGAP_Brid26 Homo septiens cDNA clone IMAGE:2168056 3° similer to gict_20977 CALCIUM-TRANSPORTING ATPASE PLASMA MENIBRANE, BRAIN ISOFORM 2 (HUMAN);	Homo sepiens TATA box binding protein (TBP)-essociated factor, RNA polymerase II, I, 28kD (TAF2I)	mRNA	Homo sepiens mRNA for KIAA1438 protein, pertial cds	601590108F1 NIH_MGC_7 Hamo sapiens aDNA clane IMAGE:3944304 51	601560108F1 NIH_MGC_7 Hamo sapiens aDNA clane IMAGE:3944304 5	601584830F1 NIH_MGC_7 Hamo sapiens aDNA dane IMAGE:3839222 5	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA	Homo septems Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein	(L+m.) and Firs (Firs) games, whilehold was	Homo septems guenylate cyclass-activating protein 2 (GUCA1B) gene, exon 1	Homo sepiens mRNA for KIAA0638 protein, partial ods	AU133385 NTZRP4 Hamo sepiens cDNA clane NTZRP4001884 6	Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds	AU130403 NT2RP3 Homo sepiens cDNA clone NT2RP3000779 5	AU130403 NT2RP3 Homo sepiens cDNA clane NT2RP3000779 6	RC1-OT0086-220300-011-d07 OT0086 Hamo sapiems cDNA	7h15h05x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMACE:3316089 3'	601298714F1 NIH_MGC_19 Hamo sepiens aDNA alone IMAGE:3828923 6	601278373F1 NIH_MGC_39 Hamo septens cDNA clane IMAGE:3610267 5	Homo sapiens mRNA for KIAA1311 protein, partial cds	EST188414 HCC cell line (matastassis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal	protein L29	601589823F1 NIH_MGC_7 Hamo septens aDNA dane IMAGE:3943591 5	Human beta-prime-adaptin (BAM22) gene, exton 5	Homo sepiens neuregulin 1 (NRG1), transcript variant SMDF, mRNA	Homo sepiens skeletal muscle LIM-protein 1 (FHL1) gana, complete cds
## 84	Database Source	NT.	EST HUMAN 6	Į.	TN.	EST_HUMAN L	EST_HUMAN 6	EST HUMAN	T		IN IN	EST_HUMAN 0	EST_HUMAN 6	EST_HUMAN 6					± EN	EST_HUMAN /	Į.	EST_HUMAN /	EST_HUMAN /	Г	EST_HUMAN 7	EST_HUMAN 6	EST_HUMAN 6			EST_HUMAN F	EST HUMAN 6	TA L		TN
	Top Hit Acessian No.		1	1	1					5032150 NT	1		1	0.0E+00 BE792472.1	4504686 NT		$\prod$	1	1	1		1	1	-		Ţ	Ļ			1	1		7669517	1
100	(Top) Hit BLAST E Value	0.0E+00 AF245505.	0.0E+00 BE296813.	0.0E+00 AB037838.	0.0E+00 AB037836.	0.0E+00	0.0E+00 BF672818.	0.0E+00 AI571737.1		0.0E+00	0.0E+00 AB037859.	0.0E+00	0.0E+00 BE795445.	0.0E+00 E	0.0E+00		0.0E+00 0780Z/.1	0.0E+00 AF173227.	0.0E+00 AB011108.	0.0E+00 AU133385	0.0E+00 M89225.1	0.0E+00 AU130403.	0.0E+00 AU130403.	0.0E+00 AW887015	0.0E+00 BF000018.	0.0E+00 BE383166.	0.0E+00 BE531283.	0.0E+00 AB037732.		0.0E+00 AA316723.	0.0E+00 BE794884.	0.0E+00 U36253.1	0.0E+00	0.0E+00 AF110763.
<b>-</b>	Expression Signal	8.56	1.03	216	215	2.35	1.01	1.1		2.57	7.78	1.25	1,25	8.15	268		1.32	5.99	110.09	122	0.92	1.28	1.28	207	1.12	5.39	3.03	0.92		11.44	1.11	3.65	1.05	1.6
	ORF SEQ D NO:	28589	28607	28629	28630		28634	28842		28643	28647	28648	28649		28664			28872	28673	28676	28877	28679	28680	28883	28686	28887	<b> </b>	28719			28741			
	SEO ID NO:	15569			l	15606	15610	15818		15619	15622	15623	15623	15633	15640		15650	15851	15855	15658	15659	15861	15661	15684	15867	ļ	ı	1	1	15728	L	15733	15734	15735
9	SEO EO	8957	2589	9092	2808	2807	2811	2820		282	2823	2624	2824	2634	2642		2653	2654	2658	2661	2002	2864	2664	2687	2870	2871	2872	2709		2732	2733	2739	2740	2741

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ngie Exon Probes Expressed in bone Mairow	Top Hit Descriptor	801691991F1 NIH_MGC_7 Hamo sapiens cDNA dane IMACE:3946983 6	801335485F1 NIH_MGC_39 Hano sepiens cDNA clane IMAGE:3688564 5	AV721647 HTB Hamo sapiens aDNA dane HTBBYE09 5'	Homo sepiens spermatogenests associated PD1 (KIAA0757) mRNA	Homo sepiens spermatogenesis associated PD1 (KIAA0757) mRNA	Homo sepiens hypothetical protein FLJ20477 (FLJ20477), mRNA	Homo sepiens hypothetical protein FLJ20477 (FLJ20477), mRNA	Homo sepiens hypertension-related calcium-regulated gene mRVA, complete cds	AV651068 GLC Homo sepiens dDNA dana GLCCLD073*	CM1-TN0141-250900-439-508 TN0141 Homo sepiens cDNA	CM1-TN0141-250900-439-bo8 TN0141 Hamo sepiens cDNA	Homo sepiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA	Homo sapiens carebellar degeneration-related protein (34kD) (CDR1) mRNA	601580903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 6	Horno sepiens chromosome 21 segment HS21C001	UI-H-BW1-amw-e-07-0-UI.s1 NCI_CGAP_Sub7 Hamo sepiens aDNA clane IMAGE:3071340 3'	Homo sapiens chondroitin sulfate proteogrycan 4 (metanoma-associated) (CSPC4), mYNA	Homo sepiens anglopoletin-3 (ANG-3), mRNA	Homo sepiens angiopoletin-3 (ANG-3), mRNA	602085578F1 NIH_MGC_83 Hamo sepiens cDNA clane IMAGE:4249915 5	Homo septems protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA	AV725534 HTC Hamo sepiens cDNA dane HTCCCA03 5	AV725534 HTC Hamo sepiens aDNA dane HTCCCA03 5	au55d04,y1 Schneider fetal brain 00004 Homo sepiens cDNA clone IMAGE:2518003 5' similar to SW 1713A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;	802071957F1 NCI_CGAP_Bm67 Homo septens cDNA clane IMACE:4214679 67	801450912F1 NIH_MGC_85 Homo sapiens cDNA done IMAGE:3854642 5	AU131494 NT2RP3 Hamo septens CDNA clane NT2RP3002672 5	AU131494 NT2RP3 Hamo sepiens cDNA clane NT2RP3002872 5	600944794F1 NIH_MGC_17 Hamo sepiens cDNA clane IMAGE:2980806 5	600944794F1 NIH_MGC_17 Homo saptens cDNA clone IMAGE:2360806 5	ghycoprotein D=Duffy group emitgen [human, blood, Genomic DNA, 3068 nt]	Hamo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isotomin C, complete cas	Homo sapiens ALR-like protein mRNA, partial cds
xon Probes =	Top Hit Detrabase Source	П	EST_HUMAN	EST_HUMAN	ᅜ	NT	NT	ΝŢ	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN TN	NT	EST_HUMAN	NT	EST_HUMAN	N	NT	ᅜ	EST_HUMAN	NT	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	Z	Z
anguis -	Top Hit Acession No.		1	0.0E+00 AV721647.1	5174486 NT	5174486	8923441 NT	8923441 NT			0.0E+00 BF377897.1	F377897.1	4757963 NT	4757963 NT	E747183.1	0.0E+00 AL163201.2	0.0E+00 BF514110.1	TN 8608034	7706275 NT	7705276 NT	0.0E+00 BF677694.1	7427522 NT	0.0E+00 AV725634.1	0.0E+00 AV725534.1	0.0E+00 AI879163.1	0.0E+00 BF630661.1	0.0E+00 BE87Z768.1	0.0E+00 AU131494.1	0.0E+00 AU131494.1	0.0E+00 BE300344.1	0.0E+00 BE300344.1	576830.1	0.0E+00 AB033281.1	0.0E+00 AF284750.1
-	Most Similar (Top) Hit BLAST E Value	0.0E+00 BE796378.	0.0E+00 BE563433.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BF377897.	0.0E+00	0.0E+00	0.0E+00 BE747183.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 E	0.0E+00	0.0E+00/	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00 S78830.1	0.0E+00	0.0E+00
	Expression Signal	8.77	13.57	123	28	29	98.0	0.98	3.23	48.84	6.5	6.5	16.0	9.94	2.96	1.71	4.09	1.02	1.58	1.58	4.03	1.58	16.3	15.3	13.6	2.83	3.53	1.98	1.88	34.94	34.94	7.12	0.75	1.6
	ORF SEQ ID NO:	28758	28762		28765			28768	28769		28770	_	28774				28792		28800	28801				28814		28819			L					26735
	SEQ ID	15741	15903	16744	15748	15746	16747	15747	15748	15749	15750	15750	15754	15754	15758	16771	15772	15778	15784	15784	15785	15791	15795	15795	1	1			_	L	L	L	15811	13798
	Probe SEQ ID NO:	2748	2751	2762	15.5	2754	2756	2755	2756	2757	2758	2758	23/23	2362	2788	212	2780	2786	27872	2782	2783	88,2	88	888	286.	8087	2809	2841	1	2842	2842	2847	2820	2826

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signel	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Deterbese Source	Top Hit Descriptor
2826	13798	28736	1.6	0.0E+00	0.0E+00 AF284750.1	M	Homo sepiens ALR-like protein mRNA, partial cds
2830	14086	27037	3.41	0.0E+00	1N 2020370.	Ę	Homo seplens cytochrome P450, subfamily I (dioxin-Inducible), polypeptide 1 (glaucoma 3, primary infamilie) (CYP181) mRNA
2880	14086	27038	341	0.05+00	4503202 NT	5	Homo sepiens cytochrome P450, subfamily I (dicein-Inducible), polypeptide 1 (glaucoma 3, primary Infamilie) (CYP-181) mRNA
2847		28832	228	0.0E+00	0.0E+00 X85980.1	Z	H. sapiens serine hydroxymethytransferase pseudogene
2848	15908		3.02	0.0E+00	0.0E+00 AF068624.1	Z	Homo sepiens 5-emindevulinate synthese 2 (ALAS2) gene, complete cds
2850	15910		1.9	0.0E+00	0.0E+00 AB040860.1	Z	Homo sepiens mRNA for KIAX1527 protein, perfuel ods
2852	15912	28835	1.07	0.0E+00	4502568	Z	Homo sapiens caspase 10, apoptosis-related cystaine protease (CASP10) mRNA
2852	15912	28836	1.07	0.0E+00	4502568 NT	Z	Homo sepiens caspase 10, apoptosts-related cysteine protease (CASP10) mRNA
				!			Homo sepiens partial rpi3 gene for ribosomal protein L3, UBZ snoRNA, UB3a snoRNA and UB3b snoRNA
2857	15917		0.98	0.0E+00			genes
2858	15918	28839	3.26	0.0E+00	2	NT	Homo septiens chromosome 21 segment HS21C001
2862	15922	28842	1.6	0.0E+00	0.0E+00 M80802.1	F	Human AHNAK mudeoprotein mRNA, 5' end
2865	15925	28844	98'0	0.0E+00	0.0E+00 BE154504.1	EST_HUMAN	PM0-HT0343-281289-003-602 HT0343 Homo sapiens cDNA
2865	15925	28845	98:0	0.0E+00	0.0E+00 BE154504.1	EST_HUMAN	PMO-HT0343-281289-003-e02 HT0343 Homo septems cDNA
2867	15927		1.48	0.0E+00	0.0E+00 X73428.1	Ā	H. sapiens Id3 gene for HLH type transcription factor
2868	15928		3.61	0.0E+00	2	卢	Homo sapiens chromosome 21 segment HS210068
2870	15930	28847	1	0.0E+00		TN.	Human transgitaminase mRNA, complete cds
2874	15933	28850	25.84	0.0E+00	0.0E+00 D50667.1	N-	Homo sapiens gammma-cytopkasmic actin (ACTGP3) psaudogene
2874	15933	28851	28.82	0.0E+00	0.0E+00 D50857.1	Ę	Homo sapiens gannma-cytoplasmic actin (ACTGP3) pseudogene
2877	L	28854	234	0.0E+00	.:	Z.	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2878	15937		6.17	0.0E+00	0.0E+00 Y10658.1	¥	H.sapiens mRNA for nuclear DNA helicase II
2879	15938		1.17	0.0E+00	0.0E+00 AF152303.1	N.	Homo sepiens protocedherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2880	15939	28855	6H.622	0.0E+00	4503470 NT	NT.	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2880	15639	28856	64.62	. 0.0E+00		z	Homo sapiens eukeryodic translation elongation factor 1 atpha 1 (EEF1A1) mRNA
88	15950	28866	2.45	0.0E+00			Homo septems sertner/threconine kinase 9 (STK9) mRNA
7887	I	28870	16.0	0.0E+00	0.0E+00 AL047599.1	LHUMAN	DKFZp588G0621_rt 586 (synonym: huter) Homo sepiens cDNA clane DKFZp588G0621
2882	L	28871	1.07	0.0E+00	7881883 NT		Homo sepiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2895	15954	28872	1.07	0.0E+00	7661883 NT		Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mPNA
2896	15955		207	0.0E+00	4503098 NT		Homo sepiens chandratiin sultate proteoglycan 4 (melanome-associated) (CSPG4), mRNA
2898		28874	5.43	0.0E+00		П	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2898	15957	28875	6.43	0.0E+00	0.0E+00 BE081898.1	I_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2903	15962	28883	0.63	0.0E+00	0806918 NT	5	Homo sepiens fow density lipoprotein-related protein 2 (LRP2), mRNA

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	Top Hit Descriptor	Homo septems low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sepiens chromosome 21 segment HS21C008	Homo saplens diromosome 21 segment HS210008	z198611.s1 NCI_CGAP_GCB1 Homo septens cDNA clone IMAGE:683517 3' struiter to contains Alu	repetitive element;	Homo sepiens hiths gene for hair keretin, exons 1 to 9	Homo sapiens EphA4 (EPHA4) mRNA	Homo sapiens eukaryotto translation elongation factor 1 alpha 1 (EEF1A1) mRNA	tm18d07.x1 NCI_CQAP_Bm25 Homo septens cDNA clone IMAGE:2167981 3' similar to TR:O16247 O16247 F44E7.2 PROTEIN :	hr18407.x1 NCI_CGAP_Bm25 Home sepiens cDNA clone IMAGE-2167981 3' similar to TR:O16247 O16247 F4467.2 PROTEIN.;	Homo septens protocadherin gannma C4 (PCDH-gamma-C4) mRNA, complete cds	qg48f04x1 Sogres_testis_NHT Homo sepiens CDNA done IMAGE:1838527 3" similar to SW:C820_HUMAN P62288 20 KD NUCLEAR CAP BINDING PROTEIN;	Homo sapiens mRNA for KIAA1287 protein, partial cds	Homo sepiens mRNA for KIAA1287 protein, partial cds	Homo sepiens mRNA for KIAA 1608 protein, partial ods	Homo sapiens mRNA for KIAA 1508 protein, partial cds	Homo sepiens KiAA0100 gene product (KIAA0100), mRNA	Homo sapiens KIAA0100 gane product (KIAA0100), mRNA	Homo sapiens myeloid/lymphoid or mioad-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AILT4) mRNA	Homo sapiens mysiold/lymphold or mbad-Insage Isukemia (trithorax (Drosophila) homolog); translocated to, 4 (MILT4) mRNA	Homo sepiens melanoma antigen, family B, 4 (MAGEB4), mRNA	Homo sepiens melanoma antigen, family B, 4 (MAGEB4), mRNA	Homo sapiens neuredn III (NRXN3) mRNA	H.saplens mRNA for M phase phosphoprotein 10	Homo sepiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6	qf43f09.x1 Sceres_festis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'	Homo sepiens prospero-related homedbox 1 (PROX1) mRNA	Homo sepiens mRNA for PKU-elpha, pertial cds	Homo sepiens KIAA0737 gene product (KIAA0737), mRNA
	Top Hit Daferbase Source			Ę		T HUMAN				T HUMAN	EST HIMAN	Т	T_HUMAN		TA.	N-	M	M	Z		Į.	Į.	K	M	¥	Į.	EST_HUMAN	NT	NT	FA.
	Top Hit Acession No.	8806918 NT	0.0E+00 AL163206.2			0.0E+00 AA215579.1		4758279 NT	4503470 NT	0.0E+00 AI581002.1	0 0E+00 AIS81002 1			0.0E+00 AB033083.1	0.0E+00 AB033083.1	0.0E+00 AB040941.1	0.0E+00 AB040941.1	7881903 NT	7661903	5174574 NT	5174574 NT	4505084	4505084 NT	4758827 NT	1	0.0E+00 AF108275.1	0.0E+00 AI149880.1	4506118 NT	0.0E+00 AB004884.1	T862278 NT
	Most Similar (Top) Hit BLAST E Vatue	0.0E+00	0.0E+00	0.0E+00		0.0E+00/	0.0E+00 Y19210.1	0.0E+00	0.0E+00	0.05+00/	0.05+00	0.0E+00/	0.05+00	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	00-100	0.0E+00	0.05+00	0.0E+00	0.0E+00 X98494.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	9.63	262	2.52		26.0	4.07	1.17	23.02	0.92	8	78.0	1.28	282	282	4.91	14.91	2.56	2.58	2.73	27.0	238	236	1.71	1.83	7.63	1.1	0.97	2.71	1.51
	ORF SEQ ID NO:	28884	28888	28889		28890		28900		28002			28910	28918	28919	2882	28921	28924	28925	28926					L	28962		28973	28974	Ш
	SEQ ID	16962	15965			15968		L	•	15978	4 8070	15080	15989	15997	16997	15998	15998	16804	16001		<u> </u>		Ш.						16053	16065
Ì	Probe SEQ ID NO:	g	8082	2808	Г	2807	2915	2018	2819	888	1 8	3 6	38	688	883	2840	88	88	2843	75	Š	305	S S	8	188	2971	88	288	2995	3007

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						•	slocator), member 5	A	A	33'					ds; cytochrome P450 21-	O, complement factor B		ST.			,		to SW.FL11_RAT									
ngie Exon Probes Expressed in Bone Marrow	Top Hit Descriptor	H.sapiens mRNA for gamma-glutamytransferase	Homo sepiens neuredn III (NRXN3) mRNA	Homo sapiens neuredn III (NRXN3) mRNA	Homo expiens interfaultin 1 receptor, type I (IL1R1) mRNA	Homo sepiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA	Hamo sepiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA	ae97b11.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'	Homo sapiens anglostatin binding protein 1 mRNA, complete ods	Homo sapiens angiostatin binding protein 1 mRNA, complete cds	Homo sepiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA	Homo sepiens titin (TTN) mRNA	Homo sepiens HLA class III region containing tenescin X (tenescin-X) gene, perdal cds; cytochrome P450 21	hydraxylass (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B	(Bf), and complement component C2 (C2) genes,>	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA	Homo sapiens A Idnase (PRKA) anchor protein 1 (AKAP1), mRNA	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA	treff08.x2 NCI_CGAP_pen1 Homo sapiens cDNA done IMAGE:2222535 3's straiter to SW-RL11_RAT P25121 60S RIBOSOMAL PROTEIN L11. ; contains Ab repetitive element.	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6	Homo sapiens telomenase reverse transcriptase (TERT) gene, exons 1-6	Homo sepiens hormonally upregulated neu tumor-essociated kinase (HUNK), mRNA	Horno septens hormonally upregulated neu fumor-essociated kinase (HUNK), mRNA	Homo sepiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA	Homo sapiens pyrtn (MEFV) gene, complete cds	Homo sapiens mRNA for KIAA1507 probein, partial cots	601464896F1 NIH_MGC_67 Homo septens cDNA clone IMAGE:3868246 6
Kon Probes EX	Top Hit Detectorse Source	Α Ή								THUMAN						<u> </u>	NT (B						EST HUMAN P		¥							EST_HUMAN 60
Single E	Top Hit Acession No.		4758827 NT	4758827 NT	504658		4502098 NT	4758055 NT	4758055 NT	1	1	0.0E+00 AF286598.1	4567590 NT	4507720 NT			0.0E+00 AF019413.1	\F055084.1	4502014 NT	4502014 NT	0.0E+00 AF265208.1	B923624 NT	0.0E+00 AI589294.1	-	-	7857213 NT	7857243 NT	4502582 NT	4502582 NT	1	Ţ	-
	Most Similar (Top) Hit BLAST E Vatus	0.0E+00 X98922.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M28699.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AA774783.	0.0E+00 AF286598.	0.0E+00/	0.0E+00	0.0E+00	-		0.0E+00/	0.0E+00 AF055084.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF128893	0.0E+00 AF128893.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AB040940.	0.0E+00
	Expression Signal	4.28	1.10	1.18	9.61	3.9	1.65	98.0	96.0	3.36	3.58	3.58	1.15	1.02			1.04	4.45	2.4	24	2.89	98'0	2.87	244	2.44	0.85	0.85	1.11	1.11	10.77	1.09	0.85
	RF SEQ ID NO:	23472	29183	28182	28191	29208	28211	29219	29220	1282 1	29229	29230	29236	29243			28250	29263	29261	29262	29276	29276	28807	28315	29316	28817	28318	20319	28320	28322	28324	28330
	Exam SEQ ID NO:	16252	16262	16262	16268	16285	16289	16295	16295	16297	16305	16305	16315	16821			16329	16332	18312	18312	16356	16357	16388	16894	16894	16395	16395	16397	16397	16400	16402	16408
	Probe SEQ ID NO:	3197	3207	3207	3213	3230	3234	3240	3240	3242	3250	3250	3261	3267			3275	3278	3288	3288	888	382	3835	88	8843	334	3344	3346	3346	3349	3351	3358

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Vatue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3368	16419	28844	0.79	0.0E+00	0.0E+00 Al832568.1	EST HUMAN	wb10f04x1 NCI_CGAP_GC6 Homo capiens dDNA clone IMAGE:2305279 3' similar to TR:Q81929 Q91929 ZINC FINGER PROTEIN.;
3407	L				0.0E+00 AU123684.1	EST_HUMAN	AU123684 NT2RN2 Homo sepiens cONA clone NT2RN2000735 5
3414			1.15	0.0E+00	7363436 NT	¥	Homo sapiens offactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3414			1.15	0.0E+00		NI.	Homo sepiens offsctory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3417					7706239 NT	NT	Homo sapiens neuroblastoma-emplified protein (LOC51594), mRNA
3418	16466	29386	1.51	0.05+00	0.0E+00 AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha11-a Isoform (CACNA11) mRNA, complete cds
3436	L			0.0E+00	7682401 NT	¥	Homo septens KIAA0952 protein (KIAA0952), mRNA
3438	L.,			0.0E+00		Į.	Homo sepiens KIAA0952 protein (KIAA0952), mRNA
3437				0.0E+00		¥	Homo sepiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3441		29406		0.0E+00		¥	Homo sepiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3450	L			0.0E+00	0.0E+00 AF110763.1	M	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3455				0.0E+00	TN 857038 NT	M	Homo sapiens death receptor 6 (DR8), mRNA
3456	16502	20420	1.05	0.0E+00	5453965 NT	M	Homo sapiens protein kinasa, AMP-ectivated, alpha 2 catalytic subunit (PRKAA2) mRNA
2456			1.05	0.0E+00	5453965 NT	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
83.28		29420	1	0.05+00	0.0E+00 AJZ77Z76.1	M	Homo sepiens mRNA for rapa-2 (rapa gene)
3450			-	0.0E+00	0.0E+00 A.1277278.1	NT	Homo sapiens mRNA for rape-2 (rapa gene)
	L_					    -	Bacteriophage P1 replication region including repA, parA, and parB genes and incA, incB, and incC
88	$_{\perp}1$				KUZZBD	Z	Froothemany operature its
3463	16509	29430	1.31	0.0E+00	7427522 NT	N.	Homo septens protein tyrosine phospinatese, receptor type, i (PTPK I), mikna
3469	16515	28435	6.12		0.0E+00 A1835159.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Hamo sapiens cDNA ctane IMAGE:2464819 3' similar to TR:073834 073634 NEURAL CELL ADHESION MOLECULE. ;
0460	40545	20496	H 42		0.05±00 41025450 4	EST HIMAN	Wp14d10.x1 NG_CGAP_Lu19 Homo septems cDNA clone IMAGE:2464819 3' stratter to TR:O73834 O73634 NEI RAI CSI I ADHESION MOI ECUI E
87.78				ļ	A 1278120 1	NT	Homo sapiene mRNA for putative ankyrth-repeat containing protein (ORF1)
8,4%	<u>L</u>			0.0E+00		¥	Homo sepiens v-foe FBJ murine estecearcoma viral choogene homolog (FOS), mRNA
3479	L			0.0E+00	6552332 NT	N.	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3485		Ŀ		١.	0.0E+00 M14123.1	LN LN	Human endogenous retrovirus HERV-K10
3480	16536	29461			0.0E+00 U43283.1	N	Human MDS1A (AML1/MDS1 fusion) mRNA, pertial cds
3407	16644	29469	1.85		0.0E+00 AF045452.1	NT	Homo septens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3497	Ш				0.0E+00 AF045462.1	TN	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3504	16551	29478	66'0		0.0E+00 AF231922.1	FN.	Homo sepiens chromosome 21 unknown mRNA

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	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C004	Homo sapiens chromosome 21 segment HS21C004		Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA	Homo sapiens mRNA for KIAA0786 protein, partial cds		Homo sepiens mRNA for KIAA0910 protein, partial cds	Home sapiens mRNA for KIAA0910 protein, partial cds	Homo sepiens KIAA0870 protein/actitus (KIAA0870), mRNA	Homo sepiens KIAA0670 protein/actinus (KIAA0670), mRNA	Γ		Human gane for Type XIX collagen at chain, exon 6	ag06g01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:812496 5' shritar to SW 4RB4 SHEEP P02446 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4. [1];	Г	Homo septens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA	Homo sapiens mRNA for KIAA1414 protein, partial cds	Homo sapiens KIAA0589 gene product (KIAA0569), mRNA	Homo sapiens ribosomal protein S2 (RPS2) mRNA	Homo sapiens v-ets avian erythrobiestosis virus E26 ancogene related (ERG), mRNA	Homo sepiens wets awan erythroblestosis virus E28 oncogene related (ERG), mRNA	Homo sepiens plasminogen activator inhibitor, type II (arginine-sarpin) (PAI2) mRNA	Pen troglodytes offactory receptor (PTR208) gene, partial ods	Homo sapiens similar to ret triegnel membrane giycoprotein POM121 (POM121L1), mRNA	Homo sapiens similar to rat Integral membrana giyooprotean POM121 (POM121L1), mRNA	Gorilla gorilla difactory receptor (GG071) gene, partial cds	Gorilla garilla olfactory receptor (GGO71) gene, partial cds		Homo sepiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds	Homo sepiens desmoplatán (DPI, DPII) (DSP) mRNA
Top Hit Detribase Source	M	Ä	K	NT	<b>EST_HUMAN</b>	M	IN	SWISSPROT	NT	NT	N	¥	EST HUMAN	EST_HUMAN	NT	EST HUMAN	Ę	¥	μ	NT .	F	NT	M	NT	IN	NT	NT	NT	NT	EST_HUMAN	IN	둗
Top Hit Acession No.	1	0.0E+00 AF124250.1	0.0E+00 AL163204.2	0.0E+00 AL163204.2	0.0E+00 AW851714.1	5729928 NT	0.0E+00 AB018339.1		0.0E+00 AB020717.1	0.0E+00 AB020717.1	7882237 NT	7662237	0.0E+00 AW298134.1	0.0E+00 AW298134.1	0.0E+00 AB004630.1	0.0E+00 AA463659.1	-	7857468 NT	0.0E+00 AB037835.1	7682183 NT	4506718 NT	7857065 NT	7657068	4505594 NT	0.0E+00 AF178733.1	7857468 NT	7657468	0.0E+00 AF127851.1	0.0E+00 AF127851.1		0.0E+00 AF152498.1	4758199 NT
Most Similar (Top) Hit BLAST E Vatue	0.0E+00	0.0E+00	0.0E+00	0.0E+00,	0.0E+00	0.0E+00	0.0E+00	0.0E+00 O14867	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00,	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	4.02	4.02	1.6	1.6	1.34	2.88	1.37	0.72	1.45	1.45	1	-	4.8	4.6	1.47	1.08	0.78	3.82	0.77	5.64	19.76	76.0	26'0	0.92	3.15	2.78	2.78	0.94	0.91	1.01	1.81	0.97
ORF SEQ ID NO:	29639	29640	29847	23648	28651	28653	29655	29657	20859	29660	2882	20683	20872	29873	29696	29697	29701	29703	29713	28723	20726	29729	29730	29733	29775	29779	29780	29787	29788	29789		29780
Eten SEQ ID NO:	16728	16728	16735	16735	16738	16740	16742	16744	16748	16746	16748	16748	16762	16762	16784	16785	16789	16792	16801	16814	16817	16822	16822	16825	16874			i	16883			16886
Probe SEQ ID NO:	3885	3685	3692	3692	3695	3697	3699	3701	3703	3703	3705	3705	3719	3718	3742	3743	3747	3750	3760	3772	3776	3781	3781	3784	<b>3834</b>	3837	3837	3843	3843	3844	3845	3846

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ngle Exon Probes Expressed in Bone Marrow	Top Hit Descriptor	Homo sepiens ATP-sensitive inventity rectifying K-channel subunit (KCNJØBIR1) gene, complete cds	Homo septems methyl CpG binding protein 2 (MECP2), mRNA	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	Homo septens 5-hydroxytryptamine (serotonin) receptor 1D (HTR1D) mRNA	Homo sapiens gene for TMEM1 and PWP2,comptete and partial cds	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds	Homo septions trenstent receptor potential channel 5 (TRPCS), mRNA	Homo sepiens chromosome X open reading frame 5 (CXORF5) mRNA	Hamo sapiens dramosome X apen reading frame 5 (CXORF5) mRNA	Human zinc finger protein ZNF134 mRNA, complete ods	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	Homo sepiens potassium vottage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA	Homo sapiens familial mental retardation protein 2 (FMR2) gene, excn 11	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA	Homo sapierrs emphiphysin gene, pertial cds	wk0+fi01 x1 NCL_CGAP_Lym12 Homo saplens cDNA clone IMAGE:2411065 3' similar to TR:O43340 O43340 R28830_2, contains element PTR7 repetitive element;	Homo sapiens ribosomal protein S8 (RPS8), mRNA	DKFZp434N0413_r1 434 (syncmyn: httes3) Homo sapiens cDNA clone DKFZp434N0413 5	Homo sapiens AP1 garma subunit binding protein 1 (AP1GBP1), mRNA	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA	Homo sepiens melanoma antigen, family B, 1 (MACEB1) mRNA	Homo expiens HBP17 heparin-binding and FGF-binding protein gene, complete cds	Homo septems ryanodine receptor 3 (RYR3) mRNA	Homo sapiens zinc finger protein (KIAA0412) mRNA	RC3-HT0860-170800-011-e12 HT0860 Homo sepiens cDNA	MXRA5 Humen matrix tissue expression library Homo sepions dDNA clone Incyta 1896728 similar to MXRA5 Matrix remodeling associated gene 5	MXRA5 Human matrix tissue expression library Homo sepiens cDNA clone Incyte 1996728 similar to MXRA5 Matrix remodelling associated gene 5	Homo sepiens F-box protein Fb3b (FBL3B) mRNA, partial cds
xon Probes	Top Hit Database Source	M	NT.	. 5	N	N	NT	Z	M	NT	¥	¥	¥	N	Ę	N	EST_HUMAN	٦	<b>EST_HUMAN</b>	NT	NT	NT	NT	NT	NT	NT	EST_HUMAN	EST HUMAN	EST_HUMAN	Z
Single E	Top Hit Acession No.	S78685.1	7710148 NT	7882183 NT	4504534 NT	0.0E+00 AB001523.1	0.0E+00 AB001523.1	6912735	4503178 NT	4503178 NT	0.0E+00 U09412.1	0.0E+00 AF114488.1	4828783 NT	0.0E+00 AF012615.1	4750171 NT	0.0E+00 AF099117.1	0.0E+00 AI864727.1	4506742 NT	0.0E+00 AL040338.1	W 2005887 NT	6005887 NT	4504138 NT	4505078 NT	0.0E+00 AF149412.1	4506758 NT	4585842 NT	0.0E+00 BF366296.1	0.0E+00 AW888221.1	<u>-</u>	
	Most Similar (Top) Hit BLAST E Vakue	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	00+30'0	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	16.29	225	1.54	1.1	1.15	1.15	77.0	71.7	71.7	434	1.13	1.28	13	2.38	0.73	2.34	13.72	1.38	1.34	1.34	1.78	1.75	1.06	1.17	1.3	1.64	1.05	1.05	1.85
	ORF SEQ ID NO:	29794	29796	29797	29800	29805	28808	29807	29815	29816	29819	29820	28822	29825	20828	29828	29838	29842	29848	29855	29856	29857		28861	29877	_	L	29891	28802	29902
	Exam SEQ ID NO:	16890		16883	L	16901	16901	16902	16907	L	16809	L	16913	16916	l_	1_	16929	16932	16937	16943	<u>.</u>	16944	16946		L	L			l	LJ
	Probe SEQ ID NO:	3850	3862	3853	3857	3862	3862	3863	3868	3868	3870	3871	3874	3877	3878	3880	3880	3882	3897	3903	3903	3904	3906	3910	3924	3928	3838	3937	3837	3947

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And Extend to the control of the con	Top Hit Descriptor	601236968F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5'	PARS-LT0031-100100-003-h09 LT0031 Homo septems aDNA	Homo sapiens cancar-testis antigen CT10 (CT10) gene, complete cds	Homo sepiens cancer-lestis antigen CT10 (CT10) gane, complete cds	Human MitC class II Iymphocyte entigen DPw4-beta-2 pseudogene, exon 2	Hamo septems chramosome 21 segment HS21C103	Hoino sapiens chromosome 21 segment HS21C084	Homo eaplens chromosome 21 segment HS21C068	mrg=mas-related [human, Genomic, 2416 nt]	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	186608.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:22447343' similar to TR:060309 060309 KIAA0563 PROTEIN.;	Homo sapiens KiAA0569 gene product (KIAA0569), mRNA	Human zinc finger protein ZNF133	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds	Hamo septems mRNA for UGA suppressor fRNA-associated antigentic protein (fRNA48 gene)	Hamo saplens chramosome 21 segment HS21C003	Homo saplens mRNA for rape-2 (rapa gene)	Homo septens mRNA for repa-2 (repa gene)	Homo saplens retinoblastoma-binding protein 4 (RBBP4) mRNA	Homo sapiens refinoblastome-binding protein 4 (RBBP4) mRNA	Homo sapiens phosphoribosy/giydnamide formy/fransferase, phosphoribosy/giydnamide synthelase,	prosprioring year and received synthesis (CAN ) minutes	Home series mRNA for KIAA0287 cess partial criss	Homo sariens IMP (Incsine monophosobate) dehydrocenese 1 (IMPOH1), mRNA	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes	2555609.11 Scares retina N2b4HR Homo septems cDNA clone IMAGE:362820 5 similar to contains Alu	repetitive element;	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds	Homo sapiens protein kinase, X-linked (PRKX) mRNA	Homo septems protein kinasa, X-finked (PRKX) mRNA	Homo sepiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA	Homo sepiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
AUI 1 1000	Top Hit . Detabase Source	EST_HUMAN 6	EST HUMAN F	I IN	NT TN	ᅜ	tN TN	1) IN	NT IN			EST HUMAN		E E	NT	Į.	i in	TN.										EST_HUMAN I					
Biglio	Top Hit Acessian No.	0.0E+00 BE378602.1	0.0E+00 AW580740.1	0.0E+00 AF116195.1	-		0.0E+00 AL163303.2	2	0.0E+00 AL163268.2	378653.1	4503470 NT	-	882183		0.0E+00 AB015610.1	0.0E+00 AJZ38617.1	0.0E+00 AL163203.2	0.0E+00 AJZ77Z78.1	0.0E+00 AJZ77Z78.1	5032026 NT	5032026		4505914 N	O.O.C. TOO A BOOGGOST 4 NOT	10207			0.0E+00 AA018975.1	0.0E+00 AF165527.1	4826947 NT	4826947	5801905 NT	4503854
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00/	0.0E+00/	0.0E+00 M23910.1	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U09366.1	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.06:400	0.001	O OF TOO	0.0E+00		0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	3.36	1.06	521	521	3,56	6.54	3.12	1.69	68'0	58.15	1.47	1.13	1.67	5.87	3.81	1.14	267	267	7.81	7.81		127	4.80	9/2	2.95		12	3.26	1.62	1.62	1.28	1.09
	ORF SEQ ID NO:	20008	29916	28945	28946	-		20081	07662	28974			20988	20989	30007	<b> </b> -	30020	30021	30022	30028	30029		3008	30042	77000	30045			30051	72172	27128	30063	30064
	SEQ ID	16662	170071	17039	17039	17049	17052	17060	17069	17074	17085	17091	17093	17894	17111	17119	17127	17128	17128	17134	17134		17145	72727	47454	17166		17156	17162	14177	14177	17175	17176
	Probe SEO ID NO:	3962	3981	4000	4000	4010	4013	4022	4031	4036	4047	4054	4057	4068	4078	4085	4083	4084	4094	4100	4100		4111	7114	7424	4122		4123	4129	4138	4138	4143	4144

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ngie exon prodes expressed in Done Mailow	Top Hit Descriptor	Homo sepiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA	Homo sapiens semenogelin II (SEMG2) mRNA	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	Homo sepiens hypothetical protein FLJ10379 (FLJ10379), mRNA	Homo sepiens mRNA for KIAA0895 protein, partial cds	W104004.x1 NCI_CGAP_GC8 Hamo sapiens cDNA clone IMAGE:2515975 3'	wu04d04.x1 NCI_CGAP_GC8 Hamo sapiens cDNA dane iMAGE:2616975 3'	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA	MR1-HT0707-100500-001-602 HT0707 Homo septems cDNA	601120778F1 NIH_MGC_20 Homo sepiens cDNA clone IMAGE:2867680 5	Homo sepiens mRNA for KIAA1125 protein, partial cds	Homo sapiens mRNA for KIAA1125 protein, partial cds	Homo sepiens transglutaminase 3 (E polypaptide, protein-glutamine-gamma-glutamytransferase) (TGM3)	mRNA	Homo sepiens nuclear receptor coactivator 3 (NCOA3), mRNA	Novel human gene on chromosome 20	ba51f04.x1 NIH_MGC_10 Homo sepiens cDNA clone IMAGE:2800095 3' straiter to SW:THI2_BOVIN Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR;	UI-HF-BIXO-edx-<-02-0-UI.r1 NIH_IMGC_38 Homo sepiens cDNA clone IMAGE:3063147 57	Homo sepiens hypothetical protein FLJ10488 (FLJ10489), mRNA	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA	Homo sepiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea unchin homolog)-like (PKDREJ) mRNA	ZUOBROT.s1 Sogres_tesds_NHT Homo septens cDNA clone IMAGE:743197 3' similar to contains Alu	repoure defination trains befreit moreon repout to the little of the factor of the fac	<b>Zuceniu. 3 Source Joseph VIII i nome seprema vivien delle minore 13 13 seminario delleggio d</b>	Homo sepiens (IIIN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens chromosome 21 segment HS21C103	Homo sepiens mRNA for oifactory receptor protein, pseudogene	Human apolipoprotein B-100 mRNA, complete cds	PM2-DT0023-080300-004-608 DT0023 Homo sepiens cDNA	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
Xon Probes E	Top Hit Database Source	¥	۲	M	N-		EST_HUMAN		EST_HUMAN	EST_HUMAN	EST HUMAN	NT	NT		攴	NT	١	EST HUMAN	EST HUMAN	¥	L	¥		ESI HUMAN	EST HUMAN	Z	¥	IN	NT	NT	EST_HUMAN	R
Single	Top Hit Acession No.	4503854 NT	4506884	8922391	8922391 NT	0.0E+00 AB020702.1	0.0E+00 A1982597.1	0.0E+00 AI982597.1	0.0E+00 BE184856.1	0.0E+00 BE184856.1	0.0E+00 BE274217.1	0.0E+00 AB032951.1	0.0E+00 AB032961.1		4507476 NT	5729725 NT	0.0E+00 AL132989.1	0.0E+00 AW675599.1	4W408788.1	0.0E+00 8922466	8922466 NT	5174832 NT		0.0E+00 AA401438.1	0 0F+00 AA401438 1	4507720 NT	4607720 NT	0.0E+00 AL163303.2	0.0E+00 AJ003145.1	J02810.1	0.0E+00 AWS3889.1	4828827 NT
	Most Similar (Top) Hit BLAST E Vatue	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/		0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.05+00/	0.0E+00	0.0E+00	0.0E+00		0.0E+00/	005+00	0.0E+88	0.0E+00	0.0E+00/	0.0E+00	0.0E+00 J02810.1	0.0E+00	0.0E+00
	Expression Signal	1.09	0.86	8.0	0.8	99'0	4.7	4.7	12	1.2	3.98	0.83	0.93		1.02	2.64	1.13	1.0	1.12	1.23	123	4.37		8.6	ď	2	1.04	78.0	1.28	2.19	0.87	0.74
	ORF SEQ ID NO:	30065	29523	20067	30068	30071	30078	30079	30081	30082		30087	30088	-	30080	16008			30106	30109	30110			30133	20137	30140	30150		30194	30211	30230	30Z36
	SEQ ID NO:	17178	16598	17179	17179	17184	17190	17190	17192	17192	17196	17201	17201		17203	17204	17206	17214	17219	172271	17221	17231		17240	17740	ı	١,		17315	17331	17348	17351
	Probe SEQ ID NO:	4144	4146	4148	4148	4153	4150	4159	4161	4161	4165	4170	4170		4172	4173	4174	4183	4188	4190	4190	4200		<del>\$</del>	4220	4235	4235	4258	. 4286	4302	4317	4322

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Most Similar Expression (Top) Hit Top Hit Acession Database Signal BLAST E No. Source	26827 NT	30239 3.59 0.0E+00 AF174590.1   NT   Homo sepiens F-box protein Fbl4 (FBL4) mRNA, partial cds	2.53 0.0E+00 AI189944.1 EST_HUMAN similar to contains MER20.b2 MER20 repetitive element;	ΤN		6563384 NT	0.77 0.0E+00 6563384 NT	1.15 0.0E+00 U10991.1 NT	1.15 0.0E+00[U10891.1 [NT	12281 NT	72 NT	N	30310 4.52 0.0E+00 L14561.1 NT pertial cds	30315 6.75 0.0E+00 230780.1 NT H.sapiens H2Bh gene	30316 6.75 0.0E+00 Z80780.1 NT H.sapiens HZB/h gene	1,31 0.0E+00 X60483.1 NT	X60483.1 NT	30329 8.47 0.0E+00 7682091 NT Homo sapiens KIAA0380 gene product (KIAA0390), mRNA	7662091 NT	1.22 0.0E+00 X8Z338,1  NT	85128 NT	1.23 0.0E+00 A.1271736.1 NT	1.01 0.0E+00 AB037781.1 NT	30376 1.2 0.0E+00 7019456 INT Homo sepiens myodin regulatory light chein inferacting protein (MIR), mRNA	6.71 0.0E+00[AF186953.1 NT	Į.	- NT	0.88 0.0E+00 W26179.1   EST_HUMAN	30304 0.88 0.0E+00 W26179.1 EST_HUMAN 2497 Human retina cDNA randomly primed sublibrary Homo saplens cDNA	2.47 0.0E+00 AF200629.1 NT	0.63 0.0E+00 T10233.1 EST_HUMAN	30425 0.63 0.0E+00 T10233.1 EST_HUMAN seq1329 b4HB3MA Cot8-HAP-Pt Homo septens cDNA clone b4HB3MA-COT8-HAP-Pt205 5
	30237	30239	1		30254	30261	30262	30268	30,269	30275			30310	30315	30316	30322	30323	30329	30830	30341	30345	30348	30348	30376		30386	30387	30393	30304		30424	30425
Exen SEQ ID NO:	4322 17351	4324 17353	4332 17360	4336 17363	4347 17374	4353 17380		L_	4359 17386	4369 17396	4387 17415	4392 17420	4398 17426	4402 17430	4402 17430	4408 17436	4408 17436	4413 17440	4413 17440	4423 . 17450	4426 17453	4427 17454	4430 17457	4463 17489	4471 17497	4476 17502	4478 17502	4480 17505	4480 17505	4495 17520	4514 17539	4514 17539

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IGIE EXUIT FIUDES EXPLESSED III DOI 19 IMAILOW	Top Hit Descriptor	Human endogenous retrovirus HERV-K10	2008608.X1 NCL_CGAP_ESQZ Homo sapiens cDNA clone INAGE:2589446 3' striilar to SW:AHNK_HUMAN Q09668 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK;	Homo sepiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA	wc56b02x1 NCI_CGAP_Pr28 Homo septens cDNA ctone IMAGE:2322903 3' similar to conteins MER22.b2 PTR5 repetitive element ;	Homo sepiens chromosome 21 segment HS21C007	PMH-HT0305-101199-002-d03 HT0305 Homo septens cDNA	Homo sapiens mRNA for putative antyrin-repeat containing protein (ORF1)	Homo sapiens mRNA for putative enkyrin-repeat containing protein (ORF1)	Homo sepiens G protein-coupled receptor 50 (GPR50) mRNA	Homo sepiens serine-fineantre protein kinase (MNBH) mRNA, complete cds	H.sapiens pancreatic polypeptide receptor PP1 gene	Homo sapiens slab/itransferase 8 (alpha-N-acet/ineurantinate: alpha-2,8-slat/itransferase, GD3 synthase) (SIAT8) mRNA	Homo sepiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon	Homo sepiens pyrin (MEFV) gene, complete cds	Homo sapiens pyrin (MEFV) gene, complete cds	Homo sepiens zinc finger protein 185 (ZNF185), mRNA	Hamo sapiens syncytin precursor, mRNA, complete cds	Homo sapiens zinc finger protein 211 (ZNF211), mRNA	Homo septens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	Homo sepiens chondrottin sutfate proteoglycen 4 (melanome-essociated) (CSPG4), mRNA	Homo sepiens calclum/calmodulin-dependent protein kinase IV (CAMK4) mKNA	Homo sepiens iduronate sulphate sulphatase (IDS) gene, complete cas	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA	Homo sepiens KIAA0390 gene product (KIAA0390), mRNA	Homo sapiens PTEN (PTEN) gene, excris 3 firrough 5	Homo sepiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility	complex()	Homo sapians mRNA for G7c protein (G7c gene located in the class) ill region of the major rustocumpatuminy promptery	Home septems mRNA for KIAA0795 protein, partial cds	Homo contains DNA for amulaid teneciment profile complete cits	TOTIO SEPTED DITA IN GLIGHTA PROMISES proved, writeway we
XOII FIODES C	Top Hit Deterbese Source	I I	EST HUMAN		EST HUMAN	T	EST_HUMAN	NT	IN		NT	N			Ę			NT								Ę		Ę				Z
Single	Top Hit Acession No.		0.0E+00 AW084964.1	51619			.1			4758487 NT	1		4506952 NT		Ļ	1	F005973 NT	0.0E+00 AF208161.1	5454175 NT	4503470 NT	4503098	4502556 NT	1.35485.1	7662091 NT	7662091 NT	\F143314.1		J245418.1				)87675.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00 M14123.1	0.0E+00	0.0E+00	0.0E+00 Alesess8.1	0.0E+00 AL163207.	0.0E+00 AW381570	0.0E+00 AJZ78120.1	0.0E+00 AJZ78120.1	0.0E+00	0.0E+00 AF108830.	0.0E+00 Z66526.1	0.05+00	0.0E+00 S78684.1	0.0E+00 AF111163.	0.0E+00 AF111163.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	100+30:0	0.0E+00	0.0E+00	0.0E+00 AF143314.		0.0E+00 AJ245418.	1	0.0E+00/AJZ45416.	V.UE-100.	0.0E+00 D87675.1
	Expression Signal	6.0	3.45	1.86	8	8,69	1.88	12	1.2	1.73	2.8	0.94	80	0.93	6	1.91	2.31	6.31	1.32	30.53	1.83	1.4	2.89	13.95	13.95	1.97		10.93		10.83	V-1	48.89
	ORF SEQ ID NO:		30441		30444		30449	30456	30457	30459	30460	30466								30510		30524		30626				30543			30545	
	Exan SEQ ID NO:	17542	17553	18318	17556	17560	17562	17568	17568	17570	17571	17576	1787.1	17582	17583	17583	18319	17597	17804	17616	17826	17831	17635	17637	17837	17653		17656				17666
	Probe SEQ ID NO:	4517	4520	153	AFR	4637	4539	4545	4646	4547	4548	4653	AREA	45.50	158	924	4578	4676	4582	4595	4605	4610	4814	4616	4616	4632		4635		4635	4637	4845

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Top Hit Descriptor	zp18g08.s1 Stratagene fetal retina 937202 Homo saplens cDNA ctone IMAGE:6088543'	Homo sapiens odz (odd Ozften-m, Drosophila) homolog 1 (ODZ1), mRNA	Homo saplans chromosome 21 segment HS21C084	y82b01.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231721 3'	y82b01.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231721 3'	Homo sepiens cyclophilin-related protein (NKTR) gene, complete cds	Homo sapiens chromosome 21 segment HS21C100	Homo sapiens gene for natrituretio protein, partial cds	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds	Novel human gene mapping to chomosome 1	Homo sepiens keratin 18 (KRT18) mRNA	Homo sapiens keratin 18 (KRT18) mRNA	Mus musculus E-cadherin binding protein E7 mRNA, complete cds	Homo sapiens ADPIATP carrier protein (ANT-2) gene, complete cds	Homo sepiens ADP/ATP carrier protein (ANT-2) gene, complete cds	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds	Homo sapiens mRNA for KIAA1047 protein, partial cds	Homo sepiens mRNA for KIAA1047 protein, partial cds	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes	Homo sepiens truncated tensecin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region	Homo sapiens mRNA for KIAA1389 protein, pertial cds	Homo sapiens mRNA for KIAA1399 protein, partial cds	Human displacement protein (OCAAT) mRNA	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA	ys83g04.r2 Strategene fetal spleen (#837205) Homo septens cDNA clone MAGE:88310 5	ya83g04.r2 Stratagene fetal spleen (#937205) Homo saplens cDNA clone IMAGE:68310 5	601158935F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3505521 5	Homo septens ecotropic viral integration site 28 (EVI28), mRNA	Homo sapiens ecotropic viral integration site 28 (EVI2B), mRNA	Human AHNAK nucleoprotein mRNA, 5' end	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
Top Hit Detabase Source	EST_HUMAN		FA FA	EST_HUMAN	EST_HUMAN	NT		M	Ę	F			Ę	¥	Į.	Į.	NT	NT.	N IN	Z		Z					EST_HUMAN				NT.	F	¥
Top Hit Acession No.	0.0E+00 AA174072.1	7857410 NT	2		ľ	1.1	2	.1	۲.		4557887 NT	4557887 NT	Ĺ.				.1	.1		1.7	-	-		6453812 NT	6453812 NT			Ţ.	5729817	5729817 NT			
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00 AL163284	0.0E+00 H92741.1	0.0E+00 H92741.1	0.0E+00 AF184110	0.0E+00 AL163300	0.0E+00 AB037521	0.0E+00 AF195858	0.0E+00 AL162331	0.0E+00	0.0E+00	0.0E+00 AF167441	0.0E+00 L78810.1	0.0E+00 L78810.1	0.0E+00 L78810.1	0.0E+00 AB028970	0.0E+00 AB028970	0.0E+00 Y18890.1	0.0E+00/AF086841	0.0E+00 AB037820.	0.0E+00 AB037820	0.0E+00 M74099.1	0.0E+00	0.0E+00	0.0E+00 T50945.1	0.0E+00 T56945.1	0.0E+00 BE278730	0.0E+00	0.0E+00	0.0E+00 M80902.1	0.0E+00 M69197.1	0.0E+00 M69197.1
Expression Signal	1.61	1.62	205	96.0	0.95	1.42	6.63	1.84	99.0	4. 2.	1.89	1.89	1.28	-	-	4	203	2.03	6.02	224	282	282	3.31	242	242	202	202	122	4.85	4.85	5.55	6.62	6.62
ORF SEQ ID NO:			-	30565	30568	30567	30568		30569	30576	30579	30580	30581	30592	30593	30594	30595	30596	30602		30619	30620	30621	30624	30626	26174	26175		30651	30652	30657	30660	30661
Exam SEQ ID NO:	17876	17877	17679	17680	17880	17881	17682	17883	17885	17690	17693	17693	17694	17703	17703	17703	17704	17704	17709	17720	17725	17726	17728	17730	17730	13244	13244	17733	17757	17757	17763	17768	17786
Probe SEQ IO NO:	4664	4656	4658	4669	4659	4680	4661	4662	4684	4669	4672	4672	4673	4682	4682	4682	4683	4683	4688	689	4704	4704	4705	4709	4709	4711	4711	4713	4737	4737	4743	4748	4746

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	Top Hit Descriptor	Hamo sapiens cyclophilin-related protein (NKTR) gene, complete ods	Homo espiens KIAA1084 protein (KIAA1084), mRNA	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA	SCN1A-brain type I sodium channel alpha-eubunit {!!!S5 transmembrane region} (human, placenta, Genomio, 1656 nt]	SCN14≠brain type i sodium channel alpha-subunit {iiSS transmembrane region} [human, placenta, Genomic. 1656 nt]	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes	Human CYP2D7AP pseudogene for cytochrome P450 2D6	Homo sepiens bromodomein edjecent to zinc finger domein, 2B (BAZ2B), mRNA	Homo sepiens bromodomain edjacent to zho finger domain, 2B (BAZ2B), mRNA	Homo sapiens alpha-3 type IX collagen (COLBAS) gene, promoter region, and excus 1-26	Homo sepiens G-protein coupled receptor (RE2), mRNA	Homo sapiens G-protein coupled receptor (RE2), mRNA	Homo sapiens protein::0008 (AD013), mRNA	Homo sepiens proteinx0008 (AD013), mRNA	UI-H-BIS-etw-c-04-0-UI,s1 NCI_CGAP_Sub5 Homo sepiens cDNA clone IMAGE:2733294 3"	Homo sepiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds	Homo sepiens HSPC024-iso mRNA, complete cds	Human MHC class I transplantation antigen (hia) gene	Human MHC class I transplantation antigen (hia) gene	Homo sepiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	M. fascicularis mRNA for metalloprobesse-like, distritegrin-like protein, IVa	Homo sepiens Williams-Beuren syndrome deletion transcript 8 (WBSCR9) mRNA, complete cds	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds	Homo sepiens fragile X mental retardation 2 (FMR2) mRNA	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA	ZINC FINGER PROTEIN 132	Homo sepiens hypothetical protein DKFZp762E1312 (DKFZp762E1312), mRNA	Homo sepiens hypothetical protein FLJ20073 (FLJ20073), mRNA	Human T <i>ar-C</i> -detta gene, econs 1-4; Tar-V-detta gene, econs 1-2; T-cell receptor alpha (Tar-alpha) gene, J1- J61 segments; and Tar-C-alpha gene, econs 1-4
	Top Hit Databese Source					<u>2</u>		Z.	N							T_HUMAN				Ī	Ī			M			SSPROT			
	Top Hit Acessian No.	0.0E+00 AF184110.1	7882479	7662181 NT	0.0E+00 S71446.1	0.0E+00.S71448.1	7.		7304922	7304922 NT	0.0E+00 AF028801.1	1N 0077700	6877700	7018320 NT	7019320	.1	0.0E+00 AF303134.1	2.1		0.0E+00 J00191.1	1 00E/10 4 00 - 70 0		-	0.0E+00 AF097416.1	4503788	4885048 NT	P52740	8922180 NT	8923080	0.0E+00 M94081.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	20.70	0.00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 P52740	0.0E+00	0.05+00	
	Expression Signed	224	24.63	29	0.96	96.0	0.86	1.25	0.81	0.81	1.56	1.12	1.12	1.12	1.12	1.49	68.0	1.83	0.68	0.68	767	1.0	0.83	1.28	3.04	13.14	1.37	1.65	4.6	1.75
	ORF SEQ ID NO:		30668		30675		L		30691	30692	30701	30704	30706	30707	30708	30740	30749		30778			30788	L	30791		30794	30795	30797	30801	30805
	SEQ ID	17770	17772	17774	17780	47780	17785	17790	17801	17801	17809	17812	17812	17814	17814	17842	17848	17849	17890	17890		17899	17801	17902	١	17905	17906	17908	17911	17915
Γ	Probe SEQ ID NO:	4750	4752	4754	4760	4760	4765	£	4781	4781	4792	4795	4786	4797	4797	4825	4831	4832	4873	4873	-	\$ 88 \$ 88	28	888	4888	<del>888</del>	4889	<b>489</b>	4894	888

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Single Exon Probes Expressed in Bone Marrow

	<u> </u>		Γ		· · · ·	Г	Г			Г					П							T.,	Т	┱	7						
Top Hit Descriptor	Human Tcr-C-delta gene, econs 1-4; Tcr-V-delta gene, econs 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1- J61 segments; and Tcr-C-alpha gene, econs 1-4	H.septens MeCP-2 gene	H.sapiena MeCP-2 gene	Homo sapiens chronosome 21 segment HS210080	Homo septems TATA box binding protein (TBP)-essociated factor, RNA polymenase II, I, 284D (TAF2I) mRNA	H. sapiens MICA gene	Homo sepiens zinc finger protein (KIAA0412) mRNA	Homo sepiens mRNA for KIAA1443 protein, pertial cds	H. sapiens fertiin alpha pseudogene	Homo sepiens mRNA for KIAA0633 protein, partial cds	Mus musculus zinc finger protein interacting with K protein 1 (ZIk1), mRNA	Homo sapiens desmoplation (DPI, DPII) (DSP) mRNA	Homo sapiens gene encoding filensin, evan 8	Homo sapiens zino-finger DNA-binding protein (HUMHOXY1), mRNA	Homo sapiens mRNA for immunoglobulin kappa light chain, anti-RhD, thered 7	Homo sapiens MHC class 1 region	Homo sepiens opioid receptor, delta 1 (OPRD1) mRNA.	Homo sapiens splice vertent AKAP350 mRNA, pertial cds	Homo sepiens flavin containing monockygenase 3 (FMO3) gene, exon 7	Homo sepiens COLAAB gene for a6(N) collagen, exon 44 and partial cds	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallytranstransferase, geranylinansfransferase) (FDPS) mFNA	qm15065x1 NG_CGAP_LL5 Homo sepiens cDNA clone IMAGE:1881821 3' similar to TR:Q61632 Q61632	LITTERIOR AND AND AND AND AND AND AND AND AND AND	noine equens glywcai + (cr c+) mous Umos carlana shalom 4 (2004) mbNa	Home Septems gryphest + (Gr C+) minute	Homo sepiens chromosome 21 segment HS210084	Homo sapiens KIAA0808 gene product (KIAA0806), mRNA	Human ribosomal protein L21 mRNA, complete cds	Human endogenous retroviral DNA (4-1), complete retroviral segment	601303729F1 NIH_MGC_21 Hano sepiens cDNA clone IMAGE:3638118 5	Homo sepiens desmoplakin (DPI, DPII) (DSP) mRNA
Top Hit Database Source	Ŋ	Į,	LN.	NT	Į.	Z	N F	¥	FX.	N.	N.	Z	NT	Z	N.	NT	Z	NT	NT	NT	Ę	Total Lill Brani	NAME OF THE PARTY		2	M	NT	TN	NT	EST_HUMAN	¥
Top Hit Acession No.	A94081.1			2	5032150 NT	(92841.1	4585642 NT	<b>+</b> -	709232.1	1	677648	4758199 NT	/16723.1	7705548 NT	J010442.1	\F055068.1	4505508 NT	VF091711.1		)63562.1	4503684 NT	, 00,	1.63   1.63.1	450408Z N	18	0.0E+00 AL163284.2	7862319 NT			.1	4758189 NT
Most Similar (Top) Hit BLAST E Value	0.0E+00 M94081.1	0.0E+00 XB462B.1	0.0E+00 X94628.1	0.0E+00 AL163280	0.0E+00	0.0E+00 X92841.1	0.0E+00	0.0E+00 AB037864	0.0E+00 Y09232.1	0.0E+00 AB014533	0.0E+00	0.0E+00	0.0E+00 Y16723.1	0.0E+00	0.0E+00 AJ010442	0.0E+00 AF055088	0.0E+00	0.0E+00 AF091711	0.0E+00 U39965.1	0.0E+00 D63562.1	0.0E+00	100	O.VETON MICH 125.	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U14967.1	0.0E+00 M10978.1	0.0E+00 BE408863.	0.0E+00
Expression Signal	1.75	1.49	1.49	238	1.16	1.59	<u>4</u>	0.69	1.25	1.17	23	1.49	76.0	1.15	25.08	25.15	1.97	201	0.91	0.89	1.62	8	800	280	0.83	1.88	1.24	8.04	1.06	2.79	3.2
ORF SEQ ID NO:	30806	30808			30820		30832	30833	30834	30835		30838	L	30840		30844		30847		20867	30859			308/8		20833			30918		30922
Exam SEQ ID NO:	17815	17917	Ш		17929	1_	17940	17941	17942	17943		17946	17947	17948	17949	17952	17954	17965	17957	17967	17963	1	0/8/1	/98/L	1/88/		18010	72081	18032		18037
Probe SEQ ID NO:	4838	4900	4900	4903	4912	4921	4923	4854	4925	4926	4927	4829	4830	4631	4832	4836	4638	4639	4941	4962	4854	7824	Ş Ş	7/84	40/2	4990	4995	2008	5018	5020	5023

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	Top Hit Descriptor Top Hit Descriptor	Source	Homo sapiens mRNA for KIAA1043 protein, partial cds	Homo sepiens hypothetical protein FL/20477 (FL/20477), mRNA	Homo sepiens hypothetical profish FL/20477 (FL/20477), mRNA	no14g09.s1 NCI_CGAP_Phe1 Hano sepiens cDNA clone IMAGE:1100704 3' cámilar to TR:E239140 EST HUMAN E239140 SPALT PROTEIN;			Г	Homo seplens MHC class 1 region	Homo saplens chromosome 21 segment HS21C009	Homo sapiens gammme-cytoplasmic actin (ACTGP3) pseudogene	Becillus amyloliquefaciens eacB gene for levansucrase (EC 2.4.1.10)	Homo septens vescular endotheltal cadherin 2 mRNA, complete ods	Homo sepiens vascular endotheltal catherh 2 mRNA, complete cds	Homo sepiens cyclophilin (USA-CYP) mRNA	Homio sepiens putative GPR37 gane, excn 2	Homo septens putative GPR37 gene, excn 2	Homo sepiens titin (TTN) mRNA	Homo septens 4F2 light chain (LOC51697), mRNA	Homo septens 4F2 light chein (LOC51597), mRNA	Human versican V2 core protein precursor splice-variant mRNA, complete cds	Homo espiens serine-threature protein Idnase (MNBH) mRNA, complete cds	Hamo septens sertine-threantine protein kinase (MNBH) mRNA, complete cds	Homó sepiers jumorji (mouse) homolog (JMJ) mRNA	Human digadendrocyte myelin glycoprotein (OMG) exans 1-2; neuroffbramatosis 1 (NF1) exans 28-49; ecotropic viral integration site 2A (EVI2A) exans 1-2; ecotropic viral integration site 2A (EVI2A) exans 1-2;	edernylate luhase (AK3) excrs 1-2	Homo sapiens T-cell receptor gamma V1 gene region	Homo sepiens mRNA for neurodin Feipha protein, complete cds	EST_HUMAN   DKFZp434l0713_71 434 (synonym: https://domo.sapiens.cDNA.clone.DKFZp434l0713 5	П	Homo sapiens keratin 12 (KRT12) gene, complete cds
-	Top Hit Acession		B028968.1 NT	8923441 NT	8923441 NT	0.0E+00 AA601248.1 ES		-	758225	U53588.1 NT	L163209.2 NT	N 1.759090	(52988.1 NT	\F240835.1 NT	0.0E+00 AF240835.1 NT	5454153 NT	712477.1 NT	712477.1 NT	•	7706245 NT	7706245 NT	J26556.1 NT	.1	NF108830.1 NT	4826777 NT		D6367.1 NT	1F057177.1 NT	\B035356.1 NT	Ţ	Ţ	NF137288.1 NT
	Most Similar (Top) Hit BLAST E	Value	0.0E+00 AB028968.	0.0E+00	0.05+00	0.0E+00	0.0E+00 AA601246	0.0E+00 AA601246	0.0E+00	0.0E+00	0.0E+00 AL163209	0.0E+00 D50657.1	0.0E+00 X52989.1	0.0E+00 AF240835	. 0.0E+00	0.0E+00	0.0E+00 Y12477.1	0.0E+00 Y12477.1	0.0E+00	0.0E+00	0.0€+00	0.0E+00 U28555.1	0.0E+00 AF108830	0.0E+00 AF108830	0.0E+00		0.0E+00 LD5367.1	0.0E+00 AF057177	0.0E+00 AB035358	0.0E+00/	0.0E+00 AF093098.	0.0E+00/
	Expression	ļ	1.24	1.97	1.97	0.75	0.76	0.76	1.3	0.8	121	24.84	3.46	96:0	0.98	98'0	1.07	1,07	1.31	0.84	0.84	1.13	1.01	1.01	1.11		1.35	1.06	0.63	209	32	203
	ORF SEQ ID NO:		30926	30835					_	30974			31009	31029	31030	31031	31057	L	31062	31092	31093	31101	31103		31116				31161			31181
	Exam SEQ ID	Ö	18044			l			<u></u>			L		L		18151	18180	18180	18185	18217	18217	18227	18229		Į.		18285	<u> </u>	18301			18430
	Probe SEQ ID	ğ	6030	504	504	5057	5057	5057	5074	5088	200	5007	5122	5141	5141	6142	5171	5171	6178	6208	5208	6218	5224	<b>622</b> 1	5236		5257	5284	5296	5305	5313	5324

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Top HII Descriptor	Homo sapiens keratin 12 (KRT12) gene, complete cds	wp08g08.x1 NCI_CGAP_K0412 Homo septens cDNA clone INAGE:2464094 3"	Homo sepiens protocadherin alpha 13 (PCDHA13), mRNA	RC3-GN0076-310800-013-bc3 GN0076 Homo sepiens cDNA	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds	Homo sepiens polycystic lidney disease-like 2 protein (PKDL2) mRNA, complete cds	H.sapiens immunoglobulin heavy chain gene, variable region	H. sapiens immunoglobulin heavy chain gene, variable region	7110c06.x1 NCI_CGAP_CLL1 Hamo septems cDNA done IMAGE:3294250 3'	ht09502x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3165194 3' similier to SW:Y054_HUMAN P42894 HYPOTHETICAL PROTEIN KIAA0054.;	601589422F1 NIH_MGC_7 Homo saptens cDNA clane IMAGE:3943804 57	601589422F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3943804 5	q404404.x1 Soares_placenta_8tx94vecks_2NbHP8tx39W Homo septens cDNA clone IMAGE:1722702.3' similar to SW:T2D3_DROME P48846 TRANSCRIPTION INITIATION FACTOR THID 86 KD SUBUNIT;	Homo sapiens eostnophil percedasse (EPP) gene, excn 7	dr68a09.y5 NCI_CGAP_KId5 Homo septens cDNA clone IMAGE:1472152 5' similar to go:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);	Homo sepiens Sp4 trenscription factor (SP4), mRNA	802118928F1 NIH_MGC_56 Hama septens cDNA clane IMAGE:4276254 67	AU134406 OVARC1 Homo sapiens cDNA clone OVARC1001894 5"	AU134406 OVARC1 Homo septens cDNA clone OVARC1001894 5	601061489F1 NIH_MGC_10 Hama sepiens aDNA dane IMAGE:3447839 6	001105891F1 NIH_MGC_15 Hamo sepiens cDNA clane IMAGE:2988310 6"	602071372F1 NCL_CGAP_Bm64 Homo sepiens cDNA clone IMAGE:4214272 5	602071372F1 NCI_CGAP_Bm64 Homo sapiens oDNA dane IMAGE:4214272 6	Homo sapiens Bloom syndrome (BLM) mRNA	Homo sapiens mRNA for KIAA0468 protein, partial cds	Hamo sapiens mRNA for KIAA0466 protein, partial ods	Homo sepiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds	Homo sepiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds	Human gane for dihydrotipoamide succinyltransfarasa, complete cds (exon 1-15)	Human gene for dihydrolipoamide succinytransferase, complete cds (excn 1-15)
Top Hit Database Source	NT	EST_HUMAN	₹ E	EST_HUMAN	NT	ᅜ	뉟	N <sub>T</sub>	<b>EST_HUMAN</b>	EST HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	Ę	EST_HUMAN	Z	EST_HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	M	М	M	M	۲	¥	<u>L</u>
Top Hit Acession No.	0.0E+00 AF137286.1	0.0E+00 AI834954.1	9256579 NT	0.0E+00 BE931080.1	0.0E+00 AF182034.1	0.0E+00 AF182034.1	X56163.1	K56163.1	0.0E+00 BE675498.1	0.0E+00 BE220753.1	0.0E+00 BE784412.1	0.0E+00 BE794412.1	A1189142.1	M29908.1	0.0E+00 AI791363.1	11421038 NT	0.0E+00 BF665982.1	0.0E+00 AU134406.1	0.0E+00 AU134408.1	BE538857.1	0.0E+00 BE292784.1	0.0E+00 BF626328.1	0.0E+00 BF526328.1	4557364 NT	0.0E+00 AB007935.1	0.0E+00 AB007935.1	0.0E+00 AF257737.1	0.0E+00 AF257737.1	D26535.1	026535.1
Most Similar (Top) Hit BLAST E Vatus	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X56163.1	0.0E+00 X56163.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M29608.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00 D26535.1	0.0E+00 D26535.1
Expression Signal	203	1.19	1.2	4.04	2.83	283	32.34	32.34	6.37	1.72	1.69	1.69	0.68	18.78	0.56	4.26	1.72	0.77	0.77	0.64	1.22	205	. 2.05	231	1.03	1.03	. 4.25	4.25	1.18	1.18
ORF SEQ ID NO:	31182	31322	31325	31340	31344	31345	31354	31355	31470	31471	31472	31473	31474	31477	31480	31488		31499	31500	31507	31633	31639	31540	33350	31567	31568	31572	31573		31590
Exam SEQ ID NO:	18430	18451	18454	18469	18473	18473	18480	18480	18559	18560	18561	18561	18562	18566	18570	25639	18588	18589	18589	18595		18609	18609	20048	18630	18630	18633	18633	18647	18647
Probe SEQ ID NO:	5324	5346	5340	5364	<b>3368</b>	6368	6378	5376	6457	6458	5459	6459	5460	25	2468	6478	5488	5489	6489	5495	5504	6099	929	5529	5532	5532	5536	5536	5550	5550

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Single Exolit Flores Expressed in Dollo Prairies	Most Similar (Top) Hit Top Hit Acession Database BLASTE No. Source	0.0E+00 BF031742.1 EST_HUMAN	0.0E+00 BF031742.1  EST_HUMAN	0.0E+00 AW470846.1 EST_HUMAN	0.0E+00 BF155670.1 EST_HUMAN	0.0E+00 BF155670.1 EST_HUMAN	0.0E+00 W33069.1 EST_HUMAN	0.0E+00 W33069.1   EST_HUMAN	0.0E+00[AF012818.1 NT	0.0E+00 BE280197.1 EST_HUMAN	0.0E+00 BE889010.1 EST_HUMAN	0.0E+00 BE388673.1 EST_HUMAN	0.0E+00 AW752848.1 EST_HUMAN	0.0E+00 11433071 NT	0.0E+00 11433071 NT	0.0E+00 BE901608.1  EST_HUMAN	0.0E+00 BE901608.1 EST_HUMAN	1.12 0.0E+00 BE901608.1 EST_HUMAN 601677735F1 NIH_MGC_21 Hamo septems cDNA clone IMAGE:3960200 5	0.0E+00 9789988 NT	0.0E+00/AATB3SUS.1 EST_NUMAN	0.0E+00 AA183606.1 EST_HUMAN	0.0E+00 U34825.1 NT	0.0E+00 U34626.1 NT	0.0E+00 AW853983.1 EST_HUMAN	0.0E+00 AW853983.1 EST_HUMAN	0.0E+00 BE268330.1 EST_HUMAN	0.0E+00 BE156561.1 EST_HUMAN	0.0E+00 M38107.1 NT	0.0E+00 BE379007.1   EST_HUMAN	0.0E+00 AU137772.1 EST HUMAN	3.66 0.0E+00 U45982.1 NT Human G protein-coupled receptor GPR-9-6 gene, complete cts
		0.0E+00 BF03	0.0E+00 BF03	0.0E+00 AW4	0.0E+00 BF15	0.0E+00 BF15	0.0E+00 W33	0.0E+00 W33	0.0E+00 AFO1	0.0E+00 BE28	0.0E+00 BE8	0.0E+00 BE38	0.0E+00 AW7	0.0E+00	0.0E+00	0.0E+00 BE90	0.0E+00 BE90	0.0E+00 BE90	0.0E+00	0.0E+00 AAT	0.0E+00 AA18	0.0E+00 U34	0.0E+00 U348	0.0E+00 AW8	0.0E+00 AW8	0.0E+00 BE2	0.0E+00 BE1	0.0E+00 M38	0.0E+00 BE3	0.0E+00 AU1	0.0E+00 U456
	Expression	0.67	0.67	1.27	0.95	0.95	1.38	1.38	2.28	282	231	0.53	0.63	1.46	1.48	1.12	1.12	1.12	86.6	1.43	1.43	11.54	11.54	0.54	0.54	1.14	1.24	0.63	1.71	1.19	3.68
	ORF SEQ ID NO:		32337	32352	32364		92371	32372		32376	32385	32388	32408		32411	32412	32413	32414		32434	32435	32460	32461		Ş	32506		82524	32558		32590
	Econ SEQ ID NO:	19128		19146	L		19160		19161	19164	18170			<u> </u>		19191	19191	19191	25654	19209	19209	18230	19230	L _	L	L	18281	18291	19327	19333	19354
	Probe SEQ ID NO:	6047	6047	6500	6072	6072	0808 0808	0809	6081	<b>6084</b>	<b>609</b>	8083 8	6109	6112	6112	6113	6113	6113	64.29	6132	6132	9456	6155	9157	6157	6197	6207	6217	4528	6260	6282

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INJUSTACIONES EXPRESSED III DOI 18 MAILOW	Top Hit Descriptor	zq81d03.1 Stratagene INT neuron (#987233) Homo sapiens cDNA clone IMAGE:648005 6' similer to TR:0854195 G854195 LEUKOCYTE SURFACE PROTEIN.;	Homo septems xylosyltransferase II (XT2), mRNA	Homo sapiens xylosyltransferase II (XT2), mRNA	Human beta2-chimaerin mRNA, complete cds	Homo sapiens carchoembryonic antigen-related ceil adhesion molecule 8 (CEACAMB), mRNA	601109532F1 NIH_MGC_16 Hamo sepiens cDNA clane INAGE:3350822 5	#91f16.x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:2248939 3' stmilar to TR:Q14839 Q14839 ML2 PROTEIN.;	Human anion exchanger (AE1) gene, excms 1-20	601587971F1 NIH_MGC_7 Homo sepiens cDNA clone IMAGE:3942329 5	801587971F1 NIH_MGC_7 Homo sepiens cDNA done INAGE:3942329 5	q50b11.x1 NCI_CGAP_Bm25 Homo sepiens cDNA clone IMAGE:1859901 3' similar to TR:Q12838 Q12838 TFIIIC ALPHA SUBUNIT;	q50b11.x1 NCI_CGAP_Bm25 Homo sepiens cDNA clone IMAGE:1859901 3' similar to TR:Q12838 Q12838	TFIIIC ALPHA SUBUNIT;	MRO-HT0923-220800-102-b05 HT0923 Homo sepiers cDNA	Homo sapiens peptide transporter 3 (LOC51286), mRNA	Human mRNA for alpha mannosidase II Isozyme, complete cds	IL3-HT0062-010909-014-A04 HT0062 Homo sepiens cDNA	7e02c12x1 NCL_CGAP_Lu24 Homo septiens cDNA done IMAGE:3291302 3' similar to SW:Y176_HUMAN 014681 HYPOTHETICAL PROTEIN KIAAA178	Homo septens KIAA0285 gene product (KIAA0285), mRNA	AV650020 GLC Homo sepiems cDNA clone GLCCAD09 3'	UI-HIF-BLO-acc-g-12-0-UI.s1 NIH_MGC_37 Hamo saplens dONA dane IMAGE:3058761 3'	yZ7b03.r1 Soares placenta NbZHP Homo sapiens cDNA clone UAAGE:149633 5	Homo septens smilande-censitive cetion channel 1, neuronal (degenerin) (ACCN1), mRNA	Human gene for the light and heavy chains of myeloperoxidase	8814607.r1 Scares_NHHMPu_S1 Homo sepiens cDNA clone IMAGE:813252.57	1257408.X1 NCI_CGAP_OV36 Homo sepiens cDNA done IMAGE:22928873' similer to SW:NTCS_HUMAN P53786 SODIUM-AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 2;	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3839616 5	601305368F1 NIH_MGC_39 Homo sapiens cDNA done IMAGE:3639616 5	MR0-BT0284-221199-002-f11 BT0284 Homo sepiens cDNA
AUII LIUUM	Top Hit Databese Source	T_HUMAN					EST_HUMAN 6	EST HUMAN N	Г	EST_HUMAN 6	EST_HUMAN 6	EST HUMAN 1			EST HUMAN IN		IN IN	EST_HUMAN II	FET HIMAN		T HUMAN	EST_HUMAN L	EST_HUMAN X		TA TA	EST_HUMAN   a	EST_HUMAN P	HUMAN		EST_HUMAN N
Single L	Top Hit Acession No.	0.0E+00 AA204740.1	11545913 NT	11545913 NT		11428367 NT	0.0E+00 BE257173.1	A1686048.1		5.1	Ţ	N198025.1		1	0.0E+00 BF367123.1	11435630 NT		2.1		882039	0.0E+00 AV650020.1	2		11428283 NT		0.0E+00 AA458375.1	0.0E+00 AI612841.1	0.0E+00 BE735989.1	1	-
	Moet Similar (Top) Hit BLAST E Vatue	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U07223.1	0.0E+00	0.0E+00	0.0E+00 AI686048.	0.0E+00 [135930.1	0.0E+00	0.0E+00	0.0E+00 Al198025.		0.0E+00 A1198025.	0.0E+00	0.0E+00	0.0E+00 D55649.1	0.0E+00	0.05400	0.0E+00	0.0E+00/	0.0E+00	0.0E+00 H01255.1	0.0E+00	0.0E+00 X15377.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/
	Expression Signal	4.53	4.05	4.05	0.58	8.33	3.68	0.97	1.28	1.28	128	0.65		0.65	1	1.77	0.79	-	77.0	88.0	8.48	3.68	5.02	1.18	8.09	0.72	1.23	3.93	3.83	0.78
	ORF SEQ ID NO:	32822	32823	32624	32642	32659	32664		32683	32691	32692	32707		32708	32710	32720	32728	32761	32768	32774		32786	32798	32809	32814	32816	32817	32823	32824	32830
	Exam SEQ ID NO:	19382	19383	18383	19401	19418	19422	19437	1944	19450	19450	19461		19461	19464	19472	19482	19498	10518	19523	18637	19546	19549	19558	19562	19584	18565	19571	19571	19575
	Probe SEQ ID NO:	6311	6312	6312	<b>6831</b>	6349	සෙස	888	8373	2883	8382	88		සහ	9639	4040	4149	6432	RAFR	8488	6472	6481	<u>8</u> 8	8483	8498	959	6501	6507	8507	6511

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					28.5		
Probe SEQ ID NO:	Esan SEO ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6511	19575	32831	0.78	0.0E+00	0.0E+00 AW748596.1	EST HUMAN	MR0-BT0264-221199-002-f11 BT0284 Homo capiens cDNA
6512	I_		29'0	0.0E+00	0.0E+00 U77629.1	Z	Homo sepiens Achaete-Scute homologue 2 (ASCL2) gene, complete cds
6514	L	32833		0.0E+00	5.1	EST_HUMAN	AU119245 HEMBA1 Homo saplens cDNA clone HEMBA1005360 5
8514	L			0.0E+00	+	EST_HUMAN	AU119245 HEMBA1 Homo septens cDNA clone HEMBA1005360 5
8519			0.86	0.0E+00		EST_HUMAN	601488712F1 NIH_MGC_67 Homo septens cDNA clone IMAGE:3871899 5
6520				0.0E+00		NT	H.sapiens germline immunoglobulin heavy chain, variable region, (13-2)
6537	_		1.84	0.0E+00	0.0E+00 Al989483.1	EST_HUMAN	ws25c07.x1 NCI_CGAP_GC8 Hamo sapiens cDNA clone IMAGE:2498220 3"
6551	L		1.76	0.0E+00		EST_HUMAN	601105344F1 NIH_MGC_15 Hamo septens cDNA dane IMAGE:2987963 5
6661	L		1.78	. 0.0E+00	0.0E+00 BE283153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Hamo sepiens cDNA clane IMAGE:2887863 5'
6584	١	32912	0.71	0.0E+00	-	EST_HUMAN	601443175F1 NIH_MGC_66 Hamo septens cDNA dane IMAGE:3847291 6
9629	1_	32962	1.2	0.0E+00	0.0E+00 AW406348.1	EST_HUMAN	UHIF-BLD-aco-h-02-0-UL/1 NIH_MGC_37 Hamo septens aDNA ctane IMAGE:3058831 5
8628	19884	32963	12	0.0E+00	0.0E+00 AW406348.1	EST_HUMAN	UI-HF-BLD-eco-h-02-0-ULr1 NIH_MGC_37 Homo sepiens cDNA clone IMAGE:3058831 5
988	L		0.89	0.0E+00	_	EST_HUMAN	AV719444 GLC Hamo sepiens aDNA clane GLCEHC06 6
6999	_			0.0E+00	0.0E+00 BE898340.1	<b>EST_HUMAN</b>	601681150F1 NIH_MGC_9 Hamo septens cDNA clone IMAGE:3951301 5
8999	19726	33002	127	0.0E+00	0.0E+00 BE898340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Home septens cDNA clone IMAGE:3951301 5'
	L.						Homo sepiens low voltage-activated T-type calcium channel alpha 1G spiice variant CavT.1a (CACNA1G)
6672	19729	33005	2.18	0.0E+00	0.1	N	mRNA, complete cds
6675	19732	33008	0.64	0.0E+00	L48546.1	NT	Homo sepiens tuberin (TSC2) gene, exans 38, 39, 40 and 41
6877	19791		1.11	0.0E+00	11420658 NT	NT	Homo eaplens transformation/transcription domain-essociated protein (TRRAP), mRNA
7000	<b>L</b>		20.00	O OF ADD	0.05400 0.04763840 1	EST HIMAN	austring.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5 similar to TR-O18390 O15390 GT24. [3] TR-O43840 TR-O43206:
3	1						au88108.y1 Schneider fedal brain 00004 Homo sapiens cDNA done IMAGE 2784159 5' similar to
88	19741	33017	3.24		0.0E+00 AW183840.1	EST_HUMAN	TR-016380 016380 GT24. [3] TR:043840 TR:043206;
	l				2072-0111	MAN ILL POPE	2520608.71 Soares_fetal_Lung_Nib-II,19W Home sapiens cDNA done IMAGE:302626 6' similar to cw>NAs unitata occase zero Eincere Decription 4s.
888	28/4P	SOUSS SOUSS	0.00	1	0.0E-00 W3/ 103.1		Anna Course fatel line Nittil 10M Home sentens of NA above IMACE-307828 67 similar to
6888	19746	3302	0.85		0.0E+00/W37163.1	EST HUMAN	SW-ZNA6_HUMAN Q02386 ZINC FINGER PROTEIN 45;
90/9	1			L	0.0E+00 BE794853.1	EST_HUMAN	601589371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943504 5
6713	I _	33048			0.0E+00 BE799873.1	EST_HUMAN	601587561F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 57
6714	L			0.0E+00	-	EST_HUMAN	QV1-GN0065-140800-318-h02 GN0065 Homo sepiens cDNA
8714	L		3.07		0.0E+00 BE767955.1	EST HUMAN	QV1-GN0085-140800-318-h02 GN0065 Hamo sepiens cDNA
67.18	1		7.15		0.0E+00 BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sepiens cDNA done IMAGE:3913311 5
6718	19774		7.15		0.0E+00 BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Hamo sepiens cDNA clone IMAGE:3913311 5
6727	19783	33062	5.42		0.0E+00 L24483.1	NT	Human antigen CD27 gene, exons 1-2

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Top Hit Descriptor	QV3-NT0022-140600-223-f01 NT0022 Homo sapiens cDNA	602185852F1 NIH_MGC_45 Hamo saplens cDNA clane IMAGE:4310078 5	Homo sepiens mRNA for dyneth heavy chain (DNAH9 gene)	Homo sapiens mRNA for dynath heavy chath (DNAH9 gene)	Human type IV sodium channel alpha potypeptide (SCN4A) gene, exon 19	UHIF-BRop-aka-d-10-0-ULr1 NIH_MGC_52.Homo sapiens cDNA clone IMAGE:3078230 5	UHIF-BRop-aka-d-10-0-UL:1 NIH_MGC_52 Hamo sapiens cDNA dane IMAGE:3078290 5'	DKFZp434D2211_r1 434 (synonym: https://displays.com/A clane DKFZp434D2211 6	DKFZp434D2211_r1 434 (synanym: htes3) Hamo sapiens cDNA clane DKFZp434D2211 5	601889823F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:4123948 5	Human diromosome 16 creatine transporter (SLOGA8) and (CDM) paratogous genes, complete ods	Novel human gene mapping to chomosome 13	Homo sepiens mRNA for vascular cacherin-2, complete cds	Homo sapiens mRNA for vascular cadharin-2, complete cds	AU137738 PLACE1 Homo septems cDNA clone PLACE1007120 6"	AU137738 PLACE1 Homo sepiens cDNA clone PLACE1007120 6"	EST368876 MAGE resequences, MAGC Hamo septens cDNA	601113958F1 NIH_MGC_16 Homo septens cDNA clone IMAGE:3354588 5	Human type VI sodium channel alpha polypeptide (SCNV4A) gene, exon 14	Homo sapiens mRNA for KIAA0468 protein, partial cds	Homo sapiens mRNA for KIAA0468 protein, partial cds	AU133213 NT2RP4 Homo capiens cDNA clone NT2RP4001656 6	Homo seplens membrane protein CH1 (CH1), mRNA	AU143708 Y79AA1 Homo septens cDNA clone Y79AA1002365 5	Homo sapiens netrin 1 (NTN1), mRNA	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917184 5	601431818F1 NIH_MGC_72 Homo septens cDNA clone IMAGE:3917184 5	Homo sapiens keretin 12 (KRT12) gene, complete cds	Homo sapiens keratin 12 (KRT12) gene, complete cds	601580948F1 NIH_MGC_9 Hamo sapiens cDNA clane IMAGE:3929722 5	601580848F1 NIH_MGC_9 Hamo sepiens cDNA clane IMAGE:3829722 5	Homo sapiens vitamin D (1,25-dihydraxyvitamin D3) receptor (VDR), mRNA	Homo sepiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
Top Hit Database Source	EST_HUMAN	<b>EST_HUMAN</b>	IN	IN	NT	<b>EST_HUMAN</b>	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	NT	٦	ᅜ	Į.	EST_HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	NT	NT	NT	EST_HUMAN	NT	EST_HUMAN	된	EST HUMAN	EST HUMAN	NT	NT	EST_HUMAN	EST HUMAN	N	Z
Top Hit Acession No.	0.0E+00 BE762770.1	0.0E+00 BF569905.1	0.0E+00 AJ404468.1	0.0E+00 AJ404468.1	01978.1	0.0E+00 AW502362.1	0.0E+00 AW502362.1	0.0E+00 AL039581.1	0.0E+00 AL039581.1	0.0E+00 BF306996.1	J41302.1	0.0E+00 AL049784.1	0.0E+00 AB026893.1	0.0E+00 AB026893.1.	0.0E+00 AU137738.1	0.0E+00 AU137738.1	0.0E+00 AW954806.1	0.0E+00 BE254103.1	.01973.1	0.0E+00[AB007835.1	4B007935.1	0.0E+00 AU133213.1	11428081 NT	0.0E+00 AU143708.1	758839	0.0E+00 BE891285.1	0.0E+00 BE891286.1	0.0E+00 AF137286.1	0.0E+00 AF137286.1	0.0E+00 BE747231.1	0.0E+00 BE747231.1	11436699 NT	11436699 NT
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 L01978.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U41302.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 L01973.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	0.67	239	0.68	0.68	4.32	1.49	1.49	0.93	0.93	5.15	2.16	121	0.69	0.69	0.68	0.68	1.23	1.14	1.23	0.68	0.68	1.38	1	224	96'0	1.34	1.34	228	2.28	0.7	0.7	4.41	4.41
ORF SEQ ID NO:			33555				33566	33574	33575	33583	33288	33312	33627	33628	33634	33635	33641	33642	33654	33664	33665	33672	33692		33697	33706	33707	31181	31182	33736	33737		33752
SEO D NO:	20216	20222	20224	20224	20228	20232	20232	20240	20240	20249	20254	20010	20286	20286	20204	20281	20297	20298	20311	20318	20318	20324	20340	20345	20346	20355	20355	18430	18430	20386	20386	20399	20399
Probe SEQ ID NO:	7182	7198	7200	7200	7204	7209	7209	7218	7218	7227	887.4	7276	7815	7316	7320	2220	7326	7327	982	7348	7348	7354	2370	7375	7376	7385	7385	7407	7407	7419	7419	7432	7432

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Top Hit Descriptor	UHIF-BK0-eas-g-07-0-UI.11 NIH_MGC_36 Homo sapiens aDNA dane IMAGE:3054924 51	ym88h10.r1 Soares adult brain N2b4HB55Y Homo saptems cDNA ctone IMAGE:166051 5	x838a05.y1 NCI_CGAP_1.u31 Home sapiens aDNA done IMAGE:2578840 5 similier to TR:008050 Q08050 HNR3/FH TRANSCRIPTION FACTOR GENESIS;	AU117553 HEMBA1 Hamo septens dDNA clane HEMBA1001691 5*	Homo sepiens glucagon-like peptide 2 receptor (GLP2R), mRNA	ZEGROZ FI Strategene muscle 937209 Homo sepiens dDNA clone IMAGE:562203 5' similer to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);	WRO-AN0083-270900-004-f07 AN0083 Homo septems cDNA	QV3-BN0046-220300-129-604 BN0046 Homo sapiens cDNA	Homo sepiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds	601889823F1 NIH_MGC_17 Hamo septems cDNA clane IMAGE:4123948 5	601889823F1 NIH_MGC_17 Homo septens cDNA clone IMAGE:4123948 5	AU118767 HEMBA1 Homo sapiens cDNA clone HEMBA1004314 6	UHIF-BRop-gire-10-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074778 5	Human mRNA for KIAA0357 gene, partial cds	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random	zu68th07.r1 Scares_testis_NHT Homo septens cDNA clone IMAGE:743125 5	zu88b07.r1 Scares_testis_NHT Hamo saplens cDNA clone IMAGE:743125 5	DKFZp434J087_r1 494 (synonym: https://dy.com.eaplens.cDNA.clone.DKFZp434J087.57	Homo sapiens dynactin 1 (DCTN1) gene, atternatively spitoed products, exons 7 through 32 and complete cds	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete	Gos HSI/74315 Human chromosome 14 Homo sepiens cDNA clone 1-4	HTM1-183F1 HTM1 Homo septems cDNA	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain	(1M) BRU STATE COURSE COURSE (SELECTION) OF COUNTY AND BRUSH BRUSH AND AND AND AND AND AND AND AND AND AND	12 IOCOSTATINITA MASO. 45 Intilio septents curto ceuto involvata intilio comercia del Trocasso Azroso	wb17g0b.x1 NCI_CGAP_GC8 Hamo capiens cDNA clone IMAGE:2306876 3' cmitar to 1 R:U76363 U75363 AIBC1.;
Top Hit Dakebase Source	П	EST_HUMAN		ſ		EST_HUMAN N	EST HUMAN		T.	EST_HUMAN 6	EST_HUMAN   0	EST_HUMAN A	EST_HUMAN L		EST_HUMAN o	EST HUMAN	Г	EST_HUMAN z	EST_HUMAN [	¥		EST HIMAN	HOWAN			ESI HUMAN	EST HUMAN A
Top Hit Acessian Na.	0.0E+00 AW402542.1	0.0E+00 R87430.1	0.0E+00 AW239328.1	0.0E+00 AU117553.1	11427135 NT	0.0E+00 AA211663.1	0.0E+00 BF228235.1	0.0E+00 AW898499.1	132832.1	0.0E+00 BF30698.1	0.0E+00 BF30698.1	0.0E+00 AU118767.1	0.0E+00 AW488551.1		0.0E+00 AI752561.1	0.0E+00 AI752561.1	0.0E+00 AA399959.1	0.0E+00 AA399959.1	0.0E+00 AL048347.2			-	1.5		11417342INI	0.0E+00 BF568605.1	0.0E+00 AI825504.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00		1		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00/AF08420:	0.0E+00		0.0=+00	0.0=+00	0.0E+00
Expression Signal	0.5	1.3	242	121	3.92	1.76	0.68	0.62	0.81	1.17	1.17	1.24	0.49	0.64	4.06	4.06	0.53	0.53	0.53	12		21 25	0.69		1.03	0.0	0.73
ORF SEQ ID NO:	33958		33978		33008		34024	34034	34037	34058	34069	34071	34107	34132	34133	34134	34200	34201	34202	34221		34222	34250		34251	34271	34282
Exan SEQ ID NO:	20595	ı	l				_		ı	l			L	20768	1	20759	1	Ε.	I		<u>L</u> .	20840	I_	l		<b>288</b>	20891
Probe SEQ ID NO:	7835	7853	7654	7878	7878	7697	7783	7710	7713	7740	7740	2750	7782	7809	7810	7810	7879	7879	7880	7887		7897	20,02		028/	7839	7850

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Single Exon Probes E  Signal (Top) Hit Top Hit Acession   Database    Signal Vatue   Surce    Source   Sourc	34283 0.73 0.0E+00 AI825504.1 EST_HUMAN	34292 3.09 0.0E+00 6912735 NT	34296 0.96 0.0E+00 N76128.1 EST_HUMAN	20910 34300 6.4 0.0E+00 BF217805.1   EST_HUMAN	20915 34308 0.53 0.0E+00 BF569862.1 EST_HUMAN	20920 34311 3.8 0.0E+00/AU129622.1 EST_HUMAN	25683 34338 0.97 0.0E+00 AW069274.1 EST_HUMAN	25603 34339 0.97 0.0E+00[AW069274.1 EST_HUMAN	20948 34341 8.56 0.0E+00 4501848 NT	20955 34348 1.05 0.0E+00 AV758467.1 EST_HUMAN	20957 34350 5.84 0.0E+00(BE739870.1 EST_HUMAN	20957 34351 6.84 0.0E+00 BE739870.1 EST_HUMAN	20958 34352 0.88 0.0E+00 6912461 NT Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA	20858 34353 0.88 0.0E+00 6912461 NT	20959 34354 3.3 0.0E+00 AU120424.1 EST_HUMAN	20959 34355 3.3 0.0E+00/AU120424.1 EST_HUMAN	20885 34381 2.13 0.0E+00 BF580287.1 EST_HUMAN	20897 34303 1.52 0.0E+00 BE787610.1 EST_HUMAN	20897 34394 1.52 0.0E+00 BE787610.1  EST_HUMAN	21037 34437 0.54 0.0E+00 AW950307.1 EST_HUMAN	21060 34458 0.52 0.0E+00 Y16785.1 NT	21066 34466 0.49 0.0E+00 11425128 NT	21067 34467 0.69 0.0E+00 AU117333.1   EST_HUMAN	21068 0.52 0.0E+00 BE613963.1 EST_HUMAN	21083 34482 4.38 0.0E+00 AWG68044.1 EST_HUMAN	21084 34488 0.75 0.0E+00 A1133435.1 EST_HUMAN	21156 34565 0.64 0.0E+00 AU133187.1 EST_HUMAN.	21200 0.66 0.0E+00 BF217200.1 EST HUMAN	21213 34820 0.87 0.0E+00 BE313013.1 EST_HUMAN	24725 34635	NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:			Signature State of the Control of th			Top Hit Database Source Source Source Source Source EST HUMAN	Top Hit Descriptor  Homo septens transient receptor potential channel of (TRPCS), mRNA  ABIG1.  Homo septens transient receptor potential channel of (TRPCS), mRNA  ABIG1.  Homo septens transient receptor potential channel of (TRPCS), mRNA  ABIG10.  ABIG10
--	---	-------------------------------	---------------------------------------	--	---	--	---	---	-------------------------------------	---	---	---	--	-------------------------------------	--	--	---	---	--	---	--------------------------------------	--------------------------------------	---	---	---	---	--	---	---	-------------	---	--	--	--	--	--	---	--

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Top Hit Descriptor	601672310F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955131 5	2633h08.r1 Soares refina N254HR Homo sepiens cDNA clone IMAGE:360831 5	601305658F1 NIH_MGC_39 Hamo septens cDNA clane IMAGE:3838803 57	Human amyldid-beta protein (APP) gene, extrn 11	Human amykiki-beta protein (APP) gene, exon 11	bb34d02.y1 NFL_MGC_10 Homo sapiens cDNA clone IMAGE:2885123 5' similar to TR:O84652 D64652 F17X2.28 PROTEIN.;	bb34d02.y1 NIH_MGC_10 Homo septions cDNA clone IMAGE:2885123 6' similar to TR:084652 064652 F17K2.28 PROTEIN.;	281504.r1 Strategene schizo brain S11 Homo sepiens cDNA clone IMAGE:728719 6' similar to TR:G300482 G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;	MRO-ST0031-061089-003-e11 ST0031 Homo sapiens cDNA	Homo sepiens mRNA for KIAA0884 protein, partial cds	AU142402 Y78AA1 Homo sapiens cDNA clone Y78AA1000277 5	601285550F1 NIH_MGC_44 Homo septens cDNA clone IMAGE:3607237 5	601285550F1 NIH_MGC_44 Hamo septens cDNA clane IMAGE3607237 5	Homo sapiens killer cell immunoglobulin-tike receptor, two domeins, short cytoplasemic tail, 1 (KIRZDS1), mRNA	2805d01.r1 Sogres fetal heart NbHH19W Homo sepiens cDNA clone IMAGE:358081 5	2805dO1.11 Scares_fatal_heart_NbHH10W Home septens cDNA clone IMAGE:358081 57	602153008F1 NIH_MGC_81 Hamo septens cDNA clane IMAGE-4294128 5	AU134114 OVARC1 Hamo septems aDNA clane OVARC1001296 5	602068632F1 NCI_CGAP_Bm64 Hamo saplans cDNA clane IMAGE:4212727 5	602069632F1 NCL_CGAP_Bm64 Homo saptens cDNA clane IMAGE:4212727 5	DKFZp761P082_r1 761 (synonym: hamy2) Homo septens cDNA clone DKFZp761P092 6	DKFZp781P092_r1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781P092 5	601485254F1 NIH_MGC_69 Hamo sepiens cDNA dans IMAGE:3887773 6	UHIF-BND-444-01-0-ULT NIH_MGC_50 Hamo septems cDNA dane IMAGE:3077496 5	aug3b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783789 3' similar to TR:060483 060463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1];	xa07d12.x1 Scares NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2667639 3' similar to contains element OFR repetitive element;	Hamo sapiens centrosomal protein 2 (CEP2), mRNA	2838d05.r1 Scares fetal liver spleen 1NFLS Homo sepiens cDNA clane IMAGE:294633 5
Top Hit Detabase Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT.	H	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	TN.	EST_HUMAN	EST_HUMAN	EST_HUMAN	5	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	5	EST_HUMAN
Top Hit Acessian No.		0.0E+00 AA017021.1	1.1			1.1	0.0E+00 AW674581.1	0.0E+00 AA397551.1	_	0.0E+00 AB020691.1				TR57278NT			0.0E+00 BF673096.1					0.0E+00 AL120124.1	0.0E+00 BE877693.1	0.0E+00 AW500549.1	0.0E+00 AW157233.1	0.0E+00 AW072395.1	21722	0.0E+00 W01616.1
Most Similar (Top) Hit BLAST E Veitue	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M34872.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00
Expression Signal	0.88	0.62	228	242	2.42	0.74	0.74	247	0.92	0.62	7.99	1.12	1.12	070	0.92	0.92	17.98	96'0	1.71	1.71	1.65	1.65	1.24	1.91	10.07	290	1.08	0.83
ORF SEQ ID NO:	34648	34682	34680	34695	34696	34727	84728	24724	34735		34737	34741	34742	34756	34768	34759			34778	34777	34810	34811		34881	34887	34006	34626	34929
Exan SEQ ID NO:	I I	21250				21313	21313	_		L	21328	21330	21330	21345	21347	21347	21349	21353	21367	21367	21389	21389	21442	21465	21473	7469	21509	21512
Page SEQ ID NO:	8288	8281	8200	8314	8314	8844	<b>88</b>	8851	8353	8358	8857	8361	8361	8478	82.83	8278	8888	8384	8688	8888	8430	8430	8473	8497	8505	8523	8541	8544

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	Top Hit Descriptor		601578195F1 NIH_MGC_9 Hamo septens cDNA clone IMAGE:3926998 6"	60 1578 165F1 NIH_MGC_9 Hamo septens cDNA clane IMAGE:3926898 5	Homo sepiens Xq pseudoautosamal region; segment 1/2	Human DNA for ceruloplasmin, exon 5	qv95c12x1 NCL_CGAP_U2 Homo sepiens cDNA clone IMAGE:1989334 3' striliar to TR:014673 Q14673 KIAA0164 PROTEIN. :	7476e04x1 NCI_CGAP_Lu24 Homo septens cDNA done IMAGE:3278882 3' similar to TR:096783 095783	STAUFEN PROTEIN.;	w60b10.x1 NCI_CGAP_Bm25 Homo septens cDNA clone INACE:2429275 3' similar to SW:COGT_HUMAN P50281 MATRIX METALLOPROTEINASE-14 PRECURSOR;	601334780F1 NIH_MGC_39 Hamo septems cDNA clane IMAGE:3688655 5	101339780F1 NIH_MGC_39 Homo septens cDNA done IMAGE:36886555 5	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	Homo sepiens Chediak-Higashi syndrome 1 (CHS1), mRNA	zv68f02.rf Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 6' strater to TR:G1304132 G1304132 TPRD. :	PASSED A Sources total failure NDAIFE By Homo septens CDNA clone IMAGE: 758919 5 striker to	TR:G1304132 G1304132 TPRD.;	273208.51 Sogres_bestis_NHT Homo sepiens cONA clone IMAGE:727958 3' strailer to gb;S85656	PROHIBITIN (HUMAN);	RC2-FN0094-120800-013-h07 FN0094 Hamo sepiens aDNA	QV3-DT0045-221288-048-c07 DT0045 Homo sepiens cDNA	QV3-DT0045-221289-046-c07 DT0045 Hamo sapiens cDNA	601462412F1 NIH_MGC_68 Hamo septens aDNA dane IMAGE:3858179 5	901452412F1 NIH_MGC_66 Homo septens cDNA clone IMAGE:3859179 5	Hamo sapiens chromosame 21 segment HS21C009	Homo sepiens chromosome 21 segment HS21C009	wm33a11.x1 NCL_CGAP_UM Hamo sepiens CDNA clane IMAGE:2437724 3' similar to TR:075457 075457	CYTOSOLIC PHOSPHOLIPASE AZ-GAMMA.;	Ine26d10.s1 NCL_CGAP_Cos Hamo saplens cDNA clone IMAGE:882269 3' similar to TR:G1138434	G1136434 KAAU187 PROTEIN.;	Homo sepiens producednem bega 3 (FCUTIDA), mitura	EQAFILAT Sogres pregnant uterus North-U Homo sapiens CLANA come invalcification in a second s	601431238F1 NIH MASC_72 Hamb squans curva dane imakut. 3810008 o
	Top Hit Database	Source	EST_HUMAN	EST_HUMAN	N	Ę	EST HIMAN	Т	EST_HUMAN	EST HUMAN	EST_HUMAN		N	NT	EST HIMAN	-	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Ŋ	N.		EST_HUMAN		EST HUMAN	Ę	EST_HUMAN	EST HUMAN
ì	Top Hit Acessian	ğ	0.0E+00 BE745597.1	E745597.1			0.05-000 81387350 4		0.0E+00 BE674157.1	1885671.1	3E563650.1	0.0E+00 BE563650.1	11427236	11427235 NT	0.05.000 0.0403102.1	1	0.0E+00 AA403192.1		0.0E+00 AA398511.1	0.0E+00 BE837593.1	0.0E+00 AW384874.1	0.0E+00 AW364874.1	0.0E+00 BE612588.1	0.0E+00 BE612588.1	0.0E+00 AL163209.2	0.0E+00 AL163209.2		0.0E+00 AI884477.1		0.0E+00 AA502294.1	11416799 NT	0.0E+00 AI580780.1	0.0E+00 BE880797.1
	Most Similar	Value	0.0E+00	0.0E+00 BE745597.	0.0E+00	0.0E+00 D45032.1	7 007 30 0	3	0.0E+00	0.0E+00 AI885671.1	0.0E+00 BE563650.	0.0E+00	0.0E+00	0,0E+00	0000	2000	0.0E+00/		0.0E+00/	0.0E+00	0.0E+00	0.00+400/	0.0E+00	0.0E+00	0.0E+00/	0.0E+00		0.0E+00		0.0E+00			0.0E+00
	Expression	reduce.	1.28	1.26	12	440	96	3	2.6	122	128	128	1,93	1.83	1 9 4	S	135		3.69	0.53	1.25	126	128	1.28	1.65	1.85		0.7		0.85	0.57	66'0	1.97
	ORF SEQ	Ö Ö	34831					365	34894	34006				35024			35027			35076					l	L	L	35123		35129		35140	
	Econ SEO EO	Š	21514	21514	21627	21548	24 50	<u> </u>	21578	2580	21593	21583	21601	21601	١_	21000	21603		21644	١_	l	1_		t	1	_	_	21698	<u> </u>			L	
	Probe SEO ID	ÿ	8546	8546	6998	8578	3	Reco	8610	2842	8825	8625	8633	8833		8838	8635		8678	8685	8888	8898	8705	8705	8720	8778		8730		8737	8742	8749	8752

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Single Exon Probes Expressed in Bone Marrow

ORF SEQ Expression (Top) Hit Top Hit Acession Signal Value Value	35166 0.55 0.0E+00/AW246765.1 [EST_HUMAN	35167 0.56 0.0E+00 AW245765.1  EST_HUMAN	35168 2.62 0.0E+00 4758695 NT	35169 2.62 0.0E+00 4758695 NT	35172 0.52 0.0E+00 U88084.1 NT	35173 0.52 0.0E+00 U88084.1 NT	35238 1.02 0.0E+00 AJ251760.1 NT	35244 3 0.0E+00 X98922.1 NT	36245 3 0.0E+00[X98922.1 NT	35246 3 0.0E+00[X98922.1 [NT	35260 1.82 0.0E+00 U82979.1  NT	95305 1.16 0.0E+00 AF022856.1  NT	35306 1.16 0.0E+00 AF022856.1 NT -	35308 0.68 0.0E+00 AU131671.1 EST_HUMAN	35325 0.81 0.0E+00 11426572 NT	1.53 0.0E+00 AW513513.1 EST_HUMAN	0.66 0.0E+00 BE783232.1  EST_HUMAN	HUM084C0238 Ciontech human fetal brain polyA+ mRNA (#8535) Homo saplens cDNA clone GEN-084C028 Ciontech human fetal brain polyA+ mRNA (#8535) Homo saplens cDNA clone GEN-084C02 35328 11.32 0.0E+00 D52850.1 EST HUMAN   6*	35361 3.89 0.0E+00 BE378495.1	35365 3.98 0.0E+00 AA410545.1 EST_HUMAN	3.27 0.0E+00 BF313946.1 EST_HUMAN	10.0	35570 1 35 0 0 E-00 AW130873 1 EST HIMAN	35380 1.38 0.0E+00 AW139673.1   EST HUMAN		0.61 0.0E+00 AI640190.1 EST_HUMAN	35398 3.23 0.0E+00 BF377897.1   EST_HUMAN	35410 0.45 0.0E+00/AL163301.2 NT	35414 2.33 0.0E+00 BE260272.1 EST_HUMAN	35418 2.98 0.0E+00 BF700165.1   EST_HUMAN	35419
ORF SEQ ID NO:																		L													
D SEQ ID NO:	8778 21745		8779 21746		8783 21750	8783 21750	8851 21818			8856 21823		913 21879	8913 21879	916 21882	8931 21897	935 21901	8937 21903	8938 21904					204	8989 21955	L.	8994 21980	8013 21979	<b>.</b>		9033 21999	9033 21999
Probe SEQ ID NO:	æ	8	8	8	8	8	8	න්	భ	<b>S</b>	ಹ	ద	త	ĕ	85	8	8		S S	8	l &	Ľ	ع الم			& 	g	65	ه	٥	6

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acessian No.	Top Hit Datebase Source	Top Hit Descriptor
9033	1.	35420	2.98	0.0E+00	0.0E+00 BF700165.1	EST HUMAN	602127664F1 NIH_MGC_56 Homo septems cDNA done IMAGE:4284542 5
9047	22013		0.63	0.0E+00	0.0E+00 AI458722.1	EST_HUMAN	843h11.x1 NCI_CGAP_Li24 Homo sapiens cDNA cione IMAGE:2150949 3
9076	L			00+30.0	0.0E+00 AL449770.1	<b>EST_HUMAN</b>	AL 449770 Homo sepiens fetal brain (Stavrides GS) Homo sepiens cDNA
788	<u> </u>	ļ	12.96	0.0E+00	0.0E+00 AA962527.1	EST HUMAN	α60g02.s1 NCI_OGAP_Lu5 Hamo sepiens cDNA dane IMAGE:1602194 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
000	L			0.0E+00	10947037 NT	Ę	Homo sepiens enkyrin 1, erythrocytic (ANK1), trenscript verlant 1, mRNA
0606	1_		4.79	0.0E+00		F	Homo sapiens ankyrin 1, erytmocytic (ANK1), transcript ventant 1, mRNA
9114	L		1.23	0.0E+00	0.0E+00 Y11107.3	된	Homo sepiens ITGB4 gene for integrin beta 4 subunit, excris 3-41
916	<u> </u>		2.41	0.0E+00	0.0E+00 BE278917.1	EST_HUMAN	601158330F1 NIH_MGC_21 Hamo septems cDNA clane IMAGE:3139734 5
9128				0.0E+00	0.0E+00 AV718377.1	EST HUMAN	AV718377 FHTB Hamo sepiens cDNA clane FHTBAAF11 5
8433		25526		0.05	0.0E+00 AW337277.1	EST HUMAN	xw73c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2833644 3' similar to gbcX53687 INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN);
9138	L			0.0E+00	0.0E+00 AU124051.1	EST_HUMAN	AU124051 NT2RM2 Homo sapiens cDNA clone NT2RM2001575 5
9214	L	L		0.0E+00	0.0E+00 AU140704.1	EST_HUMAN	AU140704 PLACE4 Hamo septens cDNA clans PLACE4000089 5"
9224				0.0E+00	0.0E+00 AB007923.1	NT	Hamo saptems mRNA for KIAA0454 protein, pertial cds
8228	_		0.61	0.0E+00	0.0E+00 R17132.1	EST_HUMAN	yg09e09.rf Soares Infant brain 1NiB Homo sapiens cDNA clone IMACE:318745
8228	22195		0.61	0.0E+00	0.0E+00 R17132.1	EST HUMAN	yg03e09.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31674 5
9233				0.0E+00	0.0E+00 AW592233.1	EST_HUMAN	hA8e09.x1 Sogres_NFL_T_GBC_S1 Hamo sepiens aDNA clone IMAGE:2835096 3
8238	<u> </u>		5.11	0.0E+00	0.0E+00 AW 682233.1	EST_HUMAN	HARBOBLAT Scenes_NFL_T_GBC_S1 Hamo septens CUNA Game IMAGE: 2833060 3
8588	<u> </u>	ļ	0.48	0.0E+00	0.0E+00 AU128804.1	EST_HUMAN	AU128804 NT2RP2 Hamp sepiens cDNA dane NT2RP2804245 5
928	22247				0.0E+00 AV714784.1	EST_HUMAN	AV714764 DCB Homo septens cDNA clone DXCBAUA06 b
9236	l	35690	3.01		0.0E+00 AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: https://emo.sapiens.curv.com/bit/2p434C1814_s1
8238		35691	3.01	0.0E+00	0.0E+00 AL040428.1	EST HUMAN	DKFZp434C1814_e1 434 (synonym: https://dx.com/members.com/com/com/com/com/com/com/com/com/com/
8	1344	26897	127	0.05+00	0.0E+00 AF133001.1	Z	Homo septems killer imitationy receptor 2-2-1 (KIRZZ1) end kuler imitatory receptor 4-2-2 (KIRZZ2) genes, partial cds
208		L			0.0E+00 AB040945.1	F	Homo sapiens mRNA for KIAA1512 protein, partial cds
8310	1		224		0.0E+00 BF675505.1	EST_HUMAN	602138483F1 NIH_MGC_83 Hamo sapiens cDNA dane IMAGE:4274708 67
	ı	l					7K28b03.X1 NCI_CGAP_OV18 Home septens cDNA chine IMAGE:3476892 3' similar to TR:036448 036448
8312	7227		0.92		BF058289.	EST_HUMAN	S GAG;
8342		35733	4.84		11422857 NT	Ł	Homo sepiens tumor protein p73 (1P73), mrava
8352	22317	35743	1.44		0.0E+00 K01241.1	Z	Human ig reamanged H-chain epsiton-3 pseudogene, constant region
9361	L				0.0E+00 AB020630.1	노	Homo sapiens mRNA for KIAA0823 protein, partial cds
8384					0.0E+00 AB020630.1	노	Homo eaplens mRNA for KIAAU823 protein, partial ods
9988	Ш	35781	1.71		0.0E+00 AV660739.1	EST_HUMAN	AVEOUTS GLC Hamp septems alma dans Gluchnetz s

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Single Exon Probes Expressed in Bone Marrow

	Top Hit Descriptor	Homo saplens polycystin-L (PKDL), mRNA	V 601588304F1 NIH_MGC_7 Hamo sepiens cDIVA clane IMAGE:3942553 5				N 601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 6	Γ			Human polymorphic loci in Xq28	Human mRNA for GABA-A receptor, alpha 1 subunit	A AU127096 NTZRP2 Homo sepiems cONA clone NTZRP2000579 5		W434412.X1 NCI_CGAP_GC8 Home septens cDNA clone IMAGE:2473150 3' stmiler to SW:MGB3_HUMAN	Т	Т	7	T	Ť	I RATEO SECRETARIA M.C.C. 24 Home contains child chine BAACE Secretaria	Т		Homo sepiens mRNA for KIAA0578 protein, partial cds		Г	Г		Homo sapiens mRNA for KIAA0594 protein, partial cds	V EST50505 Gell bladder I Homo sapiens cDNA 5' end	V EST50505 Gall bladder I Homo saplens cDNA 5' end	be54d08.y3 NIH_MGC_10 Homo sepiens cDNA clone IMAGE:2800367 5' similar to TR:060275 060275 NIAA0522 PROTEIN;
	Top Hit Detabersa Source	TN	<b>EST_HUMAN</b>	TA	NT	<b>EST_HUMAN</b>	<b>EST_HUMAN</b>	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	٦	IN	EST_HUMAN	EST_HUMAN		NAME OF THE PERSON OF THE PERS	CET UIBAAN	FA FA	TOT CHANN	TOWNS TO SERVICE STATE OF THE	NOW IT INVOICE		EST_HUMAN	뇐	<b>EST_HUMAN</b>	EST HUMAN	EST HUMAN	<b>EST_HUMAN</b>	¥	EST_HUMAN	EST_HUMAN	EST_HUMAN
3.5	Top Hit Acession No.	7706838 NT	0.0E+00 BE793328.1	0.0E+00 AB033077.1	0.0E+00 AB033077.1	0.0E+00 H73937.1	0.0E+00 BE315402.1	0.0E+00 BE315402.1	0.0E+00 BE612721.1	0.0E+00 BE612721.1	0.0E+00 M89988.1	0.0E+00 X14786.1	0.0E+00 AU127098.1	0.0E+00 Al061395.1	106 1407 1	O.UE-TOO AIBOROVI.1	0 05 00 AWOE0944 4	AW BOOK II.I	A114400014	0.0E+00 AU142002.1	OUE+UN 11450885 IN O DE-LOO BE 410788 4 ES		0.0E+00 BF002024.1	0.0E+00 AB011150.1	0.0E+00 BE794823.1	1	Į.	0.0E+00 BE883843.1	0.0E+00 AB011168.1	0.0E+00 AA344601.1	0.0E+00 AA344601.1	0.0E+00 AW673469.1
	Most Similar (Top) Hit BLAST E Veitue	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	100	0.01100	00-200	0.05	20.00	0.05+00	0.00+08		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression	3.07	222	0.48	0.48	0.98	4.19	4.19	0.59	0.59	0.52	1.74	. 0.5	1.28		08.1	7	7.10	77.	44.	04.7		4.	1.25	4.85	4.5	1.36	1.36	0.77	3.53	3.53	1.02
	ORF SEQ ID NO:	36787	3 <i>211</i> 58		35774		36798		L			35819	35835	35839	9764	35000 87878	Sepen	34870	2000	2000	1000	1	36921	35837	35938	1	35950	Į	35967	17656	35972	
	Ean SEQ ID NO:	2882	22342	22343	L	$\mathbf{I}_{-}$	22366	22368	22378	97822		18622		22401		22444	┸	L	3 5 5 5	ᆚ	2000	L	22476	22480	L		22502		22619	22523	22523	22563
	Probe SED ID NO:	8872	8877	8278	8378	<b>889</b>	9401	<b>8</b>	9411	1148	9414	9416	9433	9437	3	2447	0460	876	3 3	\$ 2	8 8		9513	9527	9528	9634	9539	8838	1998	1958	1986	9619

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Table 4
Single Exon Probes Expressed in Bone Marrow

865 88 88 88 88 88 88 88 88 88 88 88 88 88	SEO D NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:	ORF SEQ ID NO: 0 N	So of the second		Top Hit Ace No. No. No. No. No. No. No. No. No. No.	Top Hit Database Source Source Source Source Source EST HUMAN EST	Top Hit Detabase Source Baskdabs, S NIH, MGC_10 Homo sapiens cDNA clone IMAGE-2800367 6 similar to TR:OBCZ76 O80276 EST_HUMAN KIAAGZ2 PROTEIN; EST_HUMAN Baskdabs, S NIH, MGC_71 Homo sapiens cDNA clone IMAGE-2820367 6 similar to pt.1.36049 Mus musculus EST_HUMAN Baskdabs, Camplete cds (MOUSE); EST_HUMAN Baskdabs, Camplete cds (MOUSE); EST_HUMAN GOZZ316011 MC_72 Famo sapiens cDNA clone IMAGE-2820036 7 similar to pt.1.36049 Mus musculus EST_HUMAN GOZZ31671 MIH_MGC_78 Homo sapiens cDNA clone IMAGE-2820036 7 similar to pt.1.36049 Mus musculus EST_HUMAN GOZZ31671 MIH_MGC_78 Homo sapiens cDNA clone IMAGE-2820036 7 Similar to pt.1.36049 Mus musculus EST_HUMAN GOZZ31671 MIH_MGC_78 Homo sapiens cDNA clone IMAGE-2820036 7 Similar to pt.1.36049 Mus musculus EST_HUMAN GOZZ31671 MIH_MGC_78 Homo sapiens cDNA clone IMAGE-2820036 7 Similar to pt.1.36049 Mus musculus EST_HUMAN GOZZ31671 MIH_MGC_78 Homo sapiens cDNA clone IMAGE-2820036 7 Similar to pt.1.36049 Mus musculus COZZ31671 MIH_MGC_78 Homo sapiens cDNA clone IMAGE-1820036 7 Similar to Start for Out-27204 Lub Homo sapiens cDNA clone IMAGE-182003 (FLIZ2504), mRNA GOTG-2747 OLIATATA PROTEIN L. Homo sapiens hypothetical CZH2 are fregar protein FLIZ2504 (FLIZ2504), mRNA GOTG-27467 OLIATATA PROTEIN L. Homo sapiens hypothetical CZH2 are fregar protein FLIZ2504 (FLIZ2504), mRNA GOTG-27467 OLIATATA PROTEIN L. Homo sapiens hypothetical CZH2 are fregar protein FLIZ2504 (FLIZ2504), mRNA GOTG-27467 OLIATATA PROTEIN L. Homo sapiens hypothetical CZH2 are fregar protein FLIZ2504 (FLIZ2504), mRNA GOTG-27467 OLIATATA PROTEIN L. Sacres MAGE resequence MAGC Homo sapiens cDNA chone IMAGE-1881298 8° similar to SW:PLZB_HUMAN GOTG-27409 BOTG-27467 ULB Homo sapiens cDNA chone IMAGE-1881298 8° similar to SW:PLZB_HUMAN GOTG-27409 BOTG-27409 BOTC-2740
8828	77822	36133	0.06		0.0E+00 BE885128.1	EST HUMAN	601510882F1 NIH_MGC_71 Homo sepiens cDNA clone IMAGE:3912165 57 601510882F1 NIH_MGC_71 Homo sepiens cDNA clone IMAGE:3912165 57
98238	2267	36134	22.2		0.0E+00 BE885128.1 0.0E+00 BE255829.1	EST_HUMAN	801109942F1 NIH MGC_16 Homo septens GUNA done IMAGE:336772 5
8840 8843	22778	36232 36232 36234	1.35	_	0.0E+00 BE781382.1 0.0E+00 BE781382.1 0.0E+00 AW103779.1	EST_HUMAN : EST_HUMAN : EST_HUMAN	601466828F1 NIH_MGC_67 Homo septens cDNA clone IMAGE:3870007 5 601466828F1 NIH_MGC_67 Homo septens cDNA clone IMAGE:3870007 5 au86c04.y1 Schneider fetal brain 00004 Homo septens cDNA clone IMAGE:2783142 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);

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Single Exon Probes Expressed in Bone Marrow

4				Most Similar		Tes His	
SEQ ID	SEO N SO S	ORF SEQ ID NO:	Expression Signal	(Top) Hit BLASTE Vælue	Top Hit Acession No.	Database Source	Top Hit Descriptor
9854	22790	36242	0.44	0.0E+00	0.0E+00 D87675.1	Nī	Homo sepiens DNA for amyloid precursor protein, complete cds
19867	22803	36257	3.12	0.0E+00	0.0E+00 BE263191.1	EST HUMAN	601145054F2 NIH_MGC_18 Homo septens cDNA clone MAGE:3160477 67
5885	22838	36283	4.11	0.0E+00	0.0E+00 C08158.1	<b>EST_HUMAN</b>	CO6159 Human pancreatic islet Homo sapiens cDNA clone hbc5605
8885	22838	36294	4.11	0.0E+00	0.0E+00 C00158.1	EST_HUMAN	C06158 Human pancreatio islet Homo sapiens cDNA clone hbc5605
8887			282	0.0E+00	BE746215.1	<b>EST_HUMAN</b>	601578683F1 NIH_MGC_9 Homo septems cDNA done IMAGE:3927548 5
9897	22850	36307	1.81	0.0E+00	11437282 NT	ΝI	Homo sepiens solute cerrier family 21 (organic enion transporter), member 9 (SLC21A9), mRNA
9897	22850	36308	1.81	0.0E+00	11437282 NT	NT	Homo sepiens solute center family 21 (organic enton transporter), member 9 (SLC2/A9), mRNA
9897	22850	36309	1.81	0.0E+00	11437282 NT	Į.	Homo sepiens solute carrier family 21 (organic enion transporter), member 9 (SLC21A9), mRNA
8917	22738	38191	1.40	0.0E+00	0.0E+00 BE900549.1	EST_HUMAN	601673425F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3856238 6
8835		36323	0.61	0.0E+00	0.0E+00 AV701829.1	EST_HUMAN	AV701829 ADB Homo sapiens cDNA clone ADBBYH01 6
8947	22874	36336	2.59	0.0E+00	0.0E+00 AF019084.1	Ę	Hamo sepiens keratin 2e (KRT2E) gene, complete cds
2047	L			0.0E+00	0.0E+00 AF019084.1	IN.	Homo septens learth 2e (KRTZE) gene, complete cds
888	L			0.0E+00	0.0E+00 BE082977.1	EST HUMAN	RC2-BT0642-130300-017-g01 BT0642 Homo sepiens cDNA
6666	22828			0.0E+00	0.0E+00 AW500283.1	EST HUMAN	UHIF-BNO-ekg-b-12-0-UI.rl NIH_MGC_60 Hamp septens cDNA clone IMAGE:3076943 57
6566	L			0.0E+00	0.0E+00 AW 500283.1	EST_HUMAN	UHHF-BNO-akg-b-12-0-UI.11 NIH_MGC_50 Hamo septens cDNA clane IMAGE:3076943 5
	L_						
10008	22885	36399	1.45	0.0E+00	0.0E+00 AF029308.1	MT	Homo sepiens chromosome 9 duplication of the T cell receptor beta locus and trypstnogen gene families
10008	22035	36400	1 45	0.05+00	0 OF +00 AF020308 1	5	. Homo seciens chromosome 8 dunication of the T cell recentor beta locus and thysthocen care families
10010	1		0.76	0.0E+00	0.0E+00 BE783272.1	EST HUMAN	601470824F1 NIH MGC 67 Homo septens dDNA dane IMAGE:3874037 6
10010	L.,	36402	0.76	0.0E+00	0.0E+00 BE783272.1	EST HUMAN	601470824F1 NIH_MGC_67 Homo septens cDNA done IMAGE:3874037 5
10019	L	<u> </u>		0.0E+00	0.0E+00 W56829.1	EST HUMAN	zd18e11.r1 Soares_fetal_heart_NbHH19W Homo septems cDNA clone IMAGE:340844 5
1001			0.52	0.0E+00	0.0E+00 W56829.1	EST_HUMAN	zd16e11.r1 Scenes_fetal_heart_NbHH19W Home septems cDNA clone IMAGE:340844 5
10032	52859	36427	1.05	0.0E+00	0.0E+00 AB035356.1	NT	Homo sapiens mRNA for neuradn Helpha protein, complete cds
10038	22963		99'0	0.0E+00	0.0E+00 AI124780.1	EST_HUMAN	am56a11.x1 Johnston frontal cortex Homo sepiens cDNA clone IMAGE:1539548 31
10038	22965		2.73	0.0E+00	0.0E+00 AW500528.1	EST_HUMAN	UHIF-BNO-alg-c-07-0-U.r.1 NIH_MGC_60 Homo septems cDNA clane IMAGE:3077384 6
10082	23009		1.51	0.0E+00	0.0E+00 AF009688.1	Nī	Multiple sclerosts associated retrovirus polyprotein (pd.) mRNA, partial cds
10109	-23035	38512	282	000	0.0E+00 S78468.1	IN	AIGF=androgen-induced growth factor AIGF litumen, piecenta, GenomichmRNA, 498 nt. segment 5 of 5]
	1						
10109				0.0E+00		¥	AIGF=androgen-Induced growth factor AIGF (human, placenta, GenomichmRNA, 498 nt, segment 5 of 5)
10112				0.0E+00	0.0E+00 BE563320.1	EST HUMAN	601334603F1 NIH_MGC_39 Hamp septems dDNA clane IMAGE:3688680 5
10132				0.0E+00	0.0E+00 AW363135.1	EST_HUMAN	CM2-CT0311-301199-043-h11 CT0311 Hamp septems cDNA
10152	23077	36553	0.61	0.0E+00	11436432 NT	¥	Homo sapiens multimerin (MMRN), mRNA

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Single Exon Probes Expressed in Bone Marrow

ORF SEQ Expression (Top) Hit Top Hit Accession D NO: Signal BLASTE No. Source	36554 1.71 0.0E+00 11424387 NT	36564 0.82 0.0E+00 BE206710.1 EST_HUMAN	36583 2.6 0.0E+00 AU132340.1 EST_HUMAN	36584 2.6 0.0E+00 AU132349.1 EST_HUMAN	36596 1.82 0.0E+00 AW500836.1 EST_HUMAN	86802 18.11 0.0E+00 BE740490.1 EST_HUMAN	36603 16.11 0.0E+00 BE740490.1 EST_HUMAN	36804 0.45 0.0E+00 AB033057.1 NT	36605 0.45 0.0E+00 AB033057.1 NT	36818 1.78 0.0E+00 7682067 NT	36838 3.6 0.0E+00 AL042278.1  EST_HUMAN	36844 0.71 0.0E+00 AL041084.2 EST_HUMAN	36851 2.57 0.0E+00 AU132349.1 EST_HUMAN	36652 2.44 0.0E+00 AF152308.1 NT	36880 5.52 0.0E+00 AF009220.1 INT	36881 5.52 0.0E+00 AF009220.1 NT	36694 2.5 0.0E+00 BF082898.1   EST_HUMAN	36720 2.73 0.0E+00 BE280783.1 EST_HUMAN	36726 12 0.0E+00 BE388700.1   EST_HUMAN	36727 1.2 0.0E+00 BE388700.1 EST_HUMAN	36733 3.64 0.0E+00 AW236289.1 EST_HUMAN	36734 0.75 0.0E+00 AA341305.1 EST HUMAN	36745 0.63 0.0E+00 11427235[NT	36763 0.75 0.0E+00 AW964113.1   EST_HUMAN	36774 7.08 0.0E+00 AU143673.1  EST_HUMAN	36775 7.08 0.0E+00 AU143673.1  EST_HUMAN	36778 13.11 0.0E+00 AF072408.1 NT	36780 2.8 0.0E+00 11421001 NT	36781 2.8 0.0E+00 11421001 NT	36824 3.43 0.0E+00 AU136637.1 EST_HUMAN	36825 3.43 0.0E+00 AU136837.1 EST_HUMAN	36839 2.24 0.0E+00 AJ295844.1 NT Homo sapients partial NANBY / gene for Kanby / Important and partial ANY 9416
ORF SEQ ID NO:	38554	36564	36583	36584	36596	36802	38603	36804	36605	36618	36638	36844	36851	36652	36680	36681	36694			36727	36733							_				
Exan SEQ ID NO:	323078	_		L				L	<u> </u>		L	L		L		!		<u> </u>	<u> </u>	23247		L	42 23268	L			<u>.                                    </u>		L			
Probe SEQ ID NO:	10153	10162	10178	10178	10187	10183	10183	10194	10194	10208	10224	10220	10239	10240	18	10268	18	Įδ	10323	<b>5323</b>	10332	<b>5</b> 833	10342	10363	10376	10378	ខ្លើ	10382	10382	10416	10418	10432

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Probe SEQ ID NO:	Exam ORF SEQ SEQ ID NO:	EQ Expression Signal	Moet Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
10432	23354 368	36840 2.24	0.0E+00	0.0E+00 AJ295844.1	N	Homo capiens partial RANBP7 gene for RanBP7//mportin7 and partial ZNF143 gene
10437	23359 368	36847 0.75		0.0E+00 AV695712.1	EST_HUMAN	AV695712 GKC Homo sepiens cDNA done GKCDXA07 5
10437		36848 0.75		0.0E+00 AV695712.1	EST_HUMAN	AV695712 GKC Homo sepiens cDNA done GKCDXA07 5
10443	23365 368	36855 0.76	0.0E+00	0.0E+00 AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
		36858 2.64	0.0E+00	0.0E+00 AA196387.1	EST_HUMAN	과양7h11.r1 Strategene muscle 837.209 Homo sepiens cDNA clone IMAGE:628197 5
		87 1.78		0.0E+00 AA131248.1	EST_HUMAN	231f01.r1 Scares_pregnent_uterus_NbHPU Homo saplens cDNA clone IMAGE:503545 5'
10470	23392 36888	388 1.78	0.0E+00	0.0E+00 AA131248.1	EST HUMAN	zistifoturi Scenes_pregmant_uterus_NibHPU Homo saptens cDNA clone IMACE::503545 5*
	28439 36937	1.79	0.0E+00	0.0E+00 AF179308.1	IN	Homo sapiens KIF4 (KIF4) mRNA, complete cds
10581 2	23483 36978	978 0.88		0.0E+00 BE880658.1	EST_HUMAN	801481565F1 NIH_MGC_89 Hamp sepiens aDNA dane IMAGE:3883867 5
	23496 36987	11.49	Ĺ	0.0E+00 BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Hamo sapiens cDNA clone IMACE;3845403 6
10573 2	23495 36988	388 11.49	0.0E+00	0.0E+00 BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Hamo septens cDNA clone IMAGE:3845403 5
	23500 36992	392 0.62	0.0E+00	0.0E+00 AU127403.1	EST_HUMAN	AU127403 NT2RP2 Homo seplens cDNA clone NT2RP2001212 5
					EST_HUMAN	801645134F1 NIH_MGC_56 Hamo sepiens cDNA clone IMAGE:3830177 5
					EST_HUMAN	601645134F1 NIH_MGC_58 Hamo septens cDNA clone IMAGE:3930177 5
	23527 37023			0.0E+00 BE897487.1	EST_HUMAN	601432317F1 NIH_MGC_72 Hamo septens cDNA clane IMAGE:3917453 5
	23588 37037	37 0.68		0.0E+00 AA311624.1	EST_HUMAN	EST182353 Jurkat T-cells VI Homo septens cDNA 5' end
	23539 37038	38 0.56		4758827 NT	NT	Homo sapiens neurakin III (NRXNS) mRNA
				0.0E+00 BE891113.1	EST_HUMAN	601432228F1 NIH_MGC_72 Homo septens cDNA clone IMAGE:3917598 5
				11560151 NT	Ŋ	Homo sepiens hypothetical C2H2 zinc finger protein FL/22504 (FL/22504), mRNA
	23564 37060	1.39	0.0E+00		M	Homo sapiens mRNA for actin binding protein ABP020, complete cds
10643 2	23565 37061	190 0.6	0.0E+00	0.0E+00 BE304622.1	EST_HUMAN	601105459F1 NIH_MGC_15 Hamo saplens cDNA clane IMAGE:2887918 5
10643 2	23566 37062	0.6		0.0E+00 BE304522.1	EST_HUMAN	601105459F1 NIH_MGC_15 Hamo septens cDNA clone IMAGE:2987918 5
10650 2					Ę	Homo sapiens mRNA for estragen receptor bela, complets cds
	23572 37068	88 4.13		0.0E+00 AB008590.1	NT	Homo septens mRNA for estrogen receptor beta, complete cds
						2/16b08.e1 Scares_fetal_fiver_spleen_1NFLS_S1 Homo sepiens cDNA clone INAGE:450707 3' similar to
	23580 37077	1.27	0.0E+00	0.0E+00 AA704457.1	EST_HUMAN	gb:M4123_cds1 RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN);
	23582 37078	1.19	0.0E+00		NT	Human beta 1.4-galactosy-transferase mRNA, complete cds
	23584 37081	181 4.52	0.0E+00	0.0E+00 BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Bm84 Homo saplens cDNA clone IMAGE:4184939 5'
	23584 37082	982 4.62	0.0E+00	0.0E+00 BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Bm84 Hamo septens cDNA clane IMAGE:4184939 6
10687 2	23609 37103	103 5.24	0.0E+00	0.0E+00 BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sepiens cDNA clone IMAGE;3924578 5
			0.0E+00		EST_HUMAN	601439713F1 NIH_MGC_72 Homo sepiens cDNA clone IMAGE:3824578 5
	23641 37134				EST_HUMAN	AV716271 DCB Homo capiens aDNA clane DCBBDC09 5
10719 2	23641 . 37135	135 0.48		0.0E+00 AV716271.1	<b>EST_HUMAN</b>	AV716271 DCB Homo sapiens cDNA clane DCBBDC09 5'

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ORF SEQ Expression (Top) Hit Top Hit Acession Signer BLASTE No. Source	37511 1.81 0.0E+00 11431124[NT	37516 1.76 0.0E+00 AW057821.1 EST_HUMAN	37520	37521 2.54	37522 2.54 0.0E+00 AI652239.1 EST_HUMAN	37525 2.13 0.0E+00 BF306842.1   EST_HUMAN	37531 3.83 0.0E+00 11545911 NT	37532 3.83 0.0E+00 11545911 NT	37541 5.31 0.0E+00 AW404795.1  EST_HUMAN	37544 2.69 0.0E+00 11424829 NT	37545 7.34 0.0E+00 4504536 NT	37546 7.34 0.0E+00 4504536 NT	97547 2.71 0.0E+00 A1991827.1 [EST_HUMAN	37651 1.64 0.0E+00 BE882109.1  EST_HUMAN	37553 21.37 0.0E+00 BE891630.1  EST_HUMAN	37554 4.59 0.0E+00 8923939 NT	37555 4.59 0.0E+00 8923939 NT	2962 32161 6.67 0.0E+00 AA195806.1 EST HUMAN  MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);		37586 100.2 0.0E+00/AA808080.1 (EST_HUMAN	37587 4.22 0.0E+00 BE-793488.1 EST_HUMAN	37595 15.77 0.0E+00 AV727382.1 EST_HUMAN	37596 15.77 0.0E+00 AV727362.1 EST_HUMAN	37813 14.2 0.0E+00 AA484318.1 EST HUMAN	37618 24.28 0.0E+00 AW516055.1 EST HUMAN	37623 1.88
													·													
Exam SEQ ID NO:	23984	3 23088	<u> </u>	<u> 1</u>	<u> </u>	L		1 24005	5 24018	B 24021	24022		0 24023	3 24026	8 24029	8 24031	8 24031	3 18962	丄		_1	3 24073	3 24073	8 24086		
Probe SEQ ID NO:	11019	11023	11029	11030	11030	11034	11041	11041	11055	11058	11059	11050	11060	11063	11068	11068	11068	11083		11103	1.02	11113	11113	11128	11129	11134

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	Top Hit Descriptor	hg13d02x1 Soares_NPL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2946476 3' similar to contains element MSR1 repetitive element;	hg13d02x1 Soares_NPL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2845475 3' similar to contains element MSR1 repetitive element;	hg13d02xt Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2845476 3' similar to contains element MSR1 repetitive element;	H. saptens mRNA for H1 histarnine receptor	HSC3IO031 normalized infant brain cDNA Homo sapiens cDNA clone c-3ic03	Homo septens timmunoglobulin kepper-chein A14 V-region precursor (IGKV) gene, pertiel cds	Homo sapiens immunoglobulin kappa-chain A14 V-region precursor (IGKV) gene, partial cds	xw66f01 x1 NCI_CGAP_Pan1 Homo sepiens cDNA clone IMAGE:2832885 3' similar to gb:X17115 IG MU CHAIN C REGION (HUMAN);	HBI3-clh-e-01-0-UI.s1 NCI_CGAP_Sub5 Homo saptens cDNA clone IMAGE:2736849 3'	UI-H-BIS-eth-e-01-0-UI.s1 NCI_CGAP_Sub5 Hamo septens cDNA clane IMAGE:2736849 3'	Homo sepiens ribosomal protein L31 (RPL31) mRNA	601119248F1 NIH_MGC_17 Hamo septens cDNA clane IMAGE:3028219 5	Homo expiens mRNA for KIAA0545 protein, perilial ods	Homo septens of cardiac alpha-myosin heavy chain gene	601183824F1 NIH_MGC_7 Homo septens cDNA clone IMAGE:3538012 5	601582046F1 NIH_MGC_7 Homo septens dDNA clone IMAGE:3838639 6	802/41405F1 NIH_MGC_48 Hamo septiens cDNA clane IMAGE:4302432 5	AU118388 HEMBA1 Homo septiens cDNA clone HEMBA1003486 5	xn72b01x1 NG_CGAP_CML1 Homo sepiens dDNA done IMAGE-2898977 3' similar to gb:X02162_ods1 L- LACTATE DEHYDROGENASE M CHAIN (H:UMAN);	qr43c03.x1 Soares_testis_NHT Homo septens cDNA clone IMAGE:1752772.3'	qf43c03.x1 Soares_testis_NHT Homo septens cDNA clone IMAGE:1752772.3°	QV4-ST0234-121189-032-b08 ST0234 Homo septems cDNA	AU116908 HEMBA1 Homo sapiens cDNA clone HEMBA1000255 5	Homo sapiens insulin receptor (INSR), mRNA	QVD-UMD083-170400-191-d08 UM0083 Hamo sapiens aDNA	QV0-UMD083-170400-191-d06 UMD083 Hamo sepiens cDNA	602037014F1 NCI_CGAP_Bm84 Hamo septens cDNA clane IMAGE:4184979 5	601148357F1 NIH_MGC_19 Homo septems CDNA clone IMAGE:3163310 5	Homo sepiens mRNA for KIAA1117 protein, pertial cds
	Top Hit Database Source	EST_HUMAN el	EST_HUMAN 6			EST_HUMAN H		NT H	EST_HUMAN C	EST_HUMAN U	EST HUMAN U		EST_HUMAN 6	NT	NT H	EST_HUMAN 6		EST_HUMAN   0	EST_HUMAN A	EST HUMAN	П	EST_HUMAN   9	EST_HUMAN Q	T_HUMAN		EST_HUMAN O	EST_HUMAN O	EST_HUMAN 6	T_HUMAN	H L
2 26110	Top Hit Acession No.	0.0E+00 AW 593333.1	0.0E+00 AW 583333.1	0.0E+00 AW583333.1			0.0E+00 M27751.1	0.0E+00 M27751.1	0.0E+00 AW338094.1	0.0E+00 AW451230.1	0.0E+00 AW451230.1	06632	0.0E+00 BE298449.1	0.0E+00 AB011117.1	0.0E+00 Z20656.1	0.0E+00 BE264885.1	0.0E+00 BE792155.1	0.0E+00 BF684061.1	0.0E+00 AU118388.1	0.0E+00 AW 236269.1	0.0E+00 AI149809.1	0.0E+00 AI149809.1	0.0E+00 AW391937.1	AU1160	11424728 NT	0.0E+00 AW804516.1	0.0E+00 AW804516.1	0.0E+00 BF340308.1	0.0E+00 BE281209.1	0.0E+00 AB029040.1
	Most Similer (Top) Hit BLAST E Value	0.0E+00	0.000	0.05+00	0.0E+00 Z34897.1	0.0E+00 F13069.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	3.36	3.36	3.38	1.88	254	2.4	2.4	40.1	3.64	3.54	8.04	2.07	2.13	- 88:	1.88	<u>1</u>	70.33	7.68	251	4.92	4.82	2.09	1.54	823	145.89	145.89	3.26	49.67	1.74
	ORF SEQ ID NO:	37626	37627	37628	37629	37630	37643	37844	37654	37666	37656		37674	37682	37686	37690	37696		37698		37702	37703	37704		37710	37716		37718	37721	37726
	SEQ ID	24089	24089	24099	24101	24102	24117	24117	24125	24128	24128	13316	24140	24151	24154	24160	[_	24168	24170	24171	L	L	24177	24187	24191	24197	24197	24198	24200	24204
	Probe SEO ID NO:	11139	11139	11130	11141	11142	11159	11159	11167	11188	11168	1178	1184	11186	11189	11206	11214	11215	11217	11218	11223	11223	11224	11234	11238	11244	11244	11245	11247	11251

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Table 4
Single Exon Probes Expressed in Bone Marrow

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Table 4
Single Exon Probes Expressed in Bone Marrow

24427 37 244	\$6.55 au			Single E  No.  No.  No.  No.  No.  No.  No.  No	Top Hit Detabase Source Source Source Source Source EST_HUMAN EST_	gile Exon Probes Expressed in Bone Marrow  Top Hit Deachbur  Sacra  Sacr
	통으	37824 37824 37824 37832 37832 37847 37872 37872 37872 37872 37872 37876 37877 37876 37877 37876 37877 37876 37877 37876 37877 37876 37877 37877 37876 378777 3787	ORF SEQ Expression D NO: Signal 37924 4.83 37927 4.18 37932 4.18 37932 4.18 37932 2.91 37932 2.91 37932 2.91 37932 2.91 37932 3.38 37937 5.09 37972 5.09 37972 5.09 37973 3.38 37973 2.91 37978 3.38 37977 3.54 37978 3.38 37978 2.13 37978 3.38 37978 5.09 37978 3.38 37978 5.09 37978 5.09 37977 7.64 38024 1.51 38024 1.51 38056 5.23 38056 17.24	ORF SEQ Expression (Tildes)  ORF SEQ Expression (Tildes)  37824 4.83  37824 4.83  37822 4.18  37822 4.18  37822 2.91  37822 3.54  38022 3.54  38052 1.24  38052 1.24	Signal Most Shriller Top Hit Ace (Top) Hit Top Hit Hit Ace (Top) Hit Ace (Top) Hit Hit Ace (Top) Hit Ace (Top) Hit Ace (Top) Hit Ace (Top) Hit Ace (Top) Hit Ace (Top) Hit Ace (Top) Hit Ace (Top) Hit Ace (Top) Hit Ace (Top) Hit Ace (Top) Hit Ace (Top) Hit Ace (Top) Hit Ace (Top) Hit Ace (Top) Hit Ace (Top) Hit Ace (Top) Hit Ace (Top) Hit Ace (To	Dec

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID	Exan SEQ ID	ORF SEQ	Expression	Most Similar (Top) Hit	Top Hit Acession	Top Hit Destabese	Top Hit Descriptor
Ö	Ö	<u>.</u>		Value		Source	
11571			5.42	0.0E+00	0.0E+00 BF240536.1	EST_HUMAN	601875630F1 NIH_MGC_55 Hamo septems cDNA clane IMAGE:4069710 5
11582		38075	1.68	0.0E+00	0.0E+00 AB037737.1	NT	Homo saplens mRNA for KIAA1316 protein, partial cds
11582	L	38078	1.68	0.0E+00	0.0E+00 AB037737.1	NT	Homo septens mRNA for KIAA1316 protein, partial cds
11686	<u>.                                    </u>	38079	3.41	0.0E+00	11430868 NT	Ę	Homo sapiens retinchlastome-like 2 (p130) (RBL2), mRNA
11588		38080	3.41	0.0E+00	11430868 NT	E	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11500	24528	39085	206	0.05+00	0 0F+00 BF122784 1	EST HAIMAN	23_08 Human Epidemnal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sepiens cDNA done 23_08.5 smillar to Homo sepiens curin 82_023489.
							bb73405.vf NIH MGC 12 Homo sepiens cDNA clone IMAGE:3048057 5' similar to SW:CD97 HUMAN
11591	24529	38086	323	0.0E+00	0.0E+00 BE017960.1	EST_HUMAN	P48960 LEUCOCYTE ANTIGEN CD97 PRECURSOR. [1];
11595		38086	2.69	0.0E+00	0.0E+00 AA772837.1	EST_HUMAN	ae74g04.81 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:869942 3'
11605	24543	38103	6.4	0.0E+00	4603544 NT	NT TN	Homo sepiens eukaryotic translation initiation factor SA (EIFGA) mRNA
11612	24550	38110	2.25	0.0E+00	0.0E+00 BF576267.1	<b>EST_HUMAN</b>	602134132F1 NIH_MGC_81 Homo septems cONA clone IMAGE:4288502 5
11615		38114	5.5	0.05+00	3.1	EST_HUMAN	dr04g05.x1 NIH_MGC_3 Homo saplens cDNA clone INAGE:2847177 5
11620	24558		6Z 88	0.0E+00		Į.	Human gamma actin-like pseudogene, complete cds
							wf20e11.x1 Soares_Dieckgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351180 3' similar to
11624	1		25	0.0E+00		EST_HUMAN	gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
11625				0.0E+00		. 4	601889823F1 NIH_MGC_17 Homo sepiens cDNA clone IMAGE-4123948 5
11625			23	0.0E+00	0.0E+00 BF306986.1	EST_HUMAN	601889823F1 NIH_MGC_17 Hamo sepiens cDNA done IMAGE:4123948 67
11632			13.62	0.0E+00	2.1	EST_HUMAN	QV2-NIN0054-230800-333-604 NN0054 Homo sepiens cDNA
11648		38154	2,42	0.0E+00 U36264.1		K	Human beta-prime-edeptin (BAMZZ) gene, exon 16
11648		38155	2.42	0.0E+00 U38284.1		NT	Human beta-prime-edeptin (BAM22) gene, exon 16
11654	24591		4.74	0.0E+00	0.0E+00 BE897051.1	EST_HUMAN	601439805F1 NIH_MGC_72 Hamp septens cDNA done IMAGE:3824577 6
11665	24601	38177	1.54	0.0E+00	1N 8923698	Ę	Homo saplans golgin-like protein (GLP), mRNA
11688	24604		224	0.0E+00	0.0E+00 BF207682.1	EST_HUMAN	601861947F1 NIH_MGC_63 Homo septens cDNA clone IMAGE:4081715 67
11669	24605		787	0.0E+00	0.0E+00 BE257744.1	EST_HUMAN	601116705F1 NIH_MGC_16 Hamo septems aDNA dane IMAGE:3357384 5
							ba04d07.y1 NIH_MGC_7 Homo suplens cDNA clone IMAGE:2823373 5' similar to TR:078022 076022 E1B-
11682	24648	38226	4.13	0.0E+00	0.0E+00 BE206848.1	EST HUMAN	55KDA-ASSOCIATED PROTEIN.;
-				Ţ		1000	bs0407.y1 NIH_MGC_7 Home sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 076022 E1B/ perch Associated Bootenia .
8		ŀ		O.OE-400	]	Т	WALATAN LATER TO THE TOTAL TO T
11684	24650	38228	3.8	0.05+00	0.0E+00 AW /53028.1	ESI_HUMAN	CVV-C 10225-101226-071-00 C 10225 From seprens GUNA
11680	24655		4.98	0.0E+00	0.0E+00 AA558707.1	EST HUMAN	nl42c08.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M95178 ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);
11680	L	31322		0.0E+00	Γ	EST HUMAN	wp08g08x1 NCI_CGAP_Kd12 Homo sepiens cDNA clone IMAGE:2484094 S'
168	辶			0.0E+00	Ļ	EST HUMAN	dr02b08.x1 NIH_MGC_3 Homo septens cDNA clone IMAGE-2846919 67
						1	

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Single Exon Probes Expressed in bottle mairon	Most Similar  Expression (Top) Hit Top Hit Acession Signal BLASTE No. Source	1.83 0.0E+00 AW 282778.1 EST_HUMAN	37432 2.09 0.0E+00 4758827/NT Homo saplens neurewin III (NRXN3) mPNA	2.43 0.0E+00 BE985909.2 EST_HUMAN	2.43 0.0E+00 BE965909.2 EST_HUMAN	38188 3.67 0.0E+00 BE186656.1 EST_HUMAN ILE-HT0731-020500-077-f05 HT0731 Homo septens cDNA	1 EST_HUMAN	5.4 0.0E+00 ALD46540.1 EST_HUMAN	2.29 0.0E+00 BF082504.1	98214 19.22 0.0E+00 A1923118.1 EST_HUMAN RECEPTOR (HUMAN);			38280 8.71 0.0E+00 AA780913.1 EST HUMAN Q13886 ALKB HOMOLOG PROTEIN.;	3.51 0.0E+00 BE910548.1 EST_HUMAN	37440) 5.45 0.0E+00 BE678347.1 EST HUMAN CHECKPOINT SUPPRESSOR 1.;	2.02 0.0E+00 BE615868.1 EST HUMAN	2.02 0.0E+00[BE615666.1 EST_HUMAN	2.13 0.0E+00 AV757420.1 EST_HUMAN	38273 5.01 0.0E+00 L39891.1 NT Homo sapiens polycystic iddney disease-essociated protein (PKD1) gene, complete ods	5.01 0.0E+00 L39891.1  NT	.1 EST_HUMAN	.1 EST HUMAN	I EST_HUMAN	1 EST_HUMAN		2.54 0.0E+00 AU141882.1 EST_HUMAN	0.0E+00 AU141882.1 EST_HUMAN	187	O O OFTEN DEPOSES 4 EST 14 IMAN	1 AR O DE-100 AS 1 FST HIMAN	ויאס ויאס ויאס ויאס ויאס ויאס ויאס ויאס
	ORF-SEQ Expr				١.							2000	38260					ļ										·	1		j
	SEQ ED	25706	<u></u>	L	乚		L	24624			1		24681	1_		1_	1_	L	L	24683		24718	24742	24750		24759	24759	24762	Ĺ	24780	1
	Probe SEQ ID NO:	41711	11718	11724	11724	11725	11739	11730	11746	11750	44769	3	11753	11758	11788	11789	11769	41777	11808	11808	11822	11835	11860	11868	11888	11877	11877	11880		11002	3

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Single Exon Probes Expressed in Bone Marrow

Probe SEO ID	Eson SEO ID	ORF SEQ	Espression	Most Similar (Top) Hit	Top Hit Acession	Top Hit Database	Top Hit Descriptor
Ö		Ö Q	Signa	BLASTE Value	<u>d</u>	Source	
11899	24780	38367	1.48	0.0E+00	0.0E+00 AL043705.1	EST_HUMAN	DKFZp434L1227_r1 434 (synonym: htss3) Hamo septens cDNA clane DKFZp434L1227 6
11904	24785		3.36	0.0E+00.	0.0E+00 AW387776.1	<b>EST_HUMAN</b>	MR4-ST0118-261089-012-b03 ST0118 Homo septens cDNA
11904	24785	38376		0.0E+00	0.0E+00 AW387776.1	<b>EST_HUMAN</b>	MR4-ST0118-261089-012-b03 ST0118 Homo septems cDNA
11916	24797		2.43	0.0E+00	0.0E+00 AW863777.1	<b>EST_HUMAN</b>	MR3-SN0010-310300-107-h03 SN0010 Homo septens cDNA
11927	24808	38402	4.22	0.0E+00	11435244	NT	Homo saplens KIAA0247 gene product (KIAA0247), mRNA
11927			4.22	0.0E+00	11435244 NT	NT	Homo sepiens KIAA0247 gene product (KIAA0247), mRNA
11982	24813	38409		0.0E+00 U38253.1		NT	Human beta-prime-adaptin (BAMZ2) gene, excn 5
11834	24815			0.0E+00	0.0E+00 BE379254.1	<b>EST_HUMAN</b>	601237691F1 NIH_MGC_44 Homo septens cDNA dane IMAGE3608623 5
11834	24815	38412	2.03	0.0E+00	0.0E+00 BE378254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo saplens cDNA done IMAGE:3608623 5
11946	20655	34019	142	0.0E+00	0.0E+00 AA211563.1	EST HUMAN	zn5602.r1 Strategene muscle 937209 Homo septens cONA clone IMAGE:562203 6' similer to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
	<u> </u>						8856g11.s1 NCI_CGAP_GCB1 Homo sepiens cDNA clone IMAGE:824900 3' similar to gb:M37766 B-
11947		38421	236	0.0E+00	0.0E+00 AA488894.1	EST_HUMAN	LYMPHOCYTE ACTIVATION MARKER BLAST-1 PRECURSOR (HUMAN);
11952		38427	2.35	0.0E+00	0.0E+00 BE794758.1	EST_HUMAN	801580588F1 NIH_MGC_7 Home septems cDNA ctone IMAGE:3944708 5
11953	24832	38428	160.92	0.0E+00	0.0E+00 BE879633.1	EST_HUMAN	601491821F1 NIH_MGC_69 Hamo septens dDNA done IMAGE:3894220 5
11965	24844	38439	12.66	0.0E+00	0.0E+00 BE409993.1	EST_HUMAN	601209403F1 NIH_MGC_21 Homo sepiens cDNA clone IMAGE:3629544 67
41068	24845	UFF86	30.0	001100	0.05400 45223391 1	5	Homo sapions calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively solired
		2	2	3	1.1000		House of the state
11888	24845	38441	225	0.0E+00	0.0E+00 AF223391.1	M	indno sapens calcum channel abhan E subum (CACNATE) gene, exons 7-49, and panas cos, aramanvery spiced
11967	18647	31589		0.0E+00 D28835.1		NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
11967	18647	31590	122	0.0E+00 D26635.1		M	Human gane for dihydrolipoamida succinyfiransfarasa, completa cds (exon 1-15)
11968	Ш		4.01	0.0E+00	0.0E+00 BF681641.1	EST_HUMAN	602155722F1 NIH_MGC_83 Hamo sepiens dDNA done IMAGE:4286725 6
11968			4.01	0.0E+00	1	EST_HUMAN	802155722F1 NIH_MGC_83 Hamo sepiens cDNA dane IMAGE:4286725 5
11974	18348	31204	1.51	0.0E+00	1	NT	Homo sapiems gaphyrin mRNA, complete cds
11978		38451	1.67	0.0E+00	1	EST_HUMAN	AU132940 NTZRP4 Homo sepiens oDNA cione NTZRP4000629 67
11979	24856	38453	4.83	0.0E+00	0.0E+00 BE903372.1	EST_HUMAN	601676357F1 NIH_MGC_21 Homo septens cDNA done IMAGE:3958635 5
11992	24869	38484	3.47	0.0E+00	0.0E+00 BF312552.1	EST_HUMAN	601897324F1 NIH MGC_19 Hamo septems cDNA clane IMAGE:4127069 5
11992	24869	38465	3.47	0.0E+00	0.0E+00 BF312552.1	<b>EST_HUMAN</b>	601897524F1 NIH_MGC_19 Hono sapiens cDNA done IMAGE:4127089 5
11994	24871	38467	34.13	0.0E+00 X51755.1		NT	Human lambda-Immunoglobulin constant region complex (germine)
11994	24871	38468	34.13	0.0E+00 X51755.1		M	Human lambda-immunoglobulin constant region complex (germtine)
12008			3.04	0.0E+00	اب	EST_HUMAN	601488533F1 NIH_MGC_70 Hamo septems cDNA clane IMAGE:3900396 5
12007		38479	1.52	0.0E+00	_	EST HUMAN	601433908F1 NIH_MGC_72 Hamo septens aDNA dane IMAGE:3919321 5
12035	25708		56.85	. 0.0E+00	0.0E+00 BF309120.1	EST_HUMAN	601690534F1 NIH JMGC_17 Hamo sepiens cDNA done IMAGE:4131416 5

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Single Exoli Plobes Expressed in Bolie Mailow	Top Hit Acession Database No. Source	0.0E+00 BE698891.1 EST_HUMAN RC4-NN0025-120600-016-b07 NN0025 Homo sapiens cDNA	0.0E+00 BE698861.1	0.0E+00 BE29775.1 EST_HUMAN 601177407F1 NIH_MGC_17 Homo septens cDNA clone IMAGE:3532968 5	EST_HUMAN	0.0E+00[BE744311.1   EST_HUMAN   601578525F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE:3837222 5	7869505 NT		0.0E+00 11024711 NT Homo saptens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #836215. Homo saplans cDNA clone 0.0E+00 P00884.1 EST HUMAN 77E12		1 EST_HUMAN	1 EST HUMAN	4.1 EST_HUMAN		0.0E+00 BE284998.1 EST_HUMAN 601193827F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3637774 6	1 EST_HUMAN	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon (NFKBIE), 0.0E+00 11419020 NT mRNA	Homo septens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epstion (NRKBIE),	DE342542 4 EST HIMAN	MT	EST_HUMAN	7	0.0E+00 A148246.2 NT Homo captens dromosome 21 segment HS210048	117862 NT	0.0E+00 5802973 NT Homo sapiens enticoddant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA		1 EST_HUMAN	418318 NT	0.0E+00/AL046544.1   EST_HUMAN   DKFZp434GZ18_r1 434 (synonym: Mes3) Homo sapiens CDNA clane DKFZp434GZ18 5
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	20.70	0.05100	0.0	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	238	2.38	60.15	1.81	1.81	1.81	1.81	1.06	241	2.41	6.46	3.24	3.24	2.15	227	227	6.45		0.40	2	6.62	1.33	228	5.82	3.47	206	4.42	3.76	5.96
	ORF SEQ ID NO:	38505	38506	38509	38517	38518	38531	38532	38535	38537	38538	38544	38547	38548	38590	38595		38605		34300							31523	L		
	SEQ ID	24912	24912	24915	_	Ĺ	24935	24636	24940	24944	24944	24940	l	24952	24688	24983	24983	25000	1	02030	L	25828	25022	1	l		l		L	Ш
	Probe SEQ ID NO:	12037	12037	12040	12048	12048	12062	12062	12067	12071	12071	12071	12080	12080	12118	12124	12124	12131		12131	121m	12163	12173	12192	12201	12218	12251	12265	12291	12289

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Single Exon Probes Expressed in Bone Marrow

			yw40e08.s1 Soares fetal liver spiesn 1NFLS Homo sepiens cDNA clone IMAGE:245222 3' similer to SW:POL_BAEVM P10272 POL YPROTEIN;	T	Homo sapiens T-cell lymphome investon and metastasts 1 (TIAMI) mRNA	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIÁMI) mRNA	Homo sepiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mPNA	Homo sapiens X-linked anhidrottic ectodermal dysplasia protein gene (EDA), excn 2 and flanking repeat regions	T			Homo saplens somatostatin receptor subtype 3 (SSTR3) gene, 5 flanking region and partial cds	Human endogenous retrovirus, complete genome	4   an05h04.x1 Strategene schizo brain S11 Homo septens cDNA clone IMACE:1684759 3'	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sepiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds	yc59e08.r1 Scares breast 3NbHBst Homo septens cDNA clone IMAGE:182248 6' similar to gb:M64099  GAMMA-GLUTAMYLTRANSPEPTIDASE 6 PRECURSOR (HUMAN);	yc59908.r1 Soeres breast 3NbHBst Homo septens cDNA done IMAGE:182246 5' similar to gb:M54099  GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);	Human gamma-cytoplasmic actin (ACTGP9) pseudogene	Homo sapiens thyroid autoantigen 70kO (Ku antigen) (G22P1), mRNA	Homo sapiens flyroid autoantigen 70kO (Ku antigen) (G22P1), mRNA	Homo saplens GTP binding protein 1 (GTPBP1) mRNA	hi86a06.x1 Soares_NPL_T_GBC_S1 Homo septems cDNA clone IMAGE:2979154 3"		$\neg$	Lious september in the control of september and in the control	Homo squers G progressionated receptor 24 (urrk24), mixina	Homo sapiens low censary moving and a (Lrv-Z.), movin	Hamo sepiens CST gene for cerebroside suffortensferese, exon 1, 2, 3, 4, 5
	Top Hit Datebase Source	EST_HUMAN	EST_HUMAN	Ę	ΕN	TN	NT	Ę		EST_HUMAN	NT	NT	ᅜ	EST HUMAN	NT	NT	NT	EST_HUMAN	EST_HUMAN	F	NT	¥	¥	EST_HUMAN	INVESTIGATION OF THE PARTY.	FA TOWN	Z	Z	Z	뒫
	Top Hit Acession No.	0.0E+00 AI903497.1	0.0E+00 N54484.1	0.0E+00 AF106658.1	4507500 NT	4507500 NT	10092587 NT	0 0F±00 AF003528 1		2.1	0.0E+00 L20483.1	0.0E+00 AF068757.1	9635487 NT	0.0E+00 AI204914.1	6912467 NT	6912457 NT	0.0E+00 AF038365.1	0.0E+00 H30132.1	0.0E+00 H30132.1	0.0E+00 D50659.1	11418189 NT	11418189 NT	4758489 NT	AW664999	100 OF 10	44826264 NT	18202011	4885312 NI	0806918 N	0.0E+00 AB029900.1
	Most Similar (Top) Hit BLAST E Vælue	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	005+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	00.300	0.05	0.05+00	0.0E+00	0.05+00	0.0E+00
	Expression Signal	1.96	1.82	6.99	3.44	3.44	2.56	2 62		3.54	1.41	282	2.72	1.47	1.88	1.88	1.52	4.49	4.40	52.39	3.63	3.63	2.42	1.39	7	1.01	9.1	3.07	1.88	2.17
-	ORF SEQ ID NO:				28857	28858				31621					28034	28035	31787	27705	27708		31743	31744	28141			17/16			31292	
	SEQ ID	25834	25962	25167	13900	13900	25837	13820		25767	26797	25831	25300	L	15027	15027	25361	14723	14723	25377	25378	25378		25415			$\perp$	l_		25466
	Page SEQ ID NO:	12314	12357	12371	12374	12374	12383	12411		12504	12534	12561	12597	12635	12683	12683	12701	12712	12712	12724	12726	12725	12739	12780		12010	1282/	12849	12858	12863

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Table 4
Single Exon Probes Expressed in Bone Marrow

	subunit (CPSF1), mRNA							RNA
Top Hit Descriptor	Homo sapiens deavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA	Homo sapians chromosome 21 segment HS21C048	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sepiens DKFZp434P211 protein (DKFZP434P211), mRNA	Homo sepiens period (Drosophila) homolog 3 (PER3), mRNA	Human endogencus retrovirus pHE.1 (ERV9)	Homo sepiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
Top Hit Database Source	אַד	Į.	LN LN	F	ב	Ę	K	
Top Hit Acession No.	9558724 NT	0.0E+00 AL163246.2	TN 8169089	6912457 NT	TM 0207030	IN 7867387	0.0E+00 X57147.1	9966844 NT
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	2.53	3.32	2.65	1.32	3.02	1.36	1.83	1.4
ORF SEQ ID NO:	31733		28809	27473		31685		27156
Exan SEQ ID NO:	25486	26984	13692	14499	25568	25590	25613	14203
Probe SEQ ID NO:	12902	12927	12935	12986	13018	13051	13082	13103

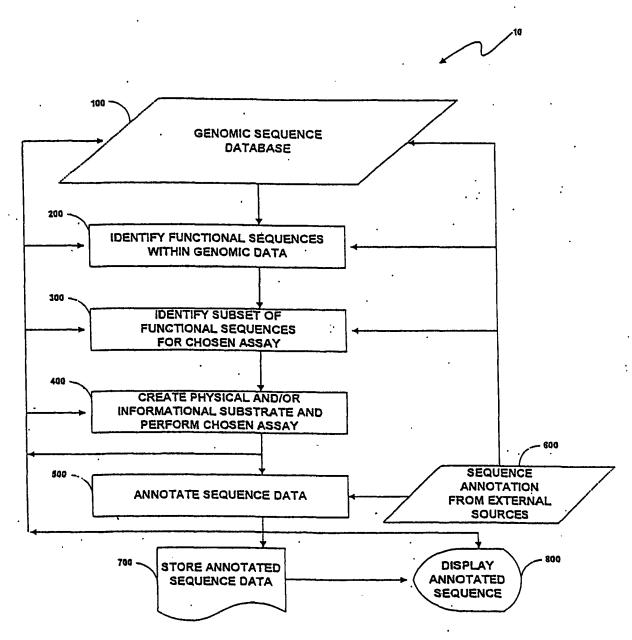


Fig. 1

PCT/US01/00668

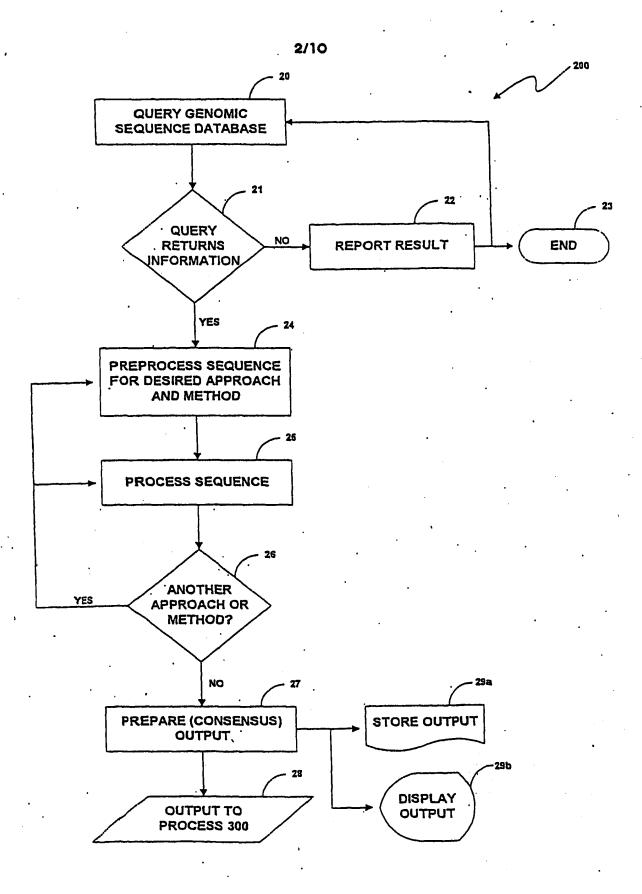


Fig. 2

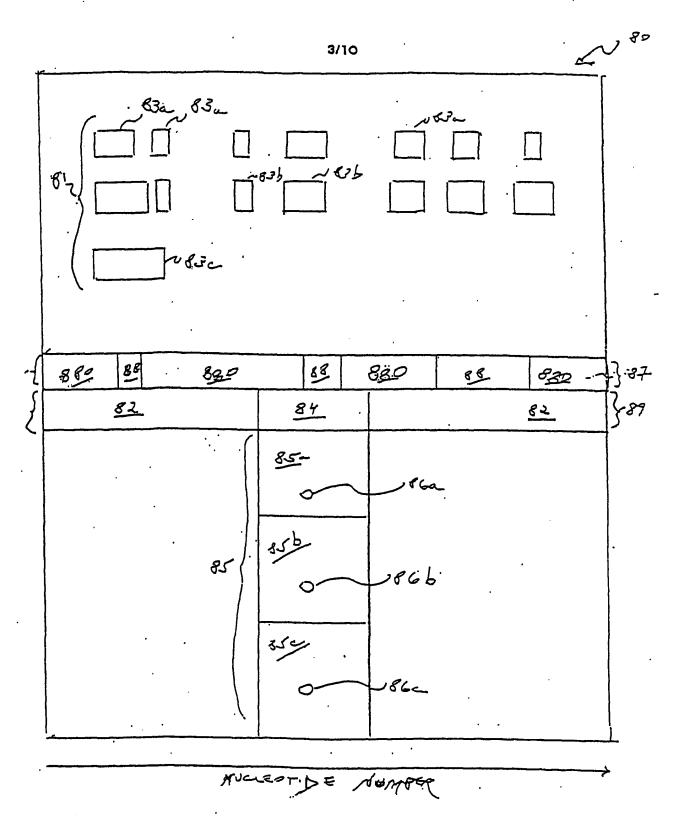


Fig. 3

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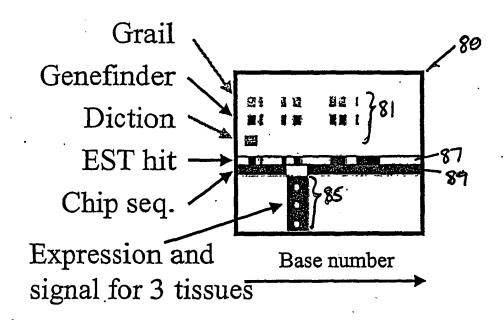


Fig. 4

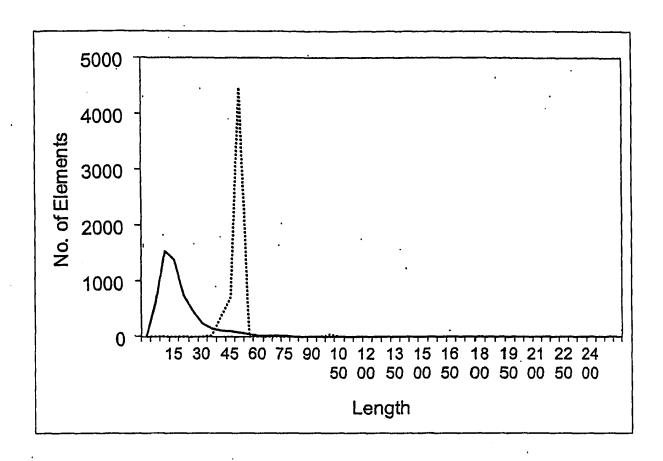


Fig. 5

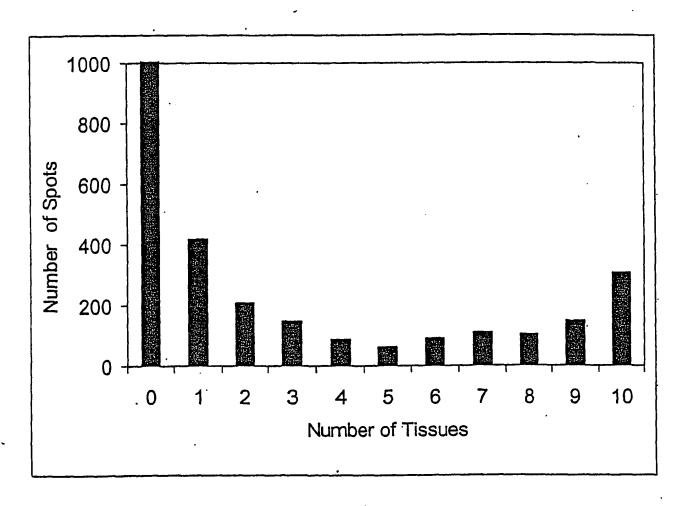
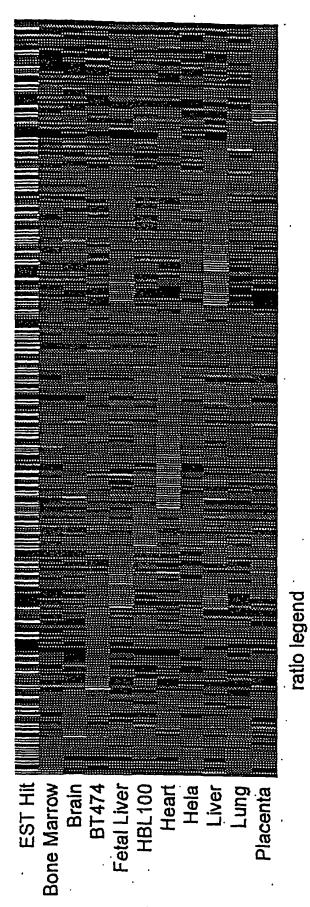


Fig. 6



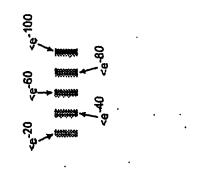


Fig. 7b

Fig. 7a

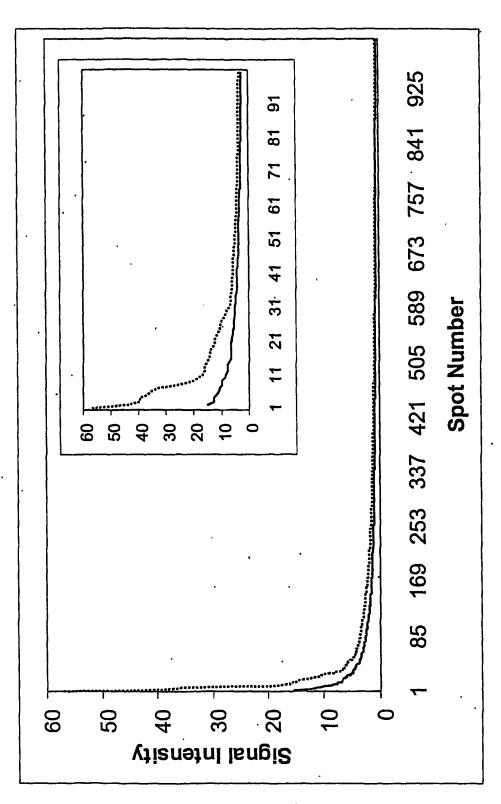


Fig. 8

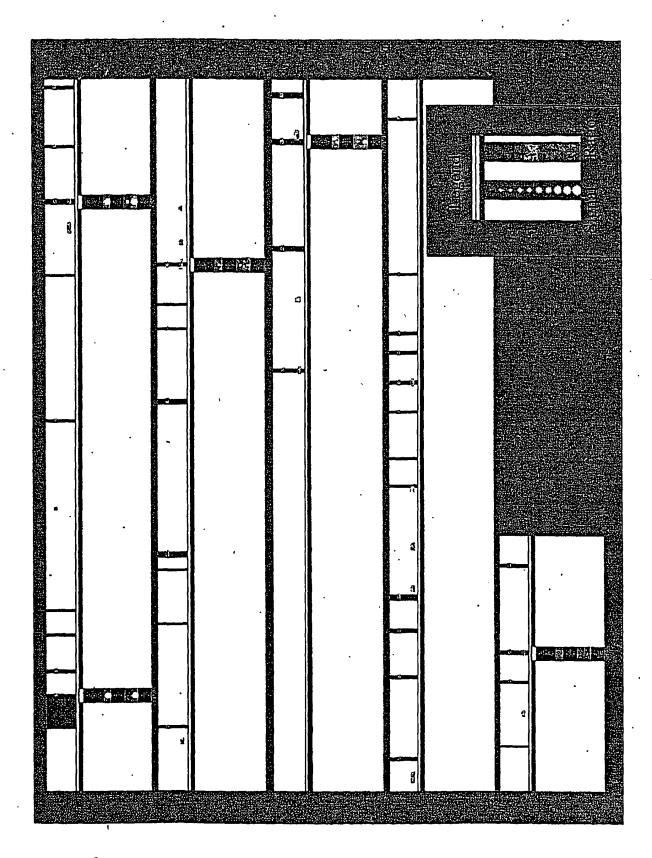
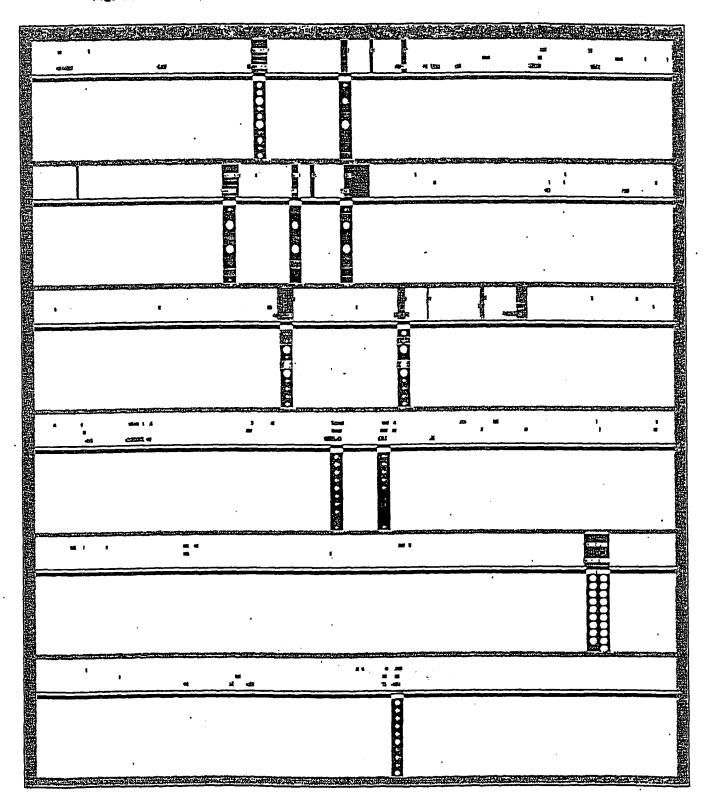


Fig. 9

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Fig. 10



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